



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 10:29 PM UTC

PDB ID : 4F5X / pdb_00004f5x
Title : Location of the dsRNA-dependent polymerase, VP1, in rotavirus particles
Authors : Estrozi, L.F.; Settembre, E.C.; Goret, G.; McClain, B.; Zhang, X.; Chen, J.Z.; Grigorieff, N.; Harrison, S.C.
Deposited on : 2012-05-13
Resolution : 5.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

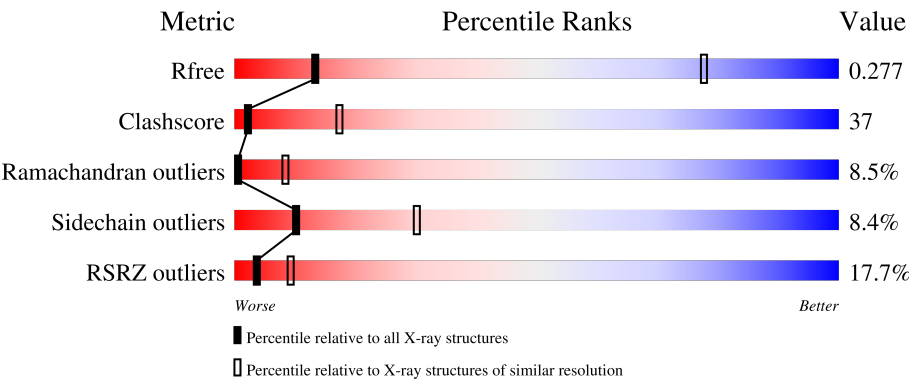
MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 5.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1009 (6.02-3.98)
Clashscore	190562	1040 (6.00-4.00)
Ramachandran outliers	187476	1015 (6.06-3.92)
Sidechain outliers	187428	1136 (6.10-3.90)
RSRZ outliers	180081	1004 (6.02-3.98)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	880	5% 14% 47% 24% 11%
1	B	880	3% 16% 47% 26% 8%
2	C	397	10% 59% 31% 9%
2	D	397	11% 55% 34% 11%
2	E	397	12% 56% 33% 9%

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Mol	Chain	Length	Quality of chain
2	F	397	
2	G	397	
2	H	397	
2	I	397	
2	J	397	
2	K	397	
2	L	397	
2	M	397	
2	N	397	
2	O	397	
3	W	1089	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 62014 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called VP2 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	781	Total	C	N	O	S	0	0	0
			6374	4049	1099	1190	36			
1	B	810	Total	C	N	O	S	0	0	0
			6624	4211	1138	1239	36			

- Molecule 2 is a protein called Intermediate capsid protein VP6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	D	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	E	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	F	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	G	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	H	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	I	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	J	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	K	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	L	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	M	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			
2	N	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O	397	Total	C	N	O	S	0	0	0
			3162	2001	550	596	15			

- Molecule 3 is a protein called RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	W	975	Total	C	N	O	S	0	0	0
			7905	5081	1308	1482	34			

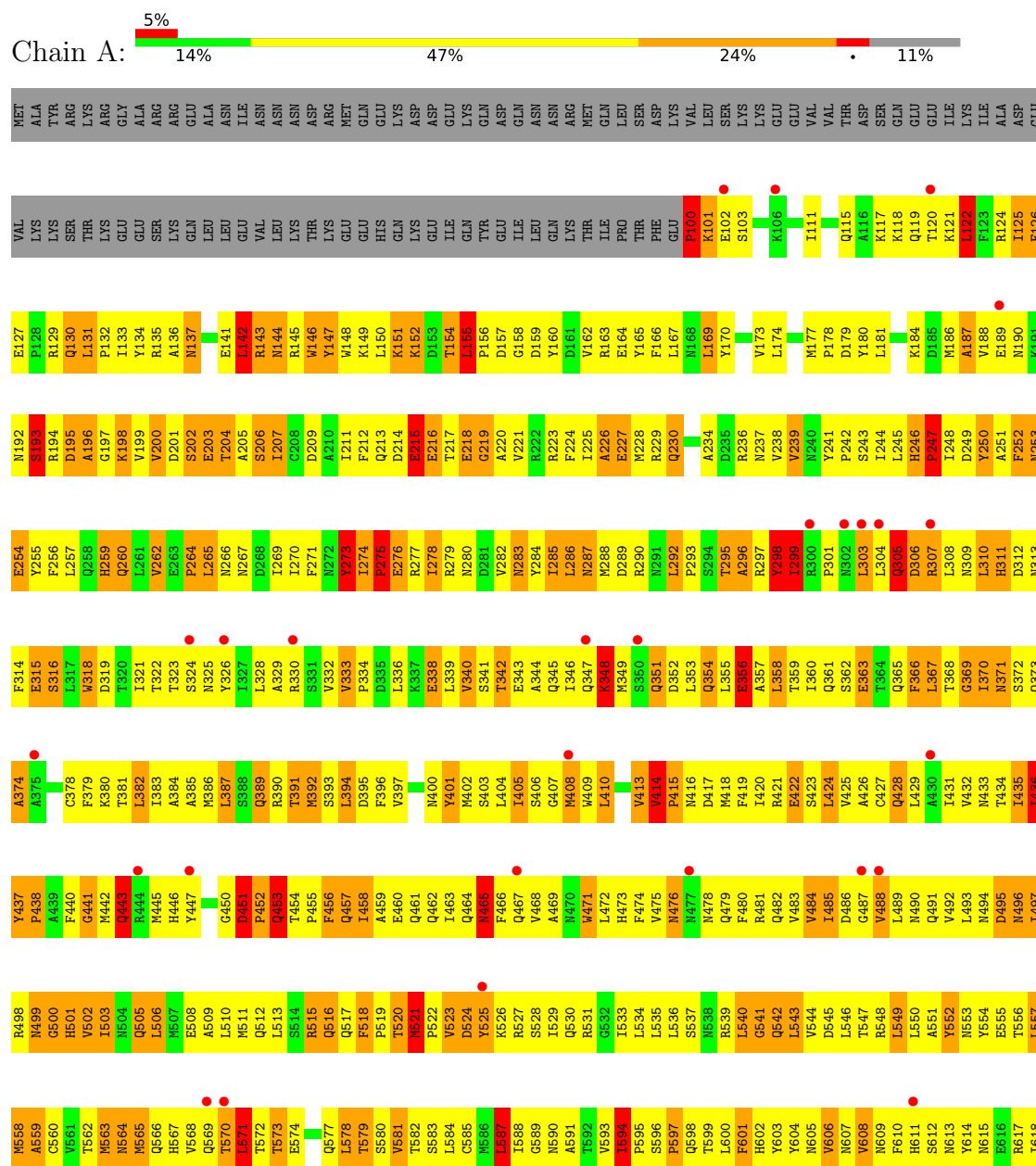
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

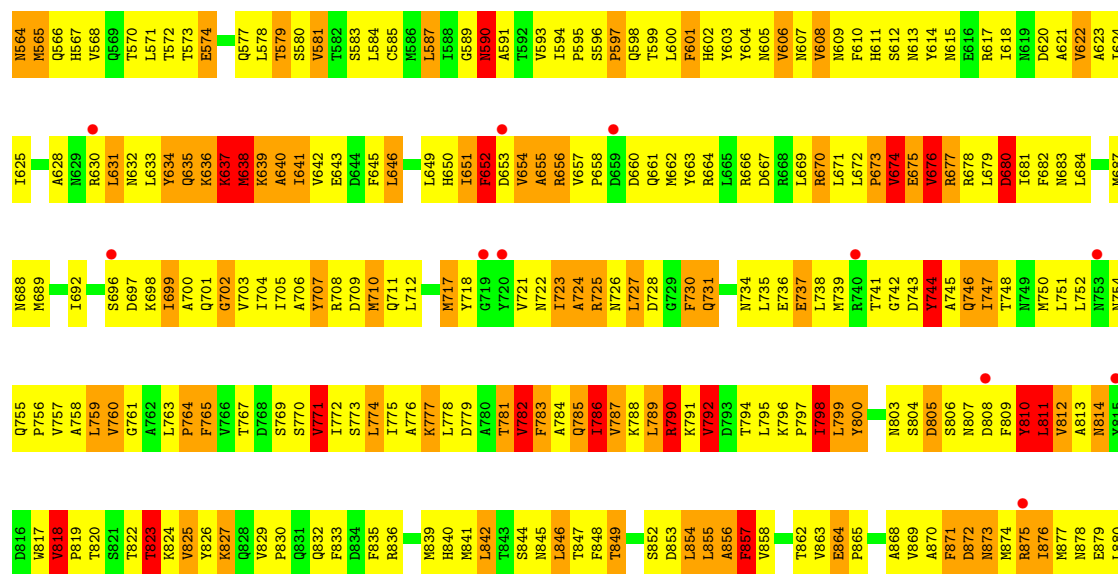
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Zn	0	0
			1	1		
4	F	1	Total	Zn	0	0
			1	1		
4	I	1	Total	Zn	0	0
			1	1		
4	L	1	Total	Zn	0	0
			1	1		
4	O	1	Total	Zn	0	0
			1	1		

3 Residue-property plots

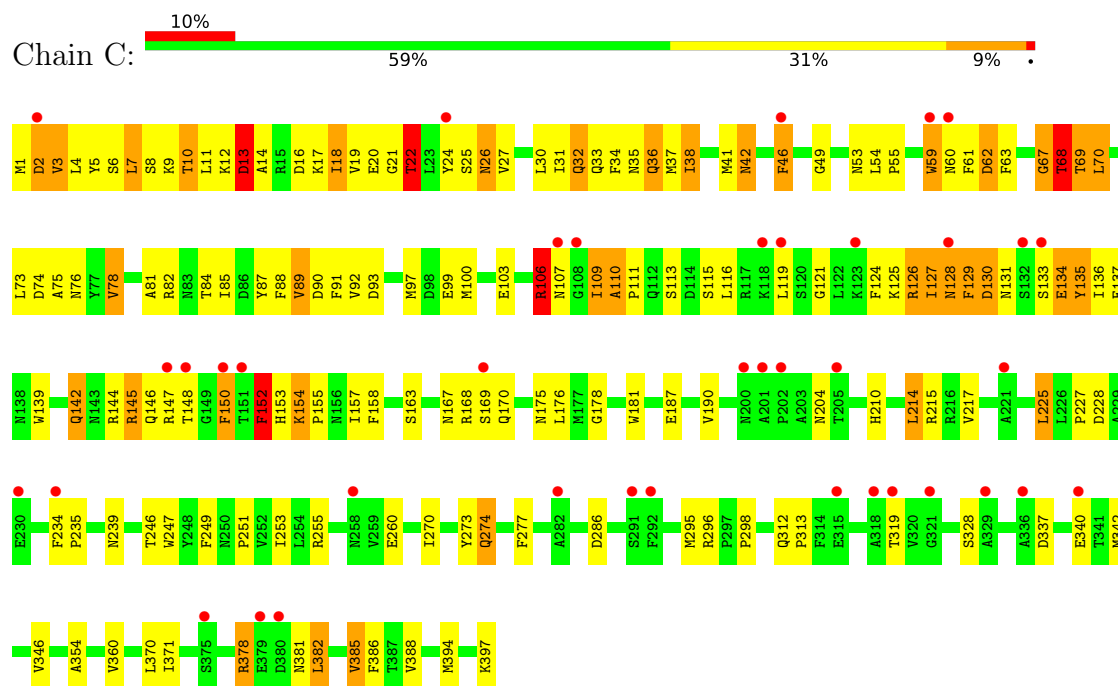
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: VP2 protein

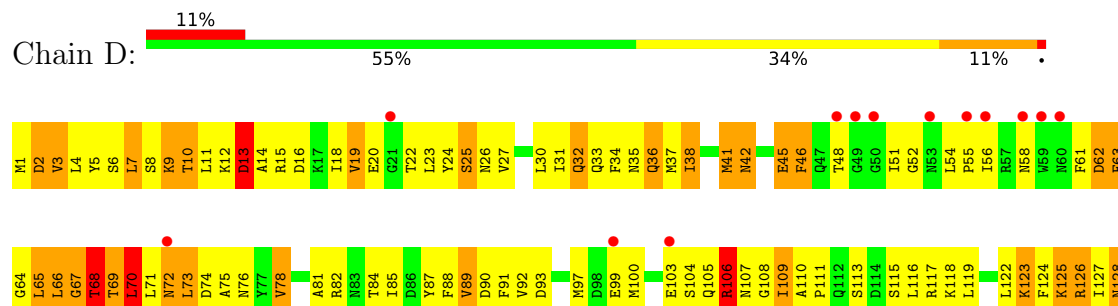


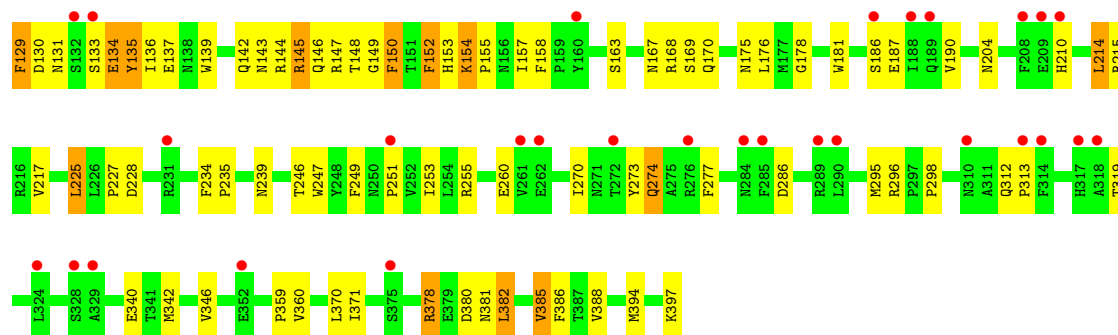


• Molecule 2: Intermediate capsid protein VP6

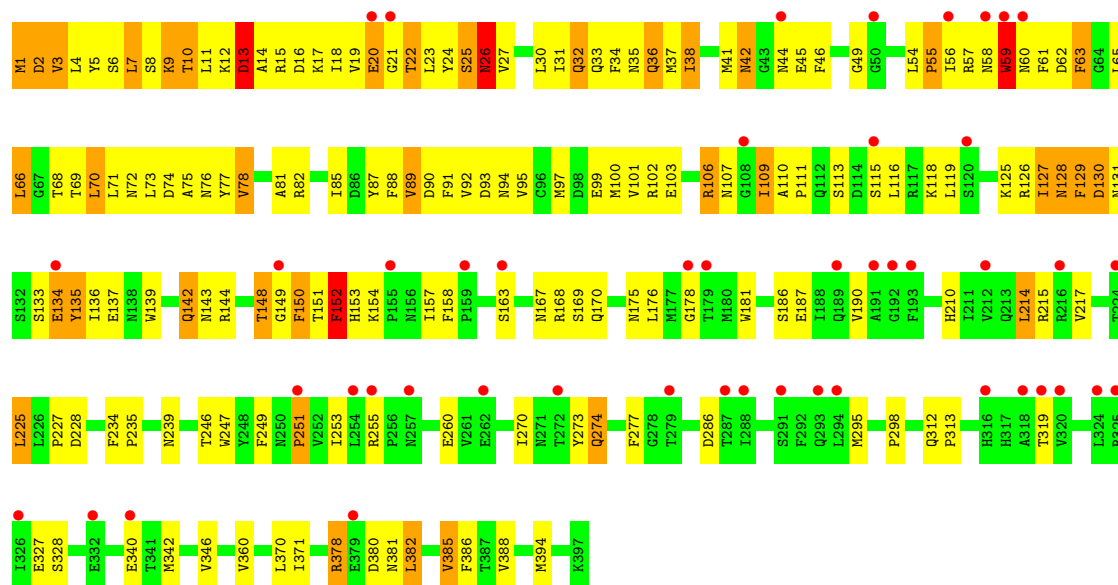


• Molecule 2: Intermediate capsid protein VP6

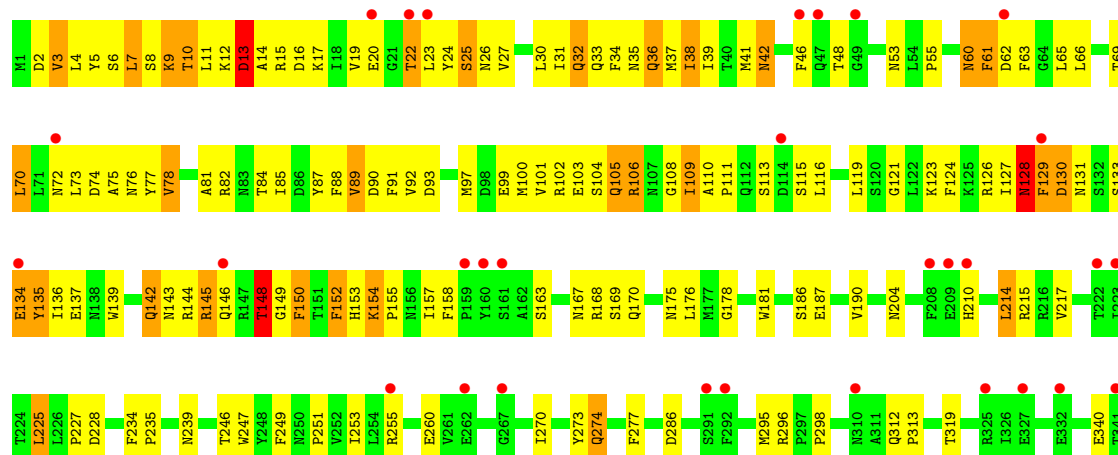




• Molecule 2: Intermediate capsid protein VP6

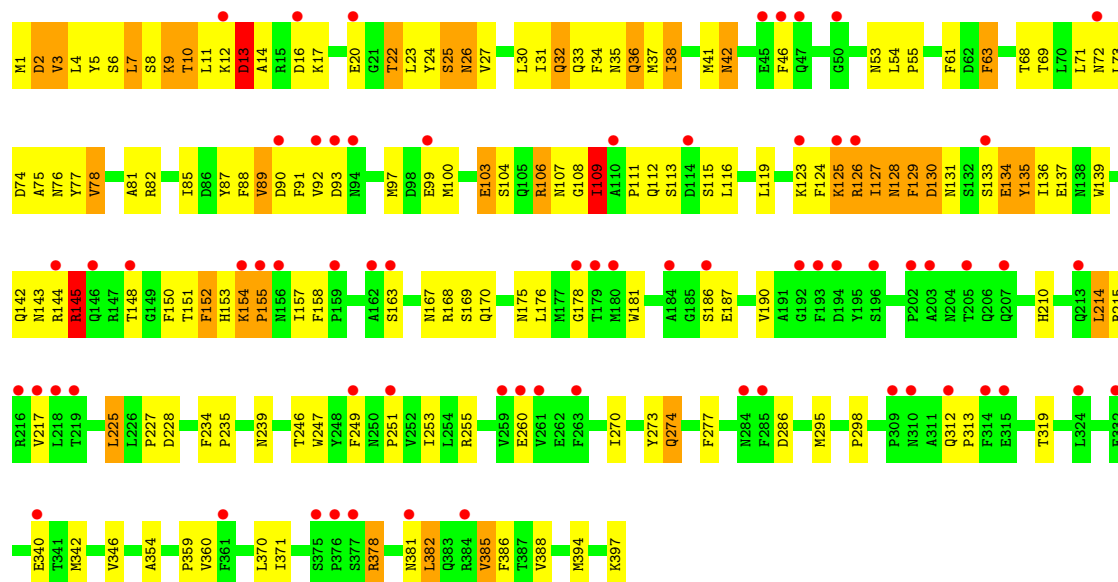


• Molecule 2: Intermediate capsid protein VP6

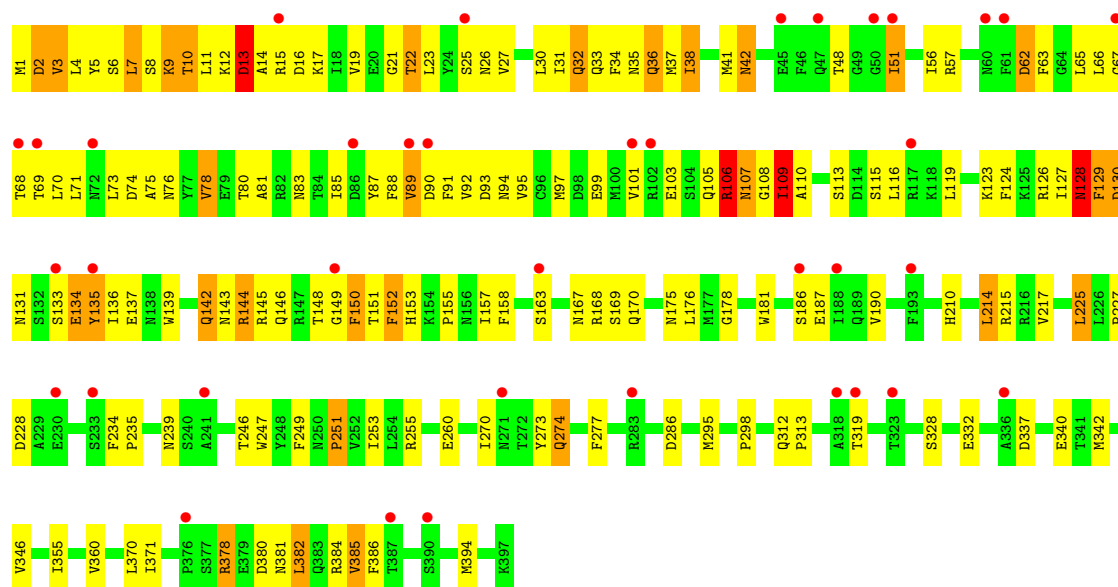




• Molecule 2: Intermediate capsid protein VP6

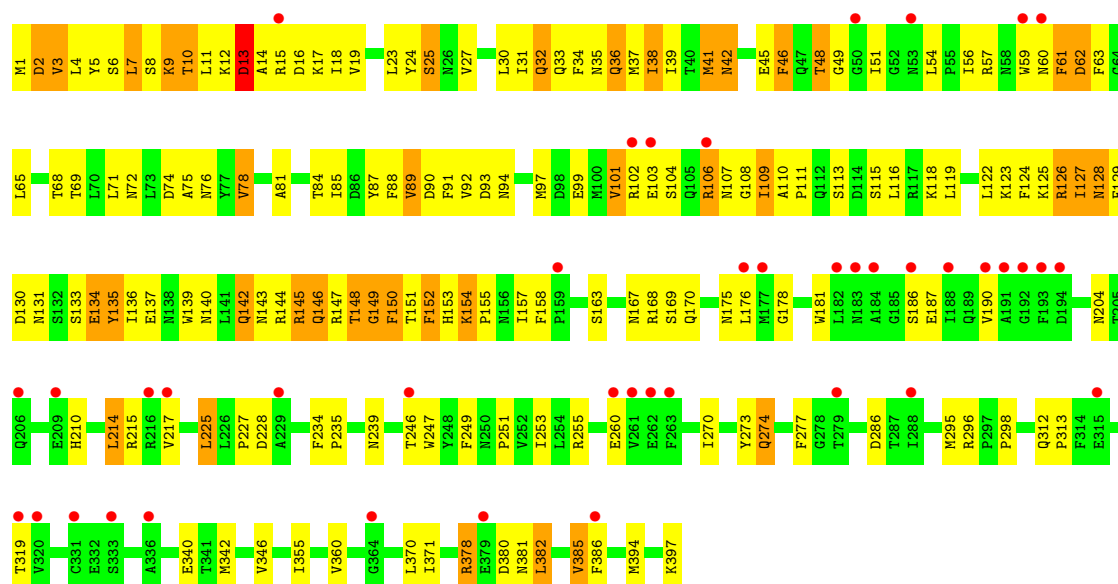


• Molecule 2: Intermediate capsid protein VP6

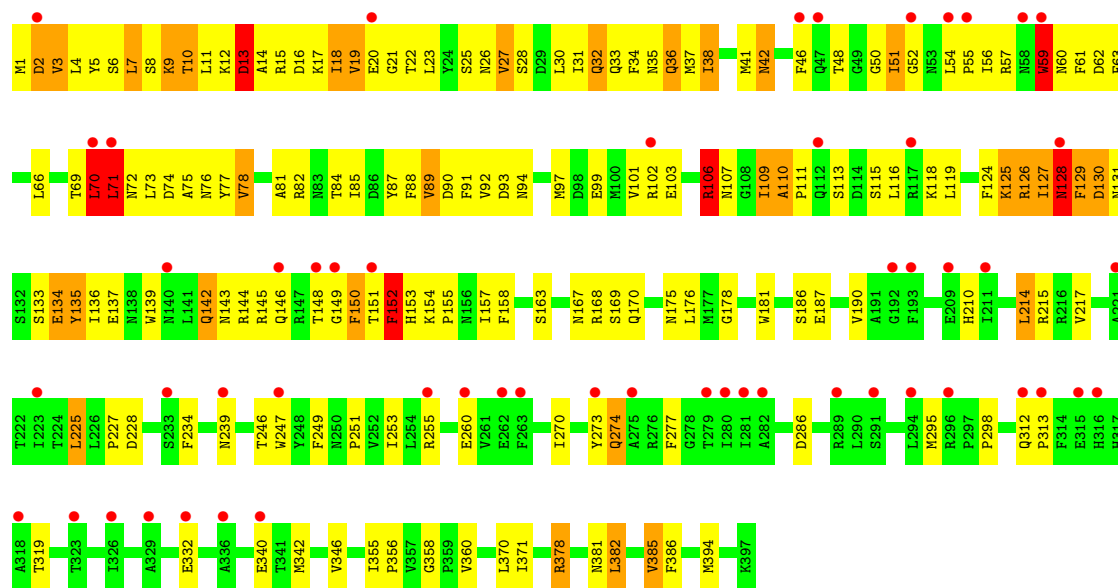


• Molecule 2: Intermediate capsid protein VP6

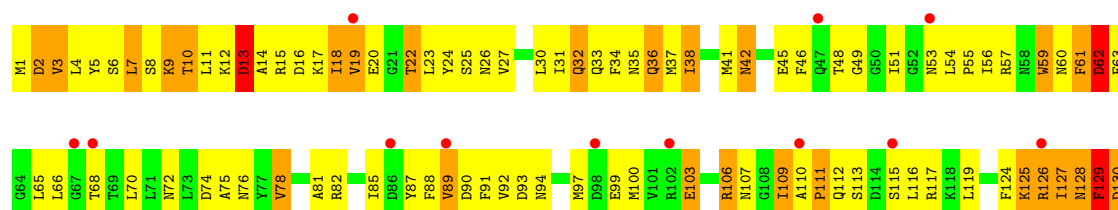


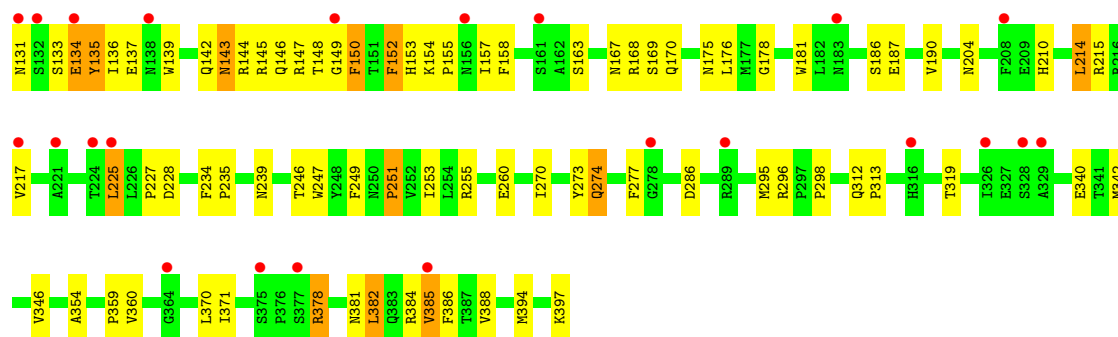


• Molecule 2: Intermediate capsid protein VP6

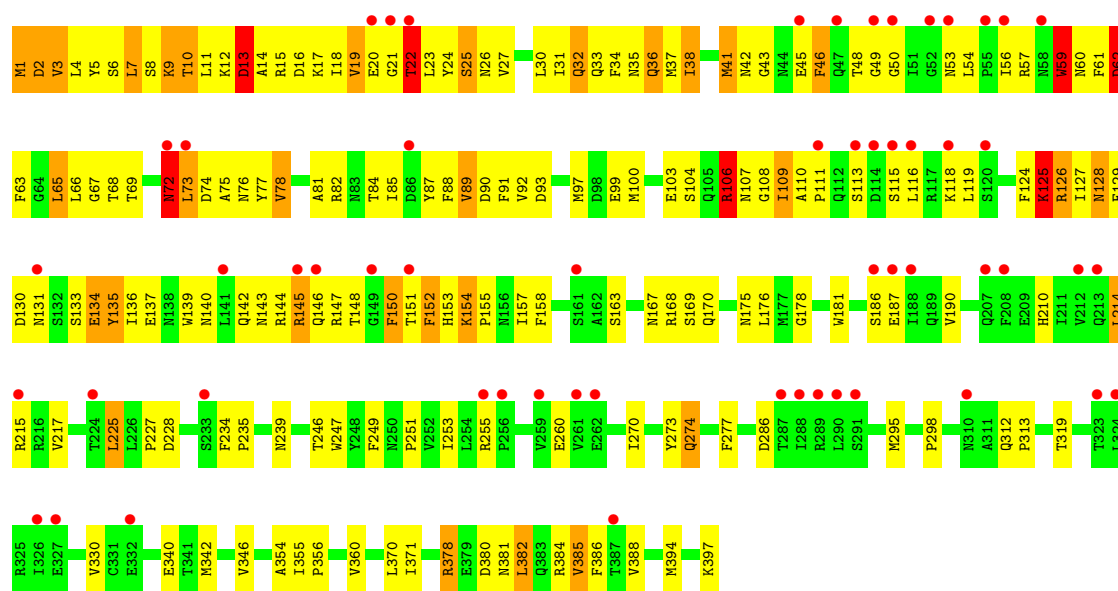


• Molecule 2: Intermediate capsid protein VP6

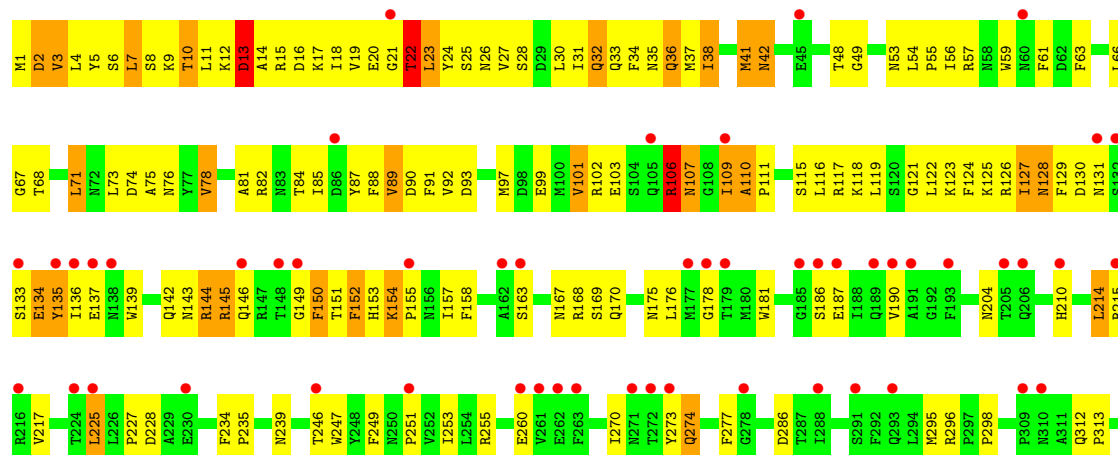




• Molecule 2: Intermediate capsid protein VP6

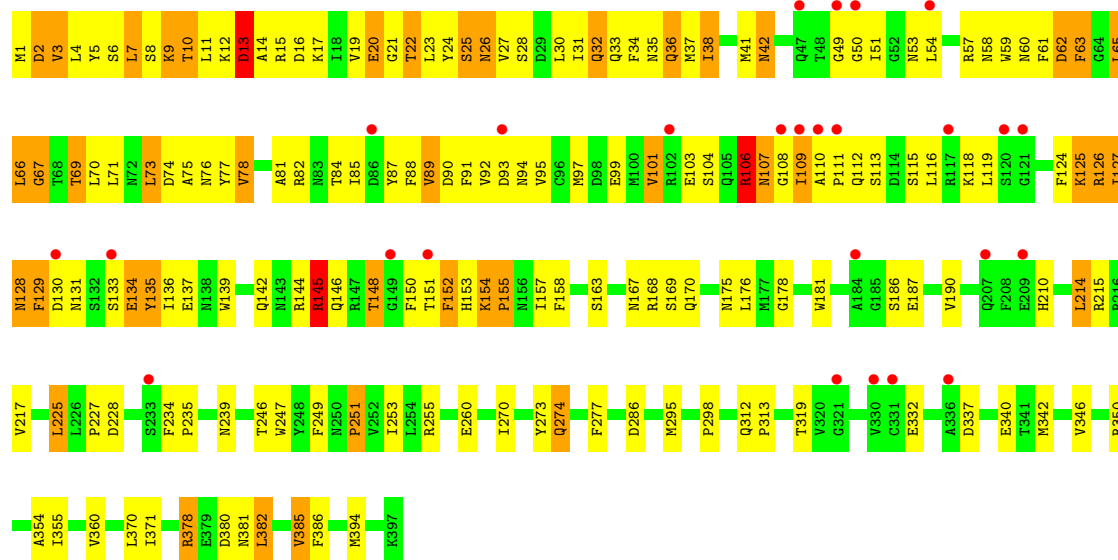


• Molecule 2: Intermediate capsid protein VP6

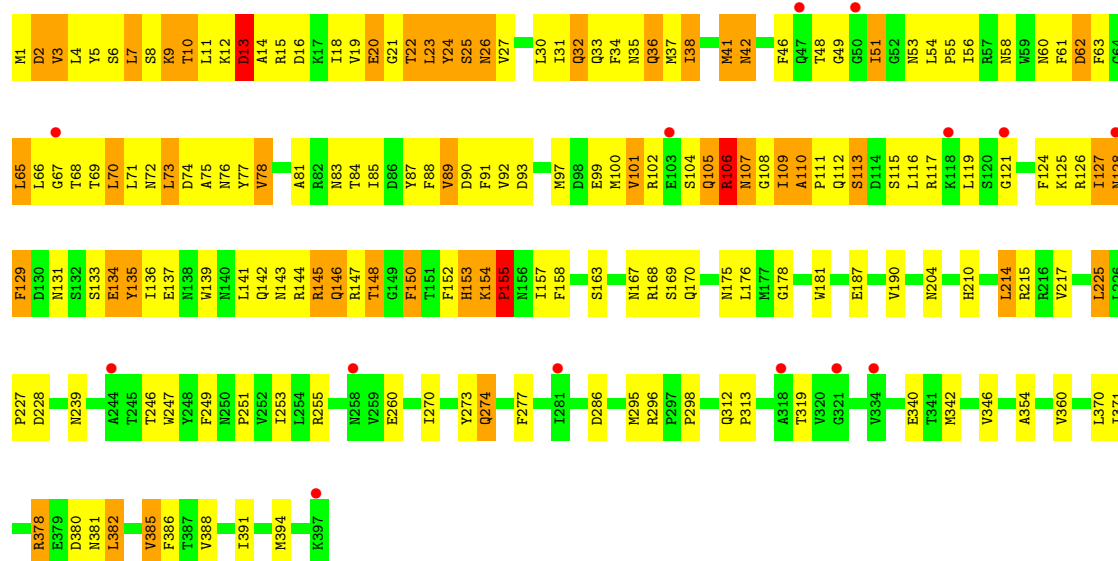




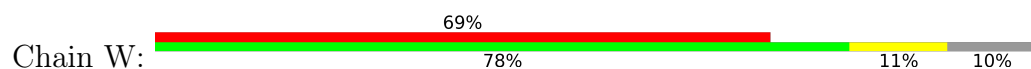
• Molecule 2: Intermediate capsid protein VP6



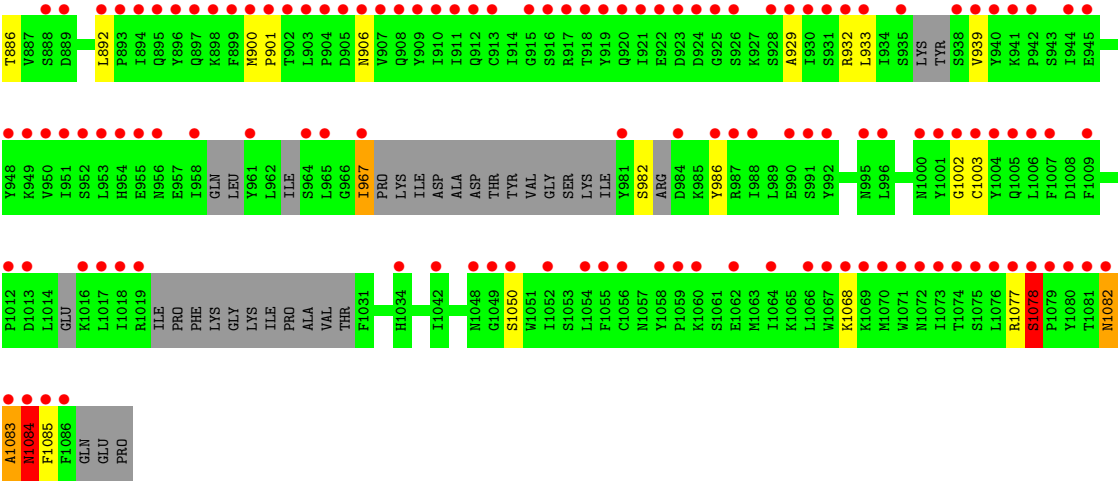
• Molecule 2: Intermediate capsid protein VP6



• Molecule 3: RNA-directed RNA polymerase



K823	N824	N825	I826	V827	S828	R829	G830	T834	E835	A836	K837	L838	N839	N840	S841	Y842	A843	P844	I845	S846	L847	E848	K849	R850	R851	A852	Q853	I854	S855	A856	L857	L858	T859	Q862	K863	P864	T865	T866	F867	K868	S869	S870	K871	I872	T873	I874	N875	D876	I877	L878	R879	D880	I881	K882	P883	F884	N885	S761	T762	K763	G764	I765	F766	S767	D768	T769	T770	F771	I772	I773	E774	Y775	G776	T777	T778	V779	D780	E781	W782	Q785	E786	A787	R788	M789	S790	I791	S792	S793	Q794	K795	S796	G797	I798	E801	I802	A803	A804	S805	S806	F807	K808	N809	N810	I811	Y812	V813	F814	P815	G816	S817	D818	Q819	Q820	L821	F822	N760	K700	R701	G702	I703	S704	D705	V706	N707	T708	L709	T710	T711	T712	A713	L714	G715	G716	S717	V718	W719	N720	R721	L722	R723	G724	F725	E726	T727	D728	R729	E730	F731	L732	L733	T734	K735	L736	W737	Q738	W739	V742	A743	G746	S747	T748	R749	L750	F751	P752	S753	E754	R755	V756	L757	T758	T759	N760	A635	V636	L637	G638	P639	A640	ASN	THR	GLU	VAL	LYS	MET	I648	Q649	D650	V651	S652	V653	D654	V655	E656	E657	T658	V659	A660	R661	E662	N663	A664	K665	V666	A667	A668	L669	V670	S671	THR	V673	E676	T681	I682	A683	G684	G685	K686	T687	F688	F689	R690	A691	C692	R693	V694	L695	L696	N697	N698	Y572	V573	I574	S575	P576	D577	G578	N579	V580	F581	K582	K583	L584	Q585	Y586	E587	V588	F589	A590	S591	G592	E593	K594	Q595	T596	K597	A598	A599	N600	S601	H602	A603	N604	L605	A606	L607	I608	K609	T610	V611	L612	SER	ARG	ILE	SER	ASN	LYS	H619	SER	PHE	A622	T623	K624	I625	V628	D629	G630	Q635	D570	S571	L500	L501	S502	Y503	G504	D505	V506	THR	ARG	F509	P439	P440	V443	D444	F445	P446	I447	P448	L449	A450	R451	R452	V453	D454	P455	G456	R457	T458	S459	V521	S522	T459	R460	I461	I462	F463	S526	S527	Q528	A400	H529	N530	F534	G541	L542	ASP	ILE	LEU	ALA	ASN	A475	V476	V477	E478	K479	T482	Y483	A484	K485	H486	Y490	A491	E492	F493	Y494	S495	Q496	S497	N498	Q499	K432	Y433	P439	P440	V443	D444	F445	P446	I447	P448	L449	A450	R451	R452	V453	D454	P455	G456	R457	T458	S459	V521	S522	T459	R460	I461	I462	F463	S396	K397	S398	S399	S400	S401	Q402	Q403	E404	S405	R406	D407	L408	K409	F410	G411	R412	R413	T414	T415	F416	S417	T418	K419	K420	N421	H422	H423	V424	N425	D426	Q427	E428	F429	N430	E431	I307	Q308	D309	W310	L311	V312	D313	R314	S315	T316	E317	D318	K318	F319	P320	L321	M322	A323	K324	L325	Y326	S327	W328	S329	F330	H331	V332	G333	F334	R335	K336	Q337	K338	M339	L340	D341	A342	A343	L344	D345	Q346	LEU	LYS	THR	GLU	TYR	Q280	M291	L292	D293	M294	M295	N296	K297	A298	V301	D302	I303	P304	K305	M306	S246	P247	M248	S249	L250	L251	V252	A253	L254	V255	D256	I257	ASN	GLY	THR	PHE	ILE	THR	ASN	GLU	LEU	LEU	GLU	PHE	SER	ASN	GLU	F334	R335	K336	Q337	K338	M339	L340	D341	A342	A343	L344	D345	Q346	LEU	LYS	THR	GLU	TYR	Q280	M291	L292	D293	M294	M295	N296	K297	A298	V301	D302	I303	P304	K305	M306	H185	N186	K187	K188	R189	R190	Y191	E192	Y193	D194	V195	K196	K197	D198	K199	P200	S201	Y202	L203	V204	T205	W206	A207	S208	S209	S210	I211	E212	M213	E155	V156	A157	E158	E124	Y125	T126	D127	S128	L129	M130	D131	P132	S133	T134	L135	L136	S137	L138	S139	D140	N141	L142	N143	A144	W145	M146	F147	R148	L149	E150	K161	V162	Y163	K164	R165	R166	L167	D168	L169	F170	T171	L172	Y173	M174	S175	T176	I177	N178	K179	L180	G181	P182	V183	A184	D64	V65	I66	E67	N68	A69	T70	L71	L72	S73	T74	L75	S76	T77	S78	Y79	D80	K81	N82	N83	A84	W85	E86	R87	K88	L89	V90	K91	Y92	S93	N91	A93	K94	G95	K96	P97	L98	E99	A100	D101	L102	T103	V104	N105	R106	E107	D108	Y109	N110	N111	N112	K113	M114	T115	E117	S118	L119	F120	T121	E123	G2	K3	Y4	N5	L6	S9	E10	Y11	L12	S13	F14	L15	N17	S18	GLN	SER	ALA	V22	Q23	I24	P25	R26	L26	Y27	Y28	S29	S30	N31	S32	E33	L34	E35	N36	R37	C38	I39	E40	F41	H42	S43	K44	C45	L46	E47	N48	S49	K50	N51	G52	L53	S54	L55	F59	V60	E61	Y62	N63
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	740.75Å 1198.07Å 1345.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 5.00 30.00 – 5.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-5.00) 24.7 (30.00-5.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.49 (at 3.78Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.293 , 0.296 0.274 , 0.277	Depositor DCC
R_{free} test set	47880 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	167.1	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 157.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.51	EDS
Total number of atoms	62014	wwPDB-VP
Average B, all atoms (Å ²)	146.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.56	0/6491	1.23	83/8806 (0.9%)
1	B	0.58	0/6745	1.21	75/9149 (0.8%)
2	C	0.62	1/3232 (0.0%)	1.05	17/4397 (0.4%)
2	D	0.63	1/3232 (0.0%)	1.03	12/4397 (0.3%)
2	E	0.62	1/3232 (0.0%)	1.04	16/4397 (0.4%)
2	F	0.62	1/3232 (0.0%)	1.02	11/4397 (0.3%)
2	G	0.61	1/3232 (0.0%)	1.03	13/4397 (0.3%)
2	H	0.62	1/3232 (0.0%)	1.00	10/4397 (0.2%)
2	I	0.63	1/3232 (0.0%)	1.03	13/4397 (0.3%)
2	J	0.62	1/3232 (0.0%)	1.04	17/4397 (0.4%)
2	K	0.63	2/3232 (0.1%)	1.03	16/4397 (0.4%)
2	L	0.62	1/3232 (0.0%)	1.03	15/4397 (0.3%)
2	M	0.63	1/3232 (0.0%)	1.05	13/4397 (0.3%)
2	N	0.62	1/3232 (0.0%)	1.03	13/4397 (0.3%)
2	O	0.64	2/3232 (0.1%)	1.08	19/4397 (0.4%)
3	W	0.51	0/8045	0.98	29/10847 (0.3%)
All	All	0.60	15/63297 (0.0%)	1.07	372/85963 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	247	TRP	NE1-CE2	-5.55	1.31	1.37
2	K	154	LYS	CA-CB	5.55	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	247	TRP	NE1-CE2	-5.51	1.31	1.37
2	C	247	TRP	NE1-CE2	-5.49	1.31	1.37
2	O	154	LYS	CA-CB	5.45	1.57	1.52
2	L	247	TRP	NE1-CE2	-5.44	1.31	1.37
2	N	247	TRP	NE1-CE2	-5.44	1.31	1.37
2	O	247	TRP	NE1-CE2	-5.44	1.31	1.37
2	H	247	TRP	NE1-CE2	-5.39	1.31	1.37
2	K	247	TRP	NE1-CE2	-5.36	1.31	1.37
2	E	247	TRP	NE1-CE2	-5.32	1.31	1.37
2	M	247	TRP	NE1-CE2	-5.21	1.31	1.37
2	J	247	TRP	NE1-CE2	-5.16	1.31	1.37
2	D	247	TRP	NE1-CE2	-5.14	1.31	1.37
2	G	247	TRP	NE1-CE2	-5.02	1.31	1.37

All (372) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	367	LEU	N-CA-C	-20.02	90.51	112.93
1	B	636	LYS	N-CA-C	-12.91	94.53	110.41
1	B	497	ILE	N-CA-C	-12.47	95.47	111.05
1	B	75	VAL	N-CA-C	-11.82	101.12	112.83
1	A	298	TYR	N-CA-C	11.39	131.01	114.16
1	A	657	VAL	CA-C-N	10.80	133.34	119.84
1	A	657	VAL	C-N-CA	10.80	133.34	119.84
2	N	127	ILE	N-CA-C	10.57	121.00	112.12
2	O	153	HIS	N-CA-C	10.40	125.09	107.93
1	A	273	TYR	CA-CB-CG	10.12	132.12	113.90
1	B	398	THR	N-CA-C	10.11	123.24	111.11
2	O	154	LYS	CA-C-N	9.81	132.11	119.84
2	O	154	LYS	C-N-CA	9.81	132.11	119.84
1	B	842	LEU	N-CA-C	9.72	124.36	108.52
1	A	200	VAL	N-CA-C	9.65	122.62	107.28
2	M	144	ARG	N-CA-C	-9.38	100.42	112.23
1	B	273	TYR	CA-CB-CG	9.24	130.53	113.90
1	A	817	TRP	N-CA-C	9.23	120.89	107.88
1	B	518	PHE	N-CA-C	9.14	118.66	108.14
1	B	825	VAL	N-CA-C	9.02	121.97	108.80
1	A	825	VAL	N-CA-C	9.01	121.88	108.46
1	B	811	LEU	N-CA-C	-8.94	96.21	109.62
1	B	518	PHE	CA-C-N	8.91	130.98	119.84
1	B	518	PHE	C-N-CA	8.91	130.98	119.84
1	A	437	TYR	CA-C-N	8.90	130.96	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	437	TYR	C-N-CA	8.90	130.96	119.84
3	W	1077	ARG	N-CA-C	8.89	126.05	111.37
1	B	422	GLU	N-CA-C	8.71	120.46	110.97
1	B	353	LEU	N-CA-C	8.67	122.85	111.75
1	B	77	LYS	N-CA-C	-8.62	99.28	113.50
1	A	155	LEU	CA-C-N	8.56	130.54	119.84
1	A	155	LEU	C-N-CA	8.56	130.54	119.84
1	A	279	ARG	N-CA-C	-8.53	101.99	111.28
3	W	1078	SER	CA-C-N	8.52	128.24	119.64
3	W	1078	SER	C-N-CA	8.52	128.24	119.64
2	O	154	LYS	N-CA-C	-8.47	94.86	112.40
2	C	154	LYS	CA-C-N	8.45	129.58	120.11
2	C	154	LYS	C-N-CA	8.45	129.58	120.11
2	M	127	ILE	N-CA-C	8.40	119.37	111.48
1	B	818	VAL	CA-C-N	8.38	129.70	119.98
1	B	818	VAL	C-N-CA	8.38	129.70	119.98
1	A	639	LYS	N-CA-C	-8.37	92.98	110.80
1	B	127	GLU	N-CA-C	-8.24	99.61	110.40
3	W	757	LEU	N-CA-C	8.11	120.20	111.36
3	W	1082	ASN	N-CA-C	8.11	128.08	110.80
2	E	71	LEU	N-CA-C	-8.01	102.14	111.03
2	O	146	GLN	N-CA-C	7.96	122.77	110.42
3	W	824	ASN	N-CA-C	7.89	122.34	112.87
1	B	726	ASN	N-CA-C	7.85	121.27	107.61
1	A	818	VAL	CA-C-N	7.84	129.65	119.84
1	A	818	VAL	C-N-CA	7.84	129.65	119.84
1	A	763	LEU	N-CA-C	7.60	120.55	108.23
2	K	127	ILE	N-CA-C	7.60	118.50	112.12
3	W	575	ILE	N-CA-C	7.50	115.33	107.76
1	A	719	GLY	N-CA-C	-7.45	100.46	112.31
3	W	254	LEU	N-CA-C	7.45	119.40	111.28
2	K	68	THR	N-CA-C	-7.43	103.78	112.92
2	E	26	ASN	N-CA-C	-7.42	104.07	113.72
2	O	26	ASN	N-CA-C	-7.41	102.49	113.61
1	B	486	ASP	N-CA-C	7.36	121.35	110.46
1	A	842	LEU	N-CA-C	7.35	121.11	109.50
2	N	87	TYR	N-CA-C	-7.29	104.52	113.41
2	J	27	VAL	N-CA-C	7.25	120.16	113.20
2	M	87	TYR	N-CA-C	-7.24	104.58	113.41
1	B	523	VAL	N-CA-C	7.23	118.02	110.72
1	B	367	LEU	N-CA-C	-7.21	103.43	113.37
2	J	87	TYR	N-CA-C	-7.20	104.63	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	87	TYR	N-CA-C	-7.19	104.64	113.41
2	D	87	TYR	N-CA-C	-7.13	104.72	113.41
1	B	587	LEU	N-CA-C	7.12	121.68	112.92
2	I	149	GLY	N-CA-C	7.11	121.03	111.72
2	O	87	TYR	N-CA-C	-7.08	104.78	113.41
2	D	66	LEU	N-CA-C	7.06	119.91	108.41
2	L	43	GLY	N-CA-C	-7.03	106.06	113.58
1	B	864	GLU	CA-C-N	7.03	128.62	119.84
1	B	864	GLU	C-N-CA	7.03	128.62	119.84
1	B	183	LEU	N-CA-C	7.02	122.40	113.55
1	A	594	ILE	CA-C-N	7.02	128.61	119.84
1	A	594	ILE	C-N-CA	7.02	128.61	119.84
2	L	87	TYR	N-CA-C	-7.01	104.86	113.41
2	I	87	TYR	N-CA-C	-7.01	104.86	113.41
2	E	87	TYR	N-CA-C	-6.99	104.88	113.41
2	K	270	ILE	N-CA-C	-6.94	105.84	111.81
2	D	46	PHE	N-CA-C	6.93	120.45	109.50
2	C	87	TYR	N-CA-C	-6.93	104.96	113.41
2	D	270	ILE	N-CA-C	-6.91	105.86	111.81
1	A	746	GLN	N-CA-C	-6.91	103.68	111.14
1	B	846	LEU	N-CA-C	6.90	120.00	108.13
2	N	270	ILE	N-CA-C	-6.89	105.89	111.81
2	I	270	ILE	N-CA-C	-6.87	105.90	111.81
2	F	87	TYR	N-CA-C	-6.87	105.03	113.41
2	H	87	TYR	N-CA-C	-6.86	105.04	113.41
2	M	270	ILE	N-CA-C	-6.85	105.92	111.81
2	J	270	ILE	N-CA-C	-6.85	105.92	111.81
2	K	87	TYR	N-CA-C	-6.84	105.06	113.41
2	G	270	ILE	N-CA-C	-6.83	105.93	111.81
2	F	270	ILE	N-CA-C	-6.83	105.94	111.81
1	A	435	ILE	N-CA-C	6.82	117.85	112.12
1	A	562	THR	N-CA-C	-6.82	104.85	113.72
2	E	270	ILE	N-CA-C	-6.81	105.95	111.81
2	O	270	ILE	N-CA-C	-6.81	105.95	111.81
1	B	798	ILE	N-CA-C	6.80	118.39	108.53
2	H	135	TYR	N-CA-C	6.76	118.73	111.36
2	H	270	ILE	N-CA-C	-6.75	106.00	111.81
2	E	113	SER	N-CA-C	6.74	119.00	110.24
2	E	135	TYR	N-CA-C	6.71	118.68	111.36
2	C	270	ILE	N-CA-C	-6.71	106.04	111.81
2	J	113	SER	N-CA-C	6.64	118.88	110.24
2	L	68	THR	N-CA-C	-6.64	103.57	112.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	W	1085	PHE	N-CA-C	6.63	124.92	110.80
2	I	154	LYS	CA-C-N	6.63	128.12	119.84
2	I	154	LYS	C-N-CA	6.63	128.12	119.84
2	J	135	TYR	N-CA-C	6.62	118.58	111.36
2	L	270	ILE	N-CA-C	-6.61	106.12	111.81
1	A	792	VAL	N-CA-C	6.59	117.79	108.17
1	B	200	VAL	N-CA-C	6.57	123.01	109.34
2	D	135	TYR	N-CA-C	6.56	118.51	111.36
1	B	79	LYS	N-CA-C	-6.56	105.03	113.16
1	A	296	ALA	N-CA-C	6.55	119.17	110.53
2	M	135	TYR	N-CA-C	6.55	118.50	111.36
2	C	113	SER	N-CA-C	6.54	119.25	110.35
1	B	151	LYS	N-CA-C	-6.52	99.89	110.20
2	I	135	TYR	N-CA-C	6.52	118.47	111.36
1	B	199	VAL	N-CA-C	6.51	118.30	108.80
2	M	110	ALA	CA-C-N	6.50	126.41	119.85
2	M	110	ALA	C-N-CA	6.50	126.41	119.85
2	E	127	ILE	N-CA-C	6.48	119.86	113.71
2	N	26	ASN	N-CA-C	-6.47	105.39	113.28
1	A	710	MET	N-CA-C	6.46	118.37	108.42
1	B	82	HIS	N-CA-C	-6.46	97.05	110.80
2	D	63	PHE	N-CA-C	6.46	120.02	109.24
2	L	135	TYR	N-CA-C	6.46	118.40	111.36
1	B	348	LYS	N-CA-C	-6.45	104.67	112.54
1	A	274	ILE	CA-C-N	6.45	127.90	119.84
1	A	274	ILE	C-N-CA	6.45	127.90	119.84
2	G	68	THR	N-CA-C	-6.42	105.30	113.01
2	C	135	TYR	N-CA-C	6.42	118.35	111.36
1	A	798	ILE	N-CA-C	6.41	118.26	108.71
1	B	272	ASN	N-CA-C	6.38	119.22	111.82
1	A	435	ILE	CB-CA-C	-6.36	104.67	110.91
1	B	213	GLN	N-CA-C	6.35	121.19	113.38
2	K	135	TYR	N-CA-C	6.34	118.27	111.36
2	O	113	SER	N-CA-C	6.34	118.48	110.24
1	B	503	ILE	N-CA-C	6.33	122.52	109.34
1	A	456	PHE	N-CA-C	-6.32	101.89	111.56
3	W	231	VAL	N-CA-C	6.31	116.47	110.53
2	C	18	ILE	N-CA-C	6.30	115.94	106.42
2	F	135	TYR	N-CA-C	6.28	118.21	111.36
2	D	154	LYS	CA-C-N	6.28	127.69	119.84
2	D	154	LYS	C-N-CA	6.28	127.69	119.84
2	G	135	TYR	N-CA-C	6.28	118.20	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	394	LEU	N-CA-C	6.27	119.79	108.69
2	C	18	ILE	CB-CA-C	-6.27	104.89	111.23
1	B	274	ILE	N-CA-C	6.26	114.72	107.89
2	J	46	PHE	N-CA-C	6.26	119.22	109.52
1	B	744	TYR	N-CA-C	-6.25	104.23	113.61
1	A	796	LYS	CA-C-N	6.22	126.57	119.92
1	A	796	LYS	C-N-CA	6.22	126.57	119.92
1	A	453	GLN	N-CA-C	-6.20	97.59	110.80
2	N	135	TYR	N-CA-C	6.20	118.12	111.36
3	W	1084	ASN	N-CA-C	6.19	123.99	110.80
2	L	46	PHE	N-CA-C	6.19	119.11	109.52
1	A	285	ILE	N-CA-C	6.17	117.01	108.12
1	A	469	ALA	N-CA-C	6.15	118.78	111.71
1	A	451	ASP	CA-C-N	6.14	127.52	119.84
1	A	451	ASP	C-N-CA	6.14	127.52	119.84
1	B	462	GLN	N-CA-C	6.13	117.94	109.54
2	O	135	TYR	N-CA-C	6.13	118.04	111.36
1	B	150	LEU	N-CA-C	6.12	118.61	109.25
1	B	637	LYS	N-CA-C	-6.12	97.76	110.80
2	I	46	PHE	N-CA-C	6.12	118.71	109.23
2	L	73	LEU	N-CA-C	6.10	119.46	110.30
2	O	110	ALA	CA-C-N	6.05	126.02	119.78
2	O	110	ALA	C-N-CA	6.05	126.02	119.78
1	A	483	VAL	N-CA-C	6.04	116.57	108.11
2	G	109	ILE	N-CA-C	6.03	116.21	110.42
2	K	154	LYS	CA-C-N	6.03	127.38	119.84
2	K	154	LYS	C-N-CA	6.03	127.38	119.84
1	B	469	ALA	N-CA-C	6.03	118.64	111.71
1	A	813	ALA	N-CA-C	-6.03	104.78	111.71
3	W	255	VAL	N-CA-C	6.03	118.03	108.87
1	A	793	ASP	N-CA-C	-6.01	97.99	110.80
2	J	59	TRP	N-CA-C	6.01	119.28	109.24
1	A	151	LYS	N-CA-C	-6.01	99.35	108.67
1	A	363	GLU	N-CA-C	6.01	120.15	112.34
1	A	776	ALA	N-CA-C	-6.01	106.04	113.19
3	W	1083	ALA	N-CA-C	5.99	123.56	110.80
2	N	10	THR	N-CA-C	-5.94	104.43	111.03
2	G	127	ILE	N-CA-C	5.93	121.69	109.34
3	W	182	VAL	CA-C-N	5.93	125.95	119.90
3	W	182	VAL	C-N-CA	5.93	125.95	119.90
2	J	110	ALA	CA-C-N	5.93	126.26	119.92
2	J	110	ALA	C-N-CA	5.93	126.26	119.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	760	VAL	N-CA-C	5.90	118.11	108.97
1	B	445	MET	N-CA-C	-5.88	106.34	112.93
1	B	232	VAL	N-CA-C	5.88	116.07	106.72
2	N	113	SER	N-CA-C	5.87	117.87	110.24
1	A	397	VAL	N-CA-C	-5.87	101.37	108.53
2	C	46	PHE	N-CA-C	5.85	118.59	109.52
1	A	100	PRO	CA-C-N	5.85	132.71	121.54
1	A	100	PRO	C-N-CA	5.85	132.71	121.54
2	D	113	SER	N-CA-C	5.84	118.29	110.35
1	B	800	TYR	N-CA-C	5.83	118.89	107.57
1	B	409	TRP	N-CA-C	-5.83	104.62	110.97
2	C	127	ILE	N-CA-C	5.83	121.46	109.34
1	B	652	PHE	N-CA-C	5.80	118.99	109.72
1	A	436	ILE	N-CA-C	5.79	118.75	112.96
2	E	66	LEU	N-CA-C	5.79	118.64	108.75
2	I	113	SER	N-CA-C	5.78	117.75	110.24
2	E	10	THR	N-CA-C	-5.77	104.62	111.03
2	E	68	THR	N-CA-C	-5.75	103.73	112.99
3	W	739	MET	N-CA-C	5.75	118.49	111.82
2	M	68	THR	N-CA-C	-5.75	104.94	112.41
1	A	433	ASN	N-CA-C	5.75	119.47	112.23
1	B	651	ILE	N-CA-C	5.75	121.29	109.34
2	I	10	THR	N-CA-C	-5.75	104.65	111.03
2	O	10	THR	N-CA-C	-5.74	104.65	111.03
2	K	19	VAL	N-CA-C	5.73	116.62	108.42
1	B	871	PHE	N-CA-C	-5.72	104.90	112.34
1	A	587	LEU	N-CA-C	5.72	119.39	111.55
1	B	565	MET	N-CA-C	5.71	116.75	107.32
2	H	10	THR	N-CA-C	-5.71	104.69	111.03
1	A	414	VAL	CA-C-N	5.69	126.96	119.84
1	A	414	VAL	C-N-CA	5.69	126.96	119.84
2	E	152	PHE	N-CA-C	5.69	117.92	108.13
1	A	760	VAL	N-CA-C	5.68	118.01	108.81
1	A	394	LEU	N-CA-C	5.67	117.48	107.61
1	A	578	LEU	N-CA-C	-5.66	105.64	112.54
1	B	541	GLY	N-CA-C	-5.66	105.92	112.83
2	L	10	THR	N-CA-C	-5.66	104.75	111.03
2	G	69	THR	N-CA-C	5.65	117.89	111.11
1	A	541	GLY	N-CA-C	-5.65	105.95	112.73
2	M	10	THR	N-CA-C	-5.65	104.76	111.03
1	A	652	PHE	N-CA-C	5.63	118.71	109.76
2	C	10	THR	N-CA-C	-5.62	104.79	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	113	SER	N-CA-C	5.62	117.99	110.35
1	B	823	THR	N-CA-C	5.62	117.38	108.79
1	A	802	ILE	N-CA-C	5.60	116.06	107.77
1	A	465	ASN	N-CA-C	-5.60	98.87	110.80
2	J	10	THR	N-CA-C	-5.60	104.82	111.03
2	J	18	ILE	CB-CA-C	-5.60	105.10	111.59
1	A	184	LYS	N-CA-C	-5.58	104.61	111.75
1	B	814	ASN	N-CA-C	-5.57	106.52	113.38
1	A	858	VAL	N-CA-C	5.57	115.90	108.27
2	G	154	LYS	CA-C-N	5.57	126.80	119.84
2	G	154	LYS	C-N-CA	5.57	126.80	119.84
2	J	70	LEU	N-CA-C	5.57	122.66	110.80
2	O	155	PRO	CA-C-N	-5.57	114.24	123.37
2	O	155	PRO	C-N-CA	-5.57	114.24	123.37
2	K	61	PHE	N-CA-C	5.56	118.52	109.06
1	B	480	PHE	N-CA-C	-5.56	105.80	112.58
1	B	273	TYR	CB-CA-C	-5.54	99.39	110.42
3	W	344	LEU	N-CA-C	5.54	118.08	111.71
1	A	356	GLU	N-CA-C	5.54	122.60	110.80
1	B	364	THR	N-CA-C	-5.54	105.73	112.88
2	C	68	THR	N-CA-C	-5.54	105.73	113.37
2	N	63	PHE	N-CA-C	5.53	118.58	109.72
1	A	812	VAL	N-CA-C	5.53	117.44	111.58
2	D	10	THR	N-CA-C	-5.53	104.90	111.03
1	B	243	SER	N-CA-C	5.52	116.65	108.86
2	J	127	ILE	N-CA-C	5.52	120.82	109.34
1	A	794	THR	N-CA-C	-5.52	105.76	113.37
2	F	10	THR	N-CA-C	-5.51	104.92	111.03
3	W	826	ILE	N-CA-C	-5.50	105.01	110.62
2	J	152	PHE	N-CA-C	5.47	117.71	109.23
3	W	67	GLU	N-CA-C	5.47	117.33	111.36
2	J	71	LEU	N-CA-C	-5.45	105.75	112.72
1	B	285	ILE	N-CA-C	5.44	116.42	108.58
1	A	115	GLN	N-CA-C	-5.44	101.41	110.17
1	A	292	LEU	N-CA-C	5.44	116.54	109.64
1	A	726	ASN	N-CA-C	5.44	121.32	114.31
1	B	444	ARG	N-CA-C	-5.43	106.63	113.20
1	A	761	GLY	N-CA-C	5.42	118.52	110.60
2	G	113	SER	N-CA-C	5.42	117.72	110.35
1	A	299	ILE	CB-CA-C	-5.42	102.40	111.29
3	W	579	ASN	N-CA-C	-5.41	106.71	113.15
2	K	10	THR	N-CA-C	-5.41	105.03	111.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	152	PHE	N-CA-C	5.39	118.25	109.24
2	F	113	SER	N-CA-C	5.39	118.10	110.50
1	A	305	GLN	N-CA-C	5.38	117.03	110.41
3	W	530	ASN	N-CA-C	5.38	117.14	111.28
1	A	800	TYR	N-CA-C	5.37	117.34	108.49
1	B	300	ARG	CA-C-N	5.36	124.98	119.56
1	B	300	ARG	C-N-CA	5.36	124.98	119.56
2	F	154	LYS	CA-C-N	5.36	126.54	119.84
2	F	154	LYS	C-N-CA	5.36	126.54	119.84
2	G	10	THR	N-CA-C	-5.36	105.08	111.03
2	C	110	ALA	CA-C-N	5.35	125.33	120.03
2	C	110	ALA	C-N-CA	5.35	125.33	120.03
2	H	144	ARG	N-CA-C	-5.35	106.80	113.38
2	J	394	MET	N-CA-C	-5.34	106.26	112.89
1	A	833	PHE	N-CA-C	5.34	118.87	107.70
2	O	127	ILE	N-CA-C	5.34	120.45	109.34
1	A	348	LYS	N-CA-C	-5.34	105.57	111.71
1	B	279	ARG	N-CA-C	-5.33	105.47	111.28
2	E	394	MET	N-CA-C	-5.33	106.28	112.89
1	B	94	THR	N-CA-C	-5.33	106.01	112.88
2	M	154	LYS	CA-C-N	5.32	126.49	119.84
2	M	154	LYS	C-N-CA	5.32	126.49	119.84
1	A	763	LEU	CA-C-N	5.31	126.48	119.84
1	A	763	LEU	C-N-CA	5.31	126.48	119.84
3	W	474	HIS	N-CA-C	5.30	116.86	111.14
2	F	106	ARG	N-CA-C	-5.29	100.55	109.07
2	D	394	MET	N-CA-C	-5.29	106.34	112.89
2	L	154	LYS	CA-C-N	5.29	126.45	119.84
2	L	154	LYS	C-N-CA	5.29	126.45	119.84
2	H	394	MET	N-CA-C	-5.28	106.34	112.89
1	B	810	TYR	N-CA-C	5.26	119.41	112.25
2	K	18	ILE	N-CA-C	5.25	115.07	106.72
2	G	394	MET	N-CA-C	-5.25	106.39	112.89
2	N	394	MET	N-CA-C	-5.24	106.39	112.89
2	M	394	MET	N-CA-C	-5.24	106.39	112.89
2	K	394	MET	N-CA-C	-5.23	106.41	112.89
2	L	394	MET	N-CA-C	-5.23	106.41	112.89
2	O	46	PHE	N-CA-C	5.22	117.62	109.52
2	N	187	GLU	N-CA-C	5.22	118.08	109.72
3	W	246	SER	N-CA-C	5.22	121.35	109.81
2	C	187	GLU	N-CA-C	5.20	118.04	109.72
2	F	187	GLU	N-CA-C	5.20	118.03	109.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	187	GLU	N-CA-C	5.20	118.03	109.72
1	B	137	ASN	N-CA-C	-5.19	105.60	112.24
2	E	63	PHE	N-CA-C	5.19	118.05	109.85
2	E	187	GLU	N-CA-C	5.19	118.02	109.72
1	A	146	TRP	N-CA-C	5.18	116.96	108.52
2	F	394	MET	N-CA-C	-5.18	106.47	112.89
2	K	187	GLU	N-CA-C	5.18	118.00	109.72
1	B	126	PHE	N-CA-C	5.17	117.33	108.90
1	B	771	VAL	N-CA-C	-5.17	104.94	110.36
2	O	394	MET	N-CA-C	-5.16	106.49	112.89
2	L	59	TRP	N-CA-C	5.16	117.48	108.76
2	H	251	PRO	O-C-N	5.16	129.40	123.06
2	I	59	TRP	N-CA-C	5.16	117.22	109.23
2	L	187	GLU	N-CA-C	5.16	117.97	109.72
1	A	250	TYR	N-CA-C	-5.15	105.10	111.33
3	W	900	MET	CA-C-N	5.15	126.28	119.84
3	W	900	MET	C-N-CA	5.15	126.28	119.84
2	H	187	GLU	N-CA-C	5.14	117.95	109.72
2	I	394	MET	N-CA-C	-5.14	106.52	112.89
1	B	83	GLN	N-CA-C	-5.13	105.38	110.97
2	H	113	SER	N-CA-C	5.13	117.32	110.35
3	W	68	ASN	N-CA-C	5.12	119.80	113.50
2	O	187	GLU	N-CA-C	5.12	117.91	109.72
2	L	384	ARG	NE-CZ-NH2	5.11	123.80	119.20
1	A	122	LEU	N-CA-C	-5.11	102.30	109.96
2	K	251	PRO	O-C-N	5.10	129.34	123.06
2	M	187	GLU	N-CA-C	5.09	117.87	109.72
1	B	746	GLN	N-CA-C	-5.09	102.97	111.37
1	B	211	ILE	CB-CA-C	-5.09	105.46	111.97
2	G	187	GLU	N-CA-C	5.08	117.86	109.72
2	E	59	TRP	N-CA-C	5.08	117.70	109.06
2	C	394	MET	N-CA-C	-5.08	106.59	112.89
1	B	250	TYR	N-CA-C	-5.08	105.01	111.11
2	D	187	GLU	N-CA-C	5.08	117.84	109.72
2	H	384	ARG	NE-CZ-NH2	5.07	123.76	119.20
1	B	829	VAL	N-CA-C	5.06	113.91	108.95
1	A	374	ALA	N-CA-C	5.06	116.48	111.07
2	I	127	ILE	N-CA-C	5.05	119.85	109.34
2	E	251	PRO	O-C-N	5.04	129.26	123.06
1	A	499	ASN	N-CA-C	5.04	116.77	111.28
3	W	573	VAL	N-CA-C	5.04	115.22	108.17
2	F	384	ARG	NE-CZ-NH2	5.04	123.73	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	740	ARG	N-CA-C	-5.03	105.99	112.68
2	J	187	GLU	N-CA-C	5.03	117.77	109.72
2	N	154	LYS	CA-C-N	5.03	126.12	119.84
2	N	154	LYS	C-N-CA	5.03	126.12	119.84
2	N	251	PRO	O-C-N	5.03	129.24	123.06
2	K	129	PHE	N-CA-C	5.02	116.05	108.07
3	W	777	THR	N-CA-C	-5.01	107.71	113.88
1	A	523	VAL	N-CA-C	5.01	119.76	109.34
3	W	226	ALA	N-CA-C	-5.01	105.82	111.28
2	K	113	SER	N-CA-C	5.00	117.56	110.50
1	B	717	MET	N-CA-C	5.00	117.62	111.82

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	273	TYR	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6374	0	6394	1083	0
1	B	6624	0	6652	1220	0
2	C	3162	0	3101	185	0
2	D	3162	0	3101	195	0
2	E	3162	0	3101	181	0
2	F	3162	0	3101	174	0
2	G	3162	0	3101	160	0
2	H	3162	0	3101	189	0
2	I	3162	0	3101	230	0
2	J	3162	0	3101	203	0
2	K	3162	0	3101	182	0
2	L	3162	0	3101	192	0
2	M	3162	0	3101	190	0
2	N	3162	0	3101	205	0
2	O	3162	0	3101	183	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	W	7905	0	7966	25	0
4	C	1	0	0	0	0
4	F	1	0	0	0	0
4	I	1	0	0	0	0
4	L	1	0	0	0	0
4	O	1	0	0	0	0
All	All	62014	0	61325	4529	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 37.

All (4529) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:75:VAL:HG22	3:W:673:VAL:CG1	1.63	1.28
1:B:771:VAL:HB	1:B:809:PHE:HB3	1.23	1.18
1:B:75:VAL:CG2	3:W:673:VAL:HG12	1.72	1.18
1:A:333:VAL:HG11	1:A:380:LYS:HA	1.27	1.15
1:B:442:MET:HE1	1:B:463:ILE:HG12	1.29	1.15
1:A:428:GLN:OE1	1:A:456:PHE:HB2	1.46	1.13
1:B:717:MET:HE1	1:B:830:PRO:HD2	1.25	1.13
2:G:145:ARG:HB3	2:G:145:ARG:HH11	1.10	1.12
2:H:83:ASN:ND2	2:I:122:LEU:HB2	1.65	1.11
1:A:451:ASP:HB3	1:A:452:PRO:HD2	1.14	1.11
1:B:432:VAL:HA	1:B:436:ILE:HD11	1.18	1.11
1:B:734:ASN:HB3	1:B:737:GLU:HB2	1.28	1.10
1:B:718:TYR:HB3	1:B:721:VAL:HG21	1.33	1.10
1:A:270:ILE:HD11	1:A:292:LEU:HD11	1.31	1.09
1:B:548:ARG:NH1	1:B:878:ASN:H	1.50	1.09
2:L:22:THR:HG23	2:L:73:LEU:HD12	1.35	1.08
1:A:699:ILE:HG12	1:A:700:ALA:H	1.18	1.07
2:G:145:ARG:HD2	2:I:143:ASN:HA	1.34	1.07
1:A:318:TRP:HA	1:A:321:ILE:HD12	1.34	1.07
1:B:200:VAL:HG21	1:B:243:SER:HB3	1.13	1.07
1:B:790:ARG:HE	1:B:790:ARG:HA	0.98	1.06
2:N:106:ARG:H	2:N:106:ARG:HD3	1.17	1.06
1:B:318:TRP:HA	1:B:321:ILE:HD12	1.37	1.06
1:A:658:PRO:HG2	1:B:348:LYS:HG2	1.38	1.05
1:B:498:ARG:HB2	2:I:32:GLN:HE22	1.15	1.05
1:A:721:VAL:HG12	1:A:722:ASN:H	1.18	1.04
1:B:510:LEU:HD11	1:B:537:SER:HA	1.36	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:VAL:HG12	1:A:200:VAL:H	1.20	1.04
1:B:457:GLN:HG3	1:B:458:ILE:H	1.22	1.03
1:B:646:LEU:HA	1:B:649:LEU:HD12	1.40	1.03
1:A:428:GLN:NE2	1:A:455:PRO:HB2	1.73	1.03
1:A:451:ASP:CB	1:A:452:PRO:HD2	1.84	1.03
1:B:274:ILE:HG23	1:B:278:ILE:HD11	1.40	1.03
1:A:510:LEU:HD22	1:A:540:LEU:HD13	1.39	1.02
1:B:444:ARG:HH21	1:B:520:THR:HG23	1.20	1.02
1:A:310:LEU:H	1:A:310:LEU:HD12	1.21	1.02
1:B:743:ASP:C	1:B:744:TYR:HD2	1.67	1.02
1:B:457:GLN:HB2	1:B:476:ASN:ND2	1.75	1.02
1:A:513:LEU:HA	1:A:516:GLN:NE2	1.75	1.01
1:B:224:PHE:O	1:B:228:MET:HG2	1.61	1.01
1:B:573:THR:HG22	1:B:574:GLU:H	0.88	1.01
1:A:521:MET:HB3	1:A:522:PRO:HD3	1.39	1.01
1:B:790:ARG:HE	1:B:790:ARG:CA	1.70	1.00
1:A:506:LEU:HD23	1:A:544:VAL:HA	1.40	1.00
2:C:106:ARG:H	2:C:106:ARG:HD3	1.26	1.00
1:A:367:LEU:HD21	3:W:929:ALA:HA	1.44	0.99
1:B:573:THR:HG22	1:B:574:GLU:N	1.71	0.99
1:A:705:ILE:HA	1:A:823:THR:HG22	1.43	0.99
1:B:674:VAL:HG21	1:B:679:LEU:HD13	1.44	0.99
1:B:473:HIS:HB2	2:I:126:ARG:HH22	1.21	0.99
1:B:510:LEU:HD22	1:B:540:LEU:HD13	1.42	0.99
1:B:573:THR:CG2	1:B:574:GLU:H	1.71	0.99
2:L:42:ASN:HA	2:L:61:PHE:HB2	1.43	0.98
1:B:371:ASN:HD22	1:B:583:SER:HB3	1.28	0.98
1:B:204:THR:HG23	1:B:244:ILE:HG22	1.44	0.98
2:H:106:ARG:HD3	2:H:106:ARG:H	1.26	0.98
1:A:275:PRO:HB2	1:A:278:ILE:HD11	1.45	0.98
1:B:265:LEU:HB3	1:B:296:ALA:HB1	1.46	0.98
1:B:435:ILE:HG22	1:B:436:ILE:H	1.29	0.98
2:J:106:ARG:HD3	2:J:106:ARG:H	1.23	0.97
1:B:700:ALA:HB2	1:B:827:LYS:HB2	1.45	0.97
1:B:700:ALA:CB	1:B:827:LYS:HB2	1.95	0.97
1:A:540:LEU:O	1:A:544:VAL:HG23	1.64	0.97
1:A:270:ILE:HG23	1:A:854:LEU:HD21	1.46	0.96
1:A:192:ASN:O	1:A:193:SER:HB3	1.65	0.96
1:B:200:VAL:HG21	1:B:243:SER:CB	1.96	0.96
2:H:83:ASN:HD21	2:I:122:LEU:HB2	1.30	0.96
1:A:660:ASP:HB3	1:B:539:ARG:HD2	1.43	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:588:ILE:HG22	1:A:589:GLY:H	1.28	0.96
1:B:458:ILE:HD12	1:B:459:ALA:N	1.81	0.95
1:A:563:MET:HE2	1:A:563:MET:HA	1.48	0.95
1:B:435:ILE:O	1:B:438:PRO:HD2	1.67	0.95
2:I:145:ARG:NH1	2:I:145:ARG:HB3	1.82	0.95
1:A:563:MET:HA	1:A:563:MET:CE	1.98	0.94
1:A:510:LEU:HD11	1:A:537:SER:HA	1.46	0.94
1:A:779:ASP:HA	1:A:798:ILE:CD1	1.98	0.93
1:B:446:HIS:O	1:B:447:TYR:HB2	1.68	0.93
2:O:27:VAL:O	2:O:31:ILE:HG12	1.66	0.93
1:A:643:GLU:HG2	1:A:662:MET:HE1	1.46	0.93
1:B:764:PRO:O	1:B:765:PHE:HB3	1.65	0.93
1:A:371:ASN:C	1:A:373:GLN:H	1.71	0.93
1:B:518:PHE:HB3	1:B:519:PRO:HD2	1.49	0.93
1:A:225:ILE:HA	1:A:228:MET:HE2	1.50	0.93
1:B:790:ARG:HA	1:B:790:ARG:NE	1.84	0.92
1:A:428:GLN:HE21	1:A:455:PRO:HB2	1.30	0.92
2:G:145:ARG:HB3	2:G:145:ARG:NH1	1.84	0.92
1:B:126:PHE:H	1:B:126:PHE:HD2	1.09	0.92
1:B:190:ASN:HD21	1:B:193:SER:HB3	1.31	0.92
1:B:722:ASN:HD22	1:B:824:LYS:HA	1.35	0.92
1:B:513:LEU:HA	1:B:516:GLN:CD	1.95	0.92
2:G:6:SER:OG	2:G:128:ASN:HA	1.70	0.92
1:A:779:ASP:HA	1:A:798:ILE:HD12	1.50	0.91
1:B:428:GLN:HB2	1:B:456:PHE:CD1	2.05	0.91
1:B:513:LEU:HA	1:B:516:GLN:NE2	1.85	0.91
1:B:366:PHE:C	1:B:368:THR:H	1.76	0.91
1:B:803:ASN:H	1:B:807:ASN:HD21	1.17	0.91
1:A:661:GLN:HE21	1:B:348:LYS:NZ	1.67	0.91
1:B:166:PHE:HE2	1:B:689:MET:HA	1.34	0.91
1:B:454:THR:HG21	1:B:476:ASN:ND2	1.86	0.91
1:B:459:ALA:HB1	1:B:463:ILE:HD11	1.51	0.90
1:A:588:ILE:HG22	1:A:589:GLY:N	1.85	0.90
2:I:135:TYR:CZ	2:I:342:MET:HE3	2.07	0.90
2:L:88:PHE:O	2:L:92:VAL:HG23	1.72	0.90
1:A:126:PHE:N	1:A:126:PHE:HD2	1.68	0.90
1:A:339:LEU:HD22	1:A:588:ILE:HA	1.53	0.90
2:L:106:ARG:H	2:L:106:ARG:HD3	1.37	0.90
2:N:145:ARG:O	2:N:146:GLN:HG3	1.71	0.90
2:C:88:PHE:O	2:C:92:VAL:HG23	1.72	0.89
1:B:509:ALA:O	1:B:513:LEU:HG	1.71	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:LEU:O	1:A:173:VAL:HG23	1.73	0.89
1:A:244:ILE:HD13	1:A:835:PHE:HE1	1.38	0.89
1:A:358:LEU:HD21	3:W:986:TYR:CE2	2.08	0.89
1:A:521:MET:HA	1:A:521:MET:HE3	1.54	0.89
1:A:660:ASP:HB3	1:B:539:ARG:HH11	1.38	0.89
2:K:106:ARG:H	2:K:106:ARG:HD3	1.37	0.89
1:A:366:PHE:C	1:A:368:THR:H	1.76	0.88
1:A:855:LEU:O	1:A:857:PHE:N	2.06	0.88
1:B:457:GLN:O	1:B:459:ALA:N	2.05	0.88
1:A:216:GLU:H	1:A:216:GLU:CD	1.81	0.88
1:B:457:GLN:HB2	1:B:476:ASN:CG	1.98	0.88
1:A:486:ASP:HB2	1:A:490:ASN:HD22	1.38	0.88
1:B:99:GLU:HB3	1:B:100:PRO:HD3	1.54	0.88
1:B:658:PRO:HB2	1:B:661:GLN:HG2	1.56	0.88
1:B:874:MET:O	1:B:875:ARG:HB2	1.73	0.88
2:M:88:PHE:O	2:M:92:VAL:HG23	1.74	0.88
1:A:194:ARG:HH11	1:A:229:ARG:HG2	1.39	0.88
2:J:106:ARG:HD3	2:J:106:ARG:N	1.87	0.88
1:B:803:ASN:H	1:B:807:ASN:ND2	1.72	0.87
1:B:182:LEU:HD11	1:B:847:THR:H	1.38	0.87
1:B:297:ARG:HG3	1:B:848:PHE:HD2	1.40	0.87
1:A:428:GLN:HB2	1:A:456:PHE:CD1	2.09	0.86
1:A:509:ALA:O	1:A:513:LEU:HG	1.75	0.86
1:B:447:TYR:O	1:B:448:ARG:HG2	1.73	0.86
2:D:88:PHE:O	2:D:92:VAL:HG23	1.73	0.86
2:O:88:PHE:O	2:O:92:VAL:HG23	1.72	0.86
2:I:76:ASN:H	2:M:76:ASN:HB2	1.37	0.86
1:B:451:ASP:H	1:B:452:PRO:HD3	1.39	0.86
1:B:413:VAL:HG12	1:B:414:VAL:N	1.88	0.86
2:N:88:PHE:O	2:N:92:VAL:HG23	1.74	0.86
1:B:473:HIS:HB2	2:I:126:ARG:NH2	1.91	0.86
1:B:745:ALA:HB1	1:B:748:THR:HB	1.57	0.86
2:H:88:PHE:O	2:H:92:VAL:HG23	1.73	0.86
2:I:24:TYR:O	2:I:27:VAL:HG22	1.74	0.86
1:B:540:LEU:O	1:B:544:VAL:HG23	1.75	0.86
1:B:182:LEU:HD23	1:B:183:LEU:H	1.40	0.86
1:A:150:LEU:HD12	1:A:696:SER:HB2	1.58	0.86
1:A:275:PRO:HB2	1:A:278:ILE:CD1	2.04	0.86
2:E:88:PHE:O	2:E:92:VAL:HG23	1.75	0.86
2:J:88:PHE:O	2:J:92:VAL:HG23	1.75	0.85
1:A:451:ASP:HB3	1:A:452:PRO:CD	2.03	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:88:PHE:O	2:I:92:VAL:HG23	1.76	0.85
1:B:590:ASN:N	1:B:590:ASN:HD22	1.74	0.85
2:C:150:PHE:HB2	2:C:152:PHE:CE1	2.11	0.85
2:F:88:PHE:O	2:F:92:VAL:HG23	1.75	0.85
2:M:106:ARG:HD3	2:M:106:ARG:H	1.40	0.85
1:B:126:PHE:HD2	1:B:126:PHE:N	1.73	0.85
2:G:88:PHE:O	2:G:92:VAL:HG23	1.75	0.85
2:H:6:SER:OG	2:H:128:ASN:HA	1.77	0.85
2:M:6:SER:OG	2:M:128:ASN:HA	1.76	0.85
1:A:239:VAL:HG22	1:A:846:LEU:HG	1.58	0.84
1:B:723:ILE:HG22	1:B:724:ALA:H	1.40	0.84
1:A:445:MET:C	1:A:447:TYR:H	1.84	0.84
1:B:306:ASP:O	1:B:308:LEU:N	2.10	0.84
1:B:518:PHE:HD2	2:H:69:THR:HB	1.40	0.84
2:K:88:PHE:O	2:K:92:VAL:HG23	1.76	0.84
1:A:660:ASP:HB3	1:B:539:ARG:CD	2.05	0.84
1:B:415:PRO:HG2	1:B:480:PHE:HD1	1.42	0.84
1:B:701:GLN:HB2	1:B:826:TYR:HD2	1.40	0.84
1:B:825:VAL:HG12	1:B:826:TYR:N	1.91	0.84
2:L:144:ARG:O	2:L:145:ARG:HB2	1.74	0.84
1:A:125:ILE:N	1:A:125:ILE:HD12	1.92	0.84
1:B:523:VAL:C	1:B:525:TYR:H	1.85	0.84
1:B:743:ASP:CG	1:B:745:ALA:H	1.85	0.84
1:A:570:THR:HG22	1:A:571:LEU:H	1.42	0.84
1:B:200:VAL:CG2	1:B:243:SER:HB3	2.05	0.84
1:B:498:ARG:NH1	2:J:25:SER:HB3	1.92	0.84
1:B:735:LEU:HG	1:B:760:VAL:O	1.78	0.84
1:B:471:TRP:HB2	1:B:512:GLN:OE1	1.77	0.84
1:A:126:PHE:N	1:A:126:PHE:CD2	2.42	0.84
1:B:503:ILE:HD11	1:B:548:ARG:HG2	1.58	0.84
2:F:82:ARG:NH1	2:H:144:ARG:HD2	1.93	0.84
2:I:76:ASN:HB2	2:M:76:ASN:HB2	1.57	0.84
1:A:771:VAL:HG13	1:A:772:ILE:H	1.43	0.84
1:B:717:MET:HE1	1:B:830:PRO:CD	2.07	0.84
1:A:361:GLN:HB2	1:A:528:SER:OG	1.78	0.83
1:B:124:ARG:C	1:B:125:ILE:HD12	2.02	0.83
1:B:428:GLN:HG2	1:B:429:LEU:N	1.92	0.83
1:B:435:ILE:HG22	1:B:436:ILE:N	1.93	0.83
2:L:23:LEU:HD21	2:N:36:GLN:OE1	1.76	0.83
1:B:743:ASP:C	1:B:744:TYR:CD2	2.54	0.83
1:A:158:GLY:H	1:A:762:ALA:HB3	1.43	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:454:THR:HG21	1:B:476:ASN:HD21	1.39	0.83
2:I:23:LEU:HD23	2:I:24:TYR:N	1.94	0.83
1:A:474:PHE:O	1:A:478:ASN:HB2	1.77	0.83
1:B:126:PHE:N	1:B:126:PHE:CD2	2.43	0.83
1:B:799:LEU:HD22	1:B:800:TYR:N	1.93	0.83
1:A:471:TRP:HB2	1:A:512:GLN:OE1	1.79	0.83
1:A:524:ASP:O	1:A:526:LYS:N	2.10	0.83
1:A:647:LYS:HG3	1:A:654:VAL:HG21	1.59	0.83
1:B:272:ASN:C	1:B:274:ILE:H	1.87	0.82
2:H:135:TYR:CZ	2:H:342:MET:HE3	2.14	0.82
2:O:6:SER:OG	2:O:128:ASN:HA	1.80	0.82
2:I:38:ILE:HG22	2:I:42:ASN:HD21	1.42	0.82
1:B:516:GLN:HA	1:B:518:PHE:HE1	1.41	0.82
1:B:590:ASN:HD22	1:B:590:ASN:H	1.25	0.82
1:A:461:GLN:HA	2:F:32:GLN:HE22	1.43	0.82
1:B:549:LEU:HD13	1:B:877:MET:HE2	1.61	0.82
1:B:428:GLN:HA	1:B:431:ILE:HD12	1.61	0.82
2:F:150:PHE:HB2	2:F:152:PHE:CE1	2.15	0.82
1:A:486:ASP:HB2	1:A:490:ASN:ND2	1.94	0.81
1:A:734:ASN:HB3	1:A:737:GLU:HG2	1.61	0.81
1:B:722:ASN:HB2	1:B:824:LYS:HB3	1.62	0.81
2:H:109:ILE:HG13	2:H:109:ILE:O	1.79	0.81
1:B:454:THR:CG2	1:B:476:ASN:HD21	1.92	0.81
1:A:406:SER:O	1:A:409:TRP:HB3	1.81	0.81
1:B:494:ASN:ND2	1:B:495:ASP:H	1.79	0.81
1:B:769:SER:HB3	1:B:807:ASN:OD1	1.80	0.81
2:L:22:THR:HB	2:N:128:ASN:O	1.79	0.81
1:A:712:LEU:HB3	1:A:721:VAL:O	1.79	0.81
1:B:218:GLU:HG3	1:B:221:VAL:HG23	1.62	0.81
1:B:193:SER:HB2	1:B:226:ALA:HA	1.62	0.81
1:B:725:ARG:H	1:B:725:ARG:HD2	1.44	0.81
1:B:498:ARG:HB2	2:I:32:GLN:NE2	1.94	0.81
1:B:511:MET:CE	2:J:70:LEU:HG	2.09	0.81
1:B:537:SER:O	1:B:540:LEU:HB3	1.81	0.81
2:H:76:ASN:HB2	2:J:76:ASN:HB2	1.60	0.81
1:A:459:ALA:O	1:A:462:GLN:HB2	1.81	0.81
1:B:118:LYS:HG2	1:B:119:GLN:H	1.46	0.81
2:I:76:ASN:CB	2:M:76:ASN:HB2	2.11	0.81
1:A:712:LEU:HG	1:A:819:PRO:HB2	1.61	0.81
1:B:315:GLU:HB3	1:B:571:LEU:HD11	1.61	0.80
2:D:128:ASN:O	2:E:22:THR:HB	1.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:24:TYR:O	2:E:27:VAL:HG22	1.82	0.80
2:O:67:GLY:O	2:O:69:THR:N	2.14	0.80
1:A:660:ASP:O	1:A:662:MET:N	2.14	0.80
1:B:510:LEU:CD1	1:B:537:SER:HA	2.11	0.80
1:A:362:SER:HB2	1:A:365:GLN:NE2	1.97	0.80
1:A:699:ILE:HG12	1:A:700:ALA:N	1.97	0.80
2:L:150:PHE:HB2	2:L:152:PHE:CE1	2.17	0.80
1:A:546:LEU:HD21	1:A:588:ILE:CD1	2.12	0.80
1:A:126:PHE:HD2	1:A:126:PHE:H	1.26	0.80
1:A:270:ILE:CD1	1:A:292:LEU:HD11	2.10	0.80
1:B:239:VAL:HG23	1:B:844:SER:O	1.81	0.80
1:A:370:ILE:HD11	3:W:933:LEU:O	1.81	0.80
1:A:769:SER:HB3	1:A:807:ASN:OD1	1.82	0.80
1:B:293:PRO:C	1:B:295:THR:H	1.90	0.80
2:N:144:ARG:O	2:N:145:ARG:HB2	1.81	0.80
1:B:563:MET:HA	1:B:563:MET:HE3	1.64	0.80
1:B:869:VAL:CG1	1:B:873:ASN:HA	2.11	0.80
1:A:371:ASN:C	1:A:373:GLN:N	2.37	0.79
1:A:437:TYR:N	1:A:438:PRO:HD2	1.97	0.79
1:B:393:SER:O	1:B:394:LEU:HD23	1.82	0.79
1:B:506:LEU:HD23	1:B:544:VAL:HA	1.62	0.79
1:A:199:VAL:HG12	1:A:200:VAL:N	1.97	0.79
1:A:303:LEU:HA	1:A:615:ASN:ND2	1.97	0.79
1:A:694:ARG:HG2	1:A:701:GLN:HE22	1.46	0.79
1:B:790:ARG:HG3	1:B:791:LYS:H	1.48	0.79
2:L:104:SER:O	2:L:108:GLY:HA3	1.82	0.79
1:A:869:VAL:HG11	1:A:873:ASN:HA	1.64	0.79
2:I:57:ARG:HH11	2:I:94:ASN:HD21	1.31	0.79
1:B:744:TYR:CD2	1:B:744:TYR:N	2.38	0.79
1:A:721:VAL:HG12	1:A:722:ASN:N	1.98	0.79
2:K:6:SER:OG	2:K:128:ASN:HA	1.82	0.79
1:A:370:ILE:HG13	3:W:933:LEU:CD1	2.13	0.79
1:A:711:GLN:C	1:A:712:LEU:HD23	2.08	0.79
1:B:457:GLN:HG3	1:B:458:ILE:N	1.98	0.79
1:B:465:ASN:HD22	1:B:468:VAL:HG23	1.47	0.79
1:A:480:PHE:CD2	1:A:493:LEU:HB3	2.18	0.79
1:A:606:VAL:HG23	1:A:607:ASN:H	1.46	0.79
1:B:673:PRO:O	1:B:674:VAL:HG13	1.83	0.79
2:H:2:ASP:HB2	2:H:128:ASN:HD21	1.46	0.79
2:N:50:GLY:O	2:N:51:ILE:HG23	1.83	0.79
1:A:869:VAL:CG1	1:A:873:ASN:HA	2.12	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:277:ARG:O	1:B:278:ILE:HG12	1.83	0.79
1:B:548:ARG:HH11	1:B:878:ASN:H	1.28	0.78
2:J:128:ASN:O	2:K:22:THR:HB	1.83	0.78
1:B:75:VAL:HG22	3:W:673:VAL:HG12	0.83	0.78
2:H:105:GLN:C	2:H:107:ASN:H	1.91	0.78
2:M:145:ARG:O	2:M:146:GLN:HG3	1.83	0.78
1:A:305:GLN:O	1:A:307:ARG:HG3	1.82	0.78
1:A:428:GLN:HG2	1:A:429:LEU:N	1.98	0.78
1:A:118:LYS:HG2	1:A:119:GLN:N	1.98	0.78
1:B:457:GLN:C	1:B:459:ALA:H	1.91	0.78
1:A:480:PHE:HD2	1:A:493:LEU:HB3	1.49	0.78
1:B:606:VAL:HG23	1:B:607:ASN:H	1.46	0.78
1:A:639:LYS:O	1:A:643:GLU:HG3	1.84	0.78
1:B:111:ILE:C	1:B:113:PRO:HD3	2.09	0.78
2:I:42:ASN:HA	2:I:61:PHE:HB2	1.66	0.78
1:B:702:GLY:HA3	1:B:759:LEU:O	1.84	0.77
2:N:144:ARG:NH2	2:N:146:GLN:HE22	1.81	0.77
1:B:374:ALA:HB1	1:B:580:SER:HB3	1.66	0.77
1:B:562:THR:HB	1:B:611:HIS:CD2	2.20	0.77
1:B:779:ASP:HA	1:B:798:ILE:CD1	2.14	0.77
1:B:406:SER:O	1:B:409:TRP:HB3	1.84	0.77
1:B:491:GLN:CD	1:B:564:ASN:HB3	2.08	0.77
2:E:93:ASP:O	2:E:97:MET:HG3	1.84	0.77
2:H:106:ARG:H	2:H:106:ARG:CD	1.98	0.77
2:I:128:ASN:HD22	2:J:19:VAL:HB	1.49	0.77
2:K:93:ASP:O	2:K:97:MET:HG3	1.85	0.77
2:M:22:THR:HG23	2:M:73:LEU:HD12	1.66	0.77
1:A:817:TRP:CG	1:A:818:VAL:H	2.02	0.77
1:B:764:PRO:O	1:B:765:PHE:CB	2.33	0.77
1:A:471:TRP:O	1:A:475:VAL:HG23	1.85	0.77
1:B:169:LEU:O	1:B:173:VAL:HG23	1.84	0.77
1:B:855:LEU:O	1:B:857:PHE:N	2.17	0.77
1:B:204:THR:CG2	1:B:244:ILE:HG22	2.14	0.77
1:B:435:ILE:C	1:B:436:ILE:HG12	2.08	0.77
2:M:139:TRP:NE1	2:M:143:ASN:HD21	1.81	0.77
2:H:93:ASP:O	2:H:97:MET:HG3	1.85	0.77
1:B:166:PHE:CE2	1:B:689:MET:HA	2.20	0.76
1:B:218:GLU:HG3	1:B:221:VAL:CG2	2.15	0.76
1:B:503:ILE:O	1:B:505:GLN:HG2	1.85	0.76
1:B:573:THR:O	1:B:574:GLU:HG2	1.84	0.76
1:B:744:TYR:HD2	1:B:744:TYR:N	1.77	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:17:LYS:HG2	2:H:130:ASP:HA	1.67	0.76
1:A:405:ILE:HG21	1:A:536:LEU:HG	1.67	0.76
1:A:614:TYR:O	1:A:618:ILE:HG12	1.85	0.76
1:B:200:VAL:HG23	1:B:242:PRO:O	1.86	0.76
1:B:731:GLN:HG2	2:D:62:ASP:HB2	1.67	0.76
1:A:548:ARG:HH12	1:A:878:ASN:H	1.34	0.76
1:A:563:MET:HE3	1:A:611:HIS:CD2	2.20	0.76
1:A:122:LEU:HG	1:A:201:ASP:OD2	1.84	0.76
1:A:461:GLN:HA	2:F:32:GLN:NE2	2.00	0.76
1:A:588:ILE:CG2	1:A:589:GLY:H	1.99	0.76
1:B:133:ILE:HD12	1:B:145:ARG:HB2	1.66	0.76
1:B:678:ARG:O	1:B:681:ILE:HG22	1.85	0.76
2:C:24:TYR:O	2:C:27:VAL:HG22	1.86	0.76
2:D:67:GLY:O	2:D:68:THR:HG23	1.85	0.76
2:I:110:ALA:HB1	2:I:111:PRO:CD	2.16	0.76
1:A:158:GLY:H	1:A:762:ALA:CB	1.99	0.76
1:A:678:ARG:O	1:A:681:ILE:HG22	1.86	0.76
1:B:199:VAL:HG12	1:B:200:VAL:N	2.00	0.76
1:B:701:GLN:HA	1:B:761:GLY:O	1.85	0.76
2:G:93:ASP:O	2:G:97:MET:HG3	1.85	0.76
1:A:503:ILE:HD13	1:A:547:THR:HB	1.68	0.76
1:B:675:GLU:HB3	1:B:678:ARG:HG2	1.68	0.76
1:A:244:ILE:HD13	1:A:835:PHE:CE1	2.21	0.76
1:A:428:GLN:HA	1:A:431:ILE:HD12	1.68	0.76
1:B:96:PRO:O	1:B:652:PHE:HB3	1.84	0.76
1:B:361:GLN:HE22	3:W:624:LYS:NZ	1.84	0.76
2:I:93:ASP:O	2:I:97:MET:HG3	1.86	0.76
2:M:135:TYR:CZ	2:M:342:MET:HE3	2.21	0.76
1:A:310:LEU:H	1:A:310:LEU:CD1	1.97	0.75
1:B:518:PHE:CB	1:B:519:PRO:HD2	2.14	0.75
1:A:501:HIS:C	1:A:503:ILE:HG13	2.11	0.75
2:C:145:ARG:HB3	2:C:145:ARG:NH1	2.02	0.75
2:F:104:SER:HB3	2:F:108:GLY:CA	2.16	0.75
1:B:781:THR:O	1:B:783:PHE:N	2.19	0.75
1:A:371:ASN:HA	1:A:374:ALA:HB3	1.68	0.75
1:A:457:GLN:HB2	1:A:476:ASN:HD21	1.52	0.75
2:E:135:TYR:CZ	2:E:342:MET:HE3	2.21	0.75
2:L:19:VAL:HG23	2:N:128:ASN:HB3	1.69	0.75
2:J:12:LYS:C	2:J:14:ALA:H	1.94	0.75
2:J:93:ASP:O	2:J:97:MET:HG3	1.87	0.75
1:B:251:ALA:HA	2:N:69:THR:HG21	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:498:ARG:CB	2:I:32:GLN:HE22	1.97	0.75
1:A:694:ARG:HG2	1:A:701:GLN:NE2	2.01	0.74
1:B:511:MET:HE3	2:J:70:LEU:HG	1.67	0.74
2:C:38:ILE:HG22	2:C:42:ASN:HD21	1.51	0.74
1:B:698:LYS:O	1:B:699:ILE:HB	1.86	0.74
2:I:76:ASN:HB2	2:M:76:ASN:CB	2.17	0.74
1:A:148:TRP:CZ3	1:A:246:HIS:HB2	2.22	0.74
1:A:537:SER:O	1:A:540:LEU:HB3	1.87	0.74
1:B:491:GLN:HG3	1:B:565:MET:H	1.50	0.74
2:J:128:ASN:HB3	2:K:19:VAL:HG23	1.69	0.74
2:N:57:ARG:HH11	2:N:94:ASN:HD21	1.33	0.74
1:A:492:VAL:HG13	1:A:558:MET:SD	2.27	0.74
1:A:647:LYS:CG	1:A:654:VAL:HG21	2.17	0.74
1:B:482:GLN:HB2	1:B:493:LEU:HD22	1.70	0.74
1:B:675:GLU:HB3	1:B:678:ARG:CG	2.17	0.74
1:B:688:ASN:O	1:B:692:ILE:HD12	1.87	0.74
1:B:614:TYR:O	1:B:618:ILE:HG12	1.87	0.74
2:O:150:PHE:HB2	2:O:152:PHE:CE1	2.23	0.74
1:A:306:ASP:C	1:A:308:LEU:H	1.95	0.74
2:D:23:LEU:HD23	2:D:24:TYR:N	2.03	0.74
2:D:93:ASP:O	2:D:97:MET:HG3	1.87	0.74
2:I:75:ALA:HB3	2:M:76:ASN:HA	1.68	0.74
2:L:93:ASP:O	2:L:97:MET:HG3	1.88	0.74
1:A:286:LEU:HD23	1:A:286:LEU:H	1.52	0.74
1:A:784:ALA:O	1:A:787:VAL:HG23	1.88	0.74
1:A:802:ILE:HA	1:A:807:ASN:HD21	1.52	0.74
1:B:190:ASN:ND2	1:B:193:SER:HB3	2.03	0.74
1:B:783:PHE:HD1	1:B:783:PHE:H	1.33	0.74
2:C:82:ARG:CZ	2:E:144:ARG:HD2	2.18	0.74
2:D:24:TYR:O	2:D:27:VAL:HG22	1.88	0.74
2:H:12:LYS:C	2:H:14:ALA:H	1.95	0.74
1:A:405:ILE:CG2	1:A:536:LEU:HG	2.18	0.74
1:A:428:GLN:HB2	1:A:456:PHE:HD1	1.51	0.74
1:B:366:PHE:C	1:B:368:THR:N	2.46	0.74
2:E:54:LEU:HD12	2:E:55:PRO:HD2	1.70	0.74
1:A:164:GLU:O	1:A:167:LEU:HB3	1.87	0.74
1:A:252:PHE:HD2	1:A:684:LEU:HD21	1.52	0.74
1:A:301:PRO:O	1:A:303:LEU:HD23	1.87	0.74
1:B:510:LEU:HD11	1:B:537:SER:CA	2.15	0.74
2:D:6:SER:OG	2:D:128:ASN:HA	1.87	0.74
1:B:368:THR:HG22	1:B:371:ASN:HD21	1.51	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:433:ASN:ND2	1:B:446:HIS:HB3	2.02	0.73
2:J:150:PHE:HB2	2:J:152:PHE:CE1	2.22	0.73
1:A:117:LYS:O	1:A:179:ASP:HB2	1.88	0.73
1:A:275:PRO:CB	1:A:278:ILE:HD11	2.18	0.73
1:B:254:GLU:HG2	2:N:69:THR:HB	1.68	0.73
2:G:106:ARG:HD3	2:G:106:ARG:H	1.53	0.73
2:G:12:LYS:C	2:G:14:ALA:H	1.96	0.73
2:I:12:LYS:C	2:I:14:ALA:H	1.95	0.73
2:M:144:ARG:HD2	2:N:82:ARG:NH1	2.02	0.73
1:A:277:ARG:HD3	1:A:559:ALA:HB2	1.71	0.73
1:A:660:ASP:CB	1:B:539:ARG:HD2	2.19	0.73
1:B:257:LEU:O	1:B:260:GLN:HG3	1.88	0.73
2:C:93:ASP:O	2:C:97:MET:HG3	1.87	0.73
2:F:42:ASN:HA	2:F:61:PHE:HB2	1.70	0.73
2:H:109:ILE:HB	2:H:380:ASP:HB3	1.68	0.73
1:A:310:LEU:HD12	1:A:310:LEU:N	2.00	0.73
1:B:540:LEU:HD23	1:B:541:GLY:N	2.03	0.73
2:E:12:LYS:C	2:E:14:ALA:H	1.96	0.73
2:M:12:LYS:C	2:M:14:ALA:H	1.96	0.73
2:N:93:ASP:O	2:N:97:MET:HG3	1.87	0.73
1:A:499:ASN:HA	1:A:505:GLN:NE2	2.04	0.73
1:B:265:LEU:HB3	1:B:296:ALA:CB	2.17	0.73
2:I:145:ARG:HB3	2:I:145:ARG:HH11	1.50	0.73
2:N:24:TYR:O	2:N:27:VAL:HG22	1.89	0.73
1:A:245:LEU:HB3	1:A:249:ASP:HB2	1.71	0.73
1:A:286:LEU:HD23	1:A:286:LEU:N	2.04	0.73
1:B:703:VAL:HG13	1:B:824:LYS:O	1.89	0.73
2:F:93:ASP:O	2:F:97:MET:HG3	1.87	0.73
2:M:93:ASP:O	2:M:97:MET:HG3	1.88	0.73
1:A:631:LEU:HB3	1:A:633:LEU:HD13	1.69	0.73
1:A:661:GLN:HE21	1:B:348:LYS:HZ1	1.37	0.73
1:B:503:ILE:O	1:B:505:GLN:N	2.22	0.73
1:B:674:VAL:HG23	1:B:679:LEU:HD22	1.69	0.73
1:B:770:SER:HB2	1:B:773:SER:OG	1.88	0.73
1:B:771:VAL:HB	1:B:809:PHE:CB	2.11	0.73
2:F:145:ARG:O	2:F:146:GLN:HG2	1.89	0.73
2:J:11:LEU:O	2:J:14:ALA:HB3	1.89	0.73
1:A:101:LYS:HZ2	3:W:382:ASP:N	1.86	0.73
1:B:277:ARG:O	1:B:279:ARG:N	2.20	0.73
1:B:594:ILE:C	1:B:594:ILE:HD12	2.13	0.73
1:B:701:GLN:O	1:B:826:TYR:HB3	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:12:LYS:C	2:D:14:ALA:H	1.95	0.73
2:D:63:PHE:CD2	2:D:84:THR:HG23	2.24	0.73
2:F:23:LEU:HD21	2:H:36:GLN:OE1	1.89	0.73
2:H:27:VAL:O	2:H:31:ILE:HG12	1.88	0.73
1:B:436:ILE:HG13	1:B:437:TYR:H	1.54	0.72
1:B:471:TRP:O	1:B:475:VAL:HG23	1.88	0.72
2:H:106:ARG:HD3	2:H:106:ARG:N	2.03	0.72
1:B:498:ARG:HH12	2:J:25:SER:HB3	1.52	0.72
1:B:521:MET:HB2	1:B:522:PRO:CD	2.19	0.72
1:B:712:LEU:CD1	1:B:722:ASN:HB3	2.18	0.72
1:A:510:LEU:CD1	1:A:537:SER:HA	2.20	0.72
2:N:12:LYS:C	2:N:14:ALA:H	1.94	0.72
1:A:370:ILE:HG13	3:W:933:LEU:HD12	1.71	0.72
1:B:492:VAL:HG11	1:B:558:MET:HG2	1.71	0.72
1:B:516:GLN:HA	1:B:518:PHE:CE1	2.25	0.72
1:B:630:ARG:O	1:B:631:LEU:HG	1.90	0.72
1:B:799:LEU:HD22	1:B:800:TYR:H	1.52	0.72
2:J:106:ARG:HG2	2:J:107:ASN:H	1.54	0.72
1:A:420:ILE:HG12	1:A:423:SER:HB2	1.69	0.72
1:A:496:ASN:HD22	1:A:498:ARG:HB2	1.53	0.72
1:A:629:ASN:O	1:A:631:LEU:N	2.17	0.72
1:B:499:ASN:O	1:B:500:GLY:C	2.33	0.72
1:B:615:ASN:O	1:B:618:ILE:HB	1.90	0.72
2:J:144:ARG:HD2	2:K:82:ARG:NH1	2.05	0.72
2:M:122:LEU:HB2	2:O:83:ASN:ND2	2.04	0.72
2:F:22:THR:HB	2:H:128:ASN:O	1.89	0.72
1:B:156:PRO:HB2	1:B:161:ASP:HB3	1.72	0.72
1:B:444:ARG:NH2	1:B:520:THR:HG23	2.03	0.72
2:K:12:LYS:C	2:K:14:ALA:H	1.96	0.72
1:A:239:VAL:CG2	1:A:846:LEU:HG	2.19	0.72
1:A:613:ASN:HD22	1:A:649:LEU:CD2	2.03	0.72
1:B:752:LEU:C	1:B:754:ASN:H	1.95	0.72
1:A:605:ASN:O	1:A:608:VAL:HB	1.90	0.72
1:A:146:TRP:O	1:A:833:PHE:HB3	1.89	0.72
1:A:721:VAL:CG1	1:A:722:ASN:H	2.01	0.72
1:B:551:ALA:O	1:B:555:GLU:HB2	1.90	0.72
1:B:825:VAL:HG12	1:B:826:TYR:H	1.53	0.72
2:C:12:LYS:C	2:C:14:ALA:H	1.96	0.72
2:D:145:ARG:O	2:D:146:GLN:HG3	1.90	0.72
2:I:135:TYR:OH	2:I:340:GLU:OE1	2.06	0.72
1:A:445:MET:O	1:A:447:TYR:N	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:355:LEU:HG	1:B:356:GLU:N	2.05	0.71
1:B:473:HIS:HB3	2:I:126:ARG:HH12	1.54	0.71
2:D:11:LEU:O	2:D:14:ALA:HB3	1.90	0.71
1:A:735:LEU:HG	1:A:760:VAL:O	1.89	0.71
1:A:764:PRO:O	1:A:797:PRO:HD2	1.91	0.71
1:B:422:GLU:HA	1:B:425:VAL:HG23	1.72	0.71
1:B:480:PHE:CE2	1:B:493:LEU:HB2	2.24	0.71
2:F:12:LYS:C	2:F:14:ALA:H	1.96	0.71
2:J:130:ASP:HA	2:K:17:LYS:HG2	1.71	0.71
2:O:93:ASP:O	2:O:97:MET:HG3	1.90	0.71
1:B:156:PRO:CB	1:B:161:ASP:HB3	2.20	0.71
2:C:144:ARG:HD2	2:D:82:ARG:CZ	2.20	0.71
2:L:6:SER:OG	2:L:128:ASN:HA	1.91	0.71
2:O:12:LYS:C	2:O:14:ALA:H	1.96	0.71
1:A:246:HIS:HB3	1:A:249:ASP:OD2	1.90	0.71
1:A:709:ASP:HB3	1:A:820:THR:HG23	1.73	0.71
1:B:194:ARG:O	1:B:196:ALA:N	2.23	0.71
1:B:428:GLN:OE1	1:B:456:PHE:HB2	1.90	0.71
2:I:11:LEU:O	2:I:14:ALA:HB3	1.91	0.71
2:I:150:PHE:HB2	2:I:152:PHE:CE1	2.25	0.71
1:A:236:ARG:HB2	1:A:238:VAL:HG23	1.72	0.71
1:B:166:PHE:CE2	1:B:689:MET:HG3	2.24	0.71
1:B:791:LYS:O	1:B:792:VAL:HG22	1.91	0.71
2:K:11:LEU:O	2:K:14:ALA:HB3	1.91	0.71
1:A:530:GLN:HA	1:A:533:ILE:HD12	1.71	0.71
1:B:605:ASN:O	1:B:608:VAL:HB	1.91	0.71
2:K:38:ILE:HG22	2:K:42:ASN:HD21	1.56	0.71
1:A:194:ARG:NH1	1:A:229:ARG:HG2	2.05	0.71
1:B:523:VAL:C	1:B:525:TYR:N	2.47	0.71
2:N:11:LEU:O	2:N:14:ALA:HB3	1.91	0.71
2:N:38:ILE:HG22	2:N:42:ASN:HD21	1.56	0.71
1:B:277:ARG:HG2	1:B:278:ILE:H	1.54	0.71
1:B:717:MET:CE	1:B:830:PRO:HD2	2.15	0.71
2:H:116:LEU:HD12	2:H:119:LEU:HB2	1.73	0.71
2:O:11:LEU:O	2:O:14:ALA:HB3	1.90	0.71
1:A:283:ASN:O	1:A:863:VAL:HG23	1.91	0.71
2:G:36:GLN:OE1	2:H:23:LEU:HD21	1.91	0.71
1:A:496:ASN:ND2	1:A:498:ARG:HB2	2.06	0.71
1:A:510:LEU:HD11	1:A:537:SER:CA	2.21	0.71
1:B:548:ARG:HH12	1:B:878:ASN:H	1.35	0.71
1:B:712:LEU:HD12	1:B:722:ASN:HB3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:4:LEU:HA	2:G:7:LEU:HD12	1.73	0.71
2:K:53:ASN:HD22	2:K:354:ALA:HB3	1.56	0.71
2:M:11:LEU:O	2:M:14:ALA:HB3	1.91	0.71
1:A:102:GLU:O	3:W:555:LEU:HD11	1.90	0.70
1:A:312:ASP:O	1:A:313:ASN:HB3	1.90	0.70
1:A:415:PRO:HG2	1:A:480:PHE:CD1	2.26	0.70
1:B:374:ALA:HB1	1:B:580:SER:HA	1.71	0.70
2:L:82:ARG:CZ	2:N:144:ARG:HD2	2.21	0.70
1:A:729:GLY:C	1:A:730:PHE:HD1	1.98	0.70
1:B:164:GLU:O	1:B:167:LEU:HB3	1.90	0.70
2:D:4:LEU:HA	2:D:7:LEU:HD12	1.73	0.70
2:M:150:PHE:HB2	2:M:152:PHE:CE1	2.26	0.70
1:A:615:ASN:O	1:A:618:ILE:HB	1.89	0.70
1:B:477:ASN:ND2	2:I:39:ILE:HG21	2.06	0.70
1:B:518:PHE:CD2	2:H:69:THR:HB	2.24	0.70
2:J:106:ARG:H	2:J:106:ARG:CD	2.03	0.70
2:J:109:ILE:HD12	2:J:109:ILE:O	1.91	0.70
1:B:259:HIS:CD2	1:B:677:ARG:HG3	2.25	0.70
2:C:11:LEU:O	2:C:14:ALA:HB3	1.90	0.70
2:K:54:LEU:HD12	2:K:55:PRO:HD2	1.71	0.70
2:N:4:LEU:HA	2:N:7:LEU:HD12	1.73	0.70
1:A:506:LEU:CD2	1:A:544:VAL:HA	2.18	0.70
1:A:551:ALA:O	1:A:555:GLU:HB2	1.92	0.70
1:B:230:GLN:HA	1:B:242:PRO:HD3	1.73	0.70
1:A:131:LEU:HD12	1:A:132:PRO:HD2	1.74	0.70
1:A:467:GLN:HB2	1:A:515:ARG:HD2	1.72	0.70
1:A:762:ALA:O	1:A:763:LEU:HG	1.92	0.70
1:B:508:GLU:HG2	1:B:512:GLN:NE2	2.07	0.70
1:B:790:ARG:HG3	1:B:791:LYS:N	2.05	0.70
2:J:116:LEU:HD12	2:J:119:LEU:HB2	1.74	0.70
2:L:12:LYS:C	2:L:14:ALA:H	1.96	0.70
2:N:167:ASN:HD22	2:N:178:GLY:HA2	1.57	0.70
1:A:508:GLU:C	1:A:512:GLN:HE21	2.00	0.70
1:A:783:PHE:HD1	1:A:783:PHE:H	1.38	0.70
2:C:167:ASN:HD22	2:C:178:GLY:HA2	1.57	0.70
2:D:153:HIS:NE2	2:E:153:HIS:NE2	2.39	0.70
2:G:167:ASN:HD22	2:G:178:GLY:HA2	1.57	0.70
1:A:482:GLN:OE1	1:A:493:LEU:HD22	1.90	0.70
1:A:503:ILE:C	1:A:505:GLN:H	1.98	0.70
1:A:560:CYS:HB2	1:A:603:TYR:HD2	1.57	0.70
1:A:793:ASP:C	1:A:795:LEU:H	2.00	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:262:VAL:CG1	1:B:297:ARG:HB3	2.21	0.70
1:B:786:ILE:HG13	1:B:787:VAL:H	1.56	0.70
2:K:167:ASN:HD22	2:K:178:GLY:HA2	1.57	0.70
2:O:154:LYS:N	2:O:155:PRO:CD	2.54	0.70
1:B:393:SER:N	1:B:573:THR:HG23	2.06	0.70
1:B:708:ARG:O	1:B:709:ASP:C	2.35	0.70
1:B:857:PHE:H	1:B:857:PHE:HD1	1.40	0.70
2:C:4:LEU:HA	2:C:7:LEU:HD12	1.74	0.70
2:J:38:ILE:HG22	2:J:42:ASN:HD21	1.56	0.70
2:J:167:ASN:HD22	2:J:178:GLY:HA2	1.57	0.70
2:O:167:ASN:HD22	2:O:178:GLY:HA2	1.57	0.70
1:A:396:PHE:HB3	1:A:578:LEU:CD1	2.22	0.70
1:A:401:TYR:HA	1:A:404:LEU:HD13	1.73	0.70
1:A:436:ILE:HD11	1:A:437:TYR:CD1	2.27	0.70
1:B:721:VAL:CG1	1:B:799:LEU:HD21	2.22	0.70
2:C:6:SER:OG	2:C:128:ASN:HA	1.92	0.70
2:E:38:ILE:HG22	2:E:42:ASN:HD21	1.57	0.70
1:A:781:THR:O	1:A:783:PHE:N	2.24	0.69
1:B:318:TRP:CA	1:B:321:ILE:HD12	2.19	0.69
1:B:670:ARG:O	1:B:671:LEU:HD23	1.92	0.69
1:B:791:LYS:O	1:B:792:VAL:HG13	1.91	0.69
1:B:805:ASP:C	1:B:807:ASN:H	1.99	0.69
2:D:239:ASN:HD22	2:D:246:THR:HG22	1.57	0.69
2:O:4:LEU:HA	2:O:7:LEU:HD12	1.74	0.69
1:A:589:GLY:C	1:A:591:ALA:H	1.99	0.69
1:B:590:ASN:H	1:B:590:ASN:ND2	1.90	0.69
2:C:22:THR:OG1	2:C:26:ASN:ND2	2.25	0.69
2:F:104:SER:HB3	2:F:108:GLY:HA2	1.74	0.69
2:O:106:ARG:H	2:O:106:ARG:HD3	1.56	0.69
1:A:437:TYR:H	1:A:438:PRO:HD2	1.56	0.69
1:A:548:ARG:HH11	1:A:877:MET:HA	1.56	0.69
1:B:182:LEU:HD11	1:B:847:THR:N	2.07	0.69
2:C:239:ASN:HD22	2:C:246:THR:HG22	1.58	0.69
2:D:150:PHE:HB2	2:D:152:PHE:CE1	2.27	0.69
2:K:150:PHE:HB2	2:K:152:PHE:CE1	2.27	0.69
2:L:11:LEU:O	2:L:14:ALA:HB3	1.93	0.69
2:L:239:ASN:HD22	2:L:246:THR:HG22	1.58	0.69
2:N:106:ARG:HD3	2:N:106:ARG:N	2.01	0.69
1:A:275:PRO:HB2	1:A:278:ILE:CG1	2.22	0.69
2:F:110:ALA:HB1	2:F:111:PRO:CD	2.22	0.69
2:I:109:ILE:HD12	2:I:109:ILE:O	1.90	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:167:ASN:HD22	2:I:178:GLY:HA2	1.57	0.69
2:J:22:THR:O	2:J:72:ASN:HA	1.92	0.69
2:E:11:LEU:O	2:E:14:ALA:HB3	1.91	0.69
2:G:11:LEU:O	2:G:14:ALA:HB3	1.92	0.69
2:M:167:ASN:HD22	2:M:178:GLY:HA2	1.57	0.69
1:A:634:TYR:HB2	1:B:875:ARG:HH22	1.57	0.69
1:B:374:ALA:HB1	1:B:580:SER:CB	2.23	0.69
2:E:5:TYR:CE2	2:E:131:ASN:HA	2.27	0.69
2:F:167:ASN:HD22	2:F:178:GLY:HA2	1.57	0.69
2:N:116:LEU:HD12	2:N:119:LEU:HB2	1.74	0.69
1:A:540:LEU:HD23	1:A:541:GLY:N	2.08	0.69
1:A:588:ILE:CG2	1:A:589:GLY:N	2.56	0.69
1:A:666:ARG:CG	1:A:667:ASP:N	2.55	0.69
1:A:803:ASN:HD22	1:A:805:ASP:HB3	1.58	0.69
1:B:772:ILE:HG23	1:B:773:SER:N	2.06	0.69
1:A:322:THR:HG22	1:A:390:ARG:HB2	1.75	0.69
1:A:451:ASP:CB	1:A:452:PRO:CD	2.68	0.69
1:A:664:ARG:HD3	1:B:538:ASN:OD1	1.92	0.69
1:A:689:MET:HA	1:A:692:ILE:HD13	1.73	0.69
1:B:368:THR:HA	1:B:579:THR:HG23	1.75	0.69
1:B:442:MET:HE1	1:B:463:ILE:CG1	2.17	0.69
1:B:783:PHE:N	1:B:783:PHE:CD1	2.60	0.69
2:D:106:ARG:H	2:D:106:ARG:HD3	1.58	0.69
2:E:109:ILE:HB	2:E:380:ASP:HB3	1.74	0.69
2:E:150:PHE:HB2	2:E:152:PHE:CE1	2.27	0.69
1:A:118:LYS:HG2	1:A:119:GLN:H	1.57	0.69
1:A:546:LEU:HD21	1:A:588:ILE:HD13	1.73	0.69
1:A:757:VAL:HG12	1:A:758:ALA:H	1.57	0.69
1:B:118:LYS:HG2	1:B:119:GLN:N	2.08	0.69
1:B:812:VAL:HG13	1:B:813:ALA:H	1.57	0.69
2:E:116:LEU:HD12	2:E:119:LEU:HB2	1.73	0.69
2:F:11:LEU:O	2:F:14:ALA:HB3	1.93	0.69
1:A:100:PRO:HB2	3:W:558:LEU:HD11	1.75	0.69
1:B:364:THR:CG2	3:W:622:ALA:HA	2.22	0.69
1:B:457:GLN:CG	1:B:458:ILE:H	1.89	0.69
1:B:633:LEU:O	1:B:633:LEU:HD23	1.92	0.69
2:H:239:ASN:HD22	2:H:246:THR:HG22	1.58	0.69
2:I:6:SER:OG	2:I:128:ASN:HA	1.92	0.69
2:K:106:ARG:HG2	2:K:107:ASN:H	1.56	0.69
2:K:144:ARG:O	2:K:145:ARG:HB2	1.92	0.69
2:L:167:ASN:HD22	2:L:178:GLY:HA2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:116:LEU:HD12	2:M:119:LEU:HB2	1.75	0.69
2:O:109:ILE:HD12	2:O:109:ILE:O	1.92	0.69
1:A:306:ASP:O	1:A:308:LEU:N	2.25	0.68
1:A:570:THR:HG22	1:A:571:LEU:N	2.07	0.68
1:A:658:PRO:HG3	1:B:345:GLN:HA	1.75	0.68
1:B:166:PHE:O	1:B:169:LEU:HB2	1.93	0.68
1:B:805:ASP:O	1:B:807:ASN:N	2.26	0.68
1:A:366:PHE:N	1:A:366:PHE:CD1	2.60	0.68
1:A:661:GLN:NE2	1:B:348:LYS:NZ	2.39	0.68
1:A:807:ASN:O	1:A:809:PHE:N	2.26	0.68
1:B:264:PRO:O	1:B:265:LEU:HB2	1.92	0.68
2:F:6:SER:OG	2:F:128:ASN:HA	1.92	0.68
2:H:106:ARG:O	2:H:107:ASN:HB2	1.93	0.68
2:J:4:LEU:HA	2:J:7:LEU:HD12	1.75	0.68
2:L:116:LEU:HD12	2:L:119:LEU:HB2	1.75	0.68
2:E:167:ASN:HD22	2:E:178:GLY:HA2	1.57	0.68
2:F:4:LEU:HA	2:F:7:LEU:HD12	1.75	0.68
2:L:110:ALA:HB1	2:L:111:PRO:CD	2.23	0.68
1:B:548:ARG:NH1	1:B:878:ASN:N	2.35	0.68
2:C:116:LEU:HD12	2:C:119:LEU:HB2	1.75	0.68
2:D:116:LEU:HD12	2:D:119:LEU:HB2	1.75	0.68
2:F:116:LEU:HD12	2:F:119:LEU:HB2	1.75	0.68
2:F:153:HIS:NE2	2:H:153:HIS:NE2	2.41	0.68
2:H:11:LEU:O	2:H:14:ALA:HB3	1.93	0.68
2:N:239:ASN:HD22	2:N:246:THR:HG22	1.58	0.68
1:A:318:TRP:CA	1:A:321:ILE:HD12	2.19	0.68
2:I:116:LEU:HD12	2:I:119:LEU:HB2	1.75	0.68
1:B:180:TYR:HD1	1:B:181:LEU:N	1.91	0.68
1:B:288:MET:HE2	1:B:288:MET:HA	1.75	0.68
2:I:239:ASN:HD22	2:I:246:THR:HG22	1.59	0.68
2:M:153:HIS:NE2	2:N:153:HIS:NE2	2.40	0.68
1:A:396:PHE:HB3	1:A:578:LEU:HD12	1.76	0.68
1:A:660:ASP:CB	1:B:539:ARG:HH11	2.04	0.68
1:B:431:ILE:HA	1:B:435:ILE:HD12	1.76	0.68
1:B:545:ASP:HB3	1:B:877:MET:SD	2.34	0.68
1:B:855:LEU:O	1:B:858:VAL:HG23	1.94	0.68
2:M:4:LEU:HA	2:M:7:LEU:HD12	1.75	0.68
1:A:659:ASP:O	1:A:662:MET:HB2	1.94	0.68
2:H:4:LEU:HA	2:H:7:LEU:HD12	1.76	0.68
2:I:4:LEU:HA	2:I:7:LEU:HD12	1.74	0.68
2:N:65:LEU:O	2:N:66:LEU:HD23	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:498:ARG:HB3	1:B:505:GLN:HE22	1.59	0.68
1:B:869:VAL:HG11	1:B:873:ASN:HA	1.74	0.68
2:H:167:ASN:HD22	2:H:178:GLY:HA2	1.57	0.68
2:J:239:ASN:HD22	2:J:246:THR:HG22	1.58	0.68
1:A:136:ALA:O	1:A:137:ASN:HB3	1.94	0.68
1:A:587:LEU:HD13	1:A:587:LEU:O	1.94	0.68
1:B:143:ARG:HG3	1:B:216:GLU:OE2	1.92	0.68
1:B:246:HIS:CD2	1:B:248:ILE:H	2.11	0.68
1:B:492:VAL:HG11	1:B:558:MET:CG	2.22	0.68
1:B:530:GLN:HA	1:B:533:ILE:HD12	1.76	0.68
2:D:167:ASN:HD22	2:D:178:GLY:HA2	1.57	0.68
2:M:239:ASN:HD22	2:M:246:THR:HG22	1.59	0.68
1:A:589:GLY:O	1:A:591:ALA:N	2.26	0.67
1:A:629:ASN:C	1:A:631:LEU:H	2.02	0.67
1:A:710:MET:HE2	1:A:824:LYS:HE2	1.75	0.67
2:H:76:ASN:HB2	2:J:76:ASN:CB	2.23	0.67
2:I:9:LYS:O	2:I:13:ASP:HB2	1.94	0.67
1:A:188:VAL:O	1:A:198:LYS:HA	1.93	0.67
1:A:436:ILE:HD12	1:A:436:ILE:C	2.18	0.67
1:A:738:LEU:C	1:A:740:ARG:H	2.02	0.67
1:B:125:ILE:HD12	1:B:125:ILE:N	2.10	0.67
1:B:258:GLN:HB3	2:N:71:LEU:HB2	1.76	0.67
1:B:721:VAL:HG12	1:B:722:ASN:N	2.08	0.67
2:G:239:ASN:HD22	2:G:246:THR:HG22	1.58	0.67
2:K:117:ARG:HH21	2:M:57:ARG:NH1	1.90	0.67
1:A:270:ILE:HG23	1:A:854:LEU:CD2	2.22	0.67
2:N:135:TYR:CZ	2:N:342:MET:HE3	2.30	0.67
1:A:306:ASP:HB3	1:A:310:LEU:CD1	2.24	0.67
1:B:305:GLN:HE21	1:B:564:ASN:CG	2.03	0.67
1:B:605:ASN:HD21	1:B:855:LEU:HD12	1.58	0.67
1:B:745:ALA:O	1:B:748:THR:N	2.28	0.67
2:D:38:ILE:HD12	2:D:65:LEU:HD23	1.75	0.67
2:E:4:LEU:HA	2:E:7:LEU:HD12	1.75	0.67
2:F:19:VAL:HG23	2:H:128:ASN:HB3	1.77	0.67
2:H:76:ASN:H	2:J:76:ASN:HB2	1.60	0.67
2:I:104:SER:O	2:I:108:GLY:HA3	1.94	0.67
2:K:116:LEU:HD12	2:K:119:LEU:HB2	1.76	0.67
2:L:4:LEU:HA	2:L:7:LEU:HD12	1.75	0.67
2:N:73:LEU:N	2:N:73:LEU:HD23	2.09	0.67
1:A:136:ALA:O	1:A:137:ASN:CB	2.43	0.67
1:A:310:LEU:O	1:A:318:TRP:HD1	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:183:LEU:HD12	1:B:844:SER:HB3	1.77	0.67
2:I:63:PHE:CD2	2:I:84:THR:HG23	2.28	0.67
2:O:239:ASN:HD22	2:O:246:THR:HG22	1.58	0.67
1:A:571:LEU:O	1:A:571:LEU:HD13	1.94	0.67
1:B:869:VAL:HG22	1:B:875:ARG:HA	1.76	0.67
2:F:239:ASN:HD22	2:F:246:THR:HG22	1.58	0.67
2:K:239:ASN:HD22	2:K:246:THR:HG22	1.58	0.67
1:B:666:ARG:CG	1:B:667:ASP:N	2.57	0.67
1:B:782:VAL:HG11	1:B:796:LYS:O	1.94	0.67
1:B:791:LYS:C	1:B:792:VAL:HG13	2.20	0.67
2:O:9:LYS:O	2:O:13:ASP:HB2	1.95	0.67
1:B:108:LEU:HD22	1:B:108:LEU:N	2.10	0.67
1:B:154:THR:O	1:B:155:LEU:HD23	1.94	0.67
1:B:394:LEU:C	1:B:396:PHE:H	2.02	0.67
2:I:76:ASN:N	2:M:76:ASN:HB2	2.09	0.67
2:K:4:LEU:HA	2:K:7:LEU:HD12	1.75	0.67
1:A:219:GLY:O	1:A:221:VAL:N	2.28	0.67
1:A:223:ARG:O	1:A:226:ALA:HB3	1.95	0.67
1:A:367:LEU:CD2	3:W:929:ALA:HA	2.22	0.67
1:A:839:MET:HG2	1:A:840:HIS:H	1.60	0.67
1:B:371:ASN:ND2	1:B:583:SER:HB3	2.06	0.67
2:G:116:LEU:HD12	2:G:119:LEU:HB2	1.76	0.67
2:K:9:LYS:O	2:K:13:ASP:HB2	1.95	0.67
1:A:409:TRP:HH2	1:A:547:THR:HG1	1.42	0.67
1:A:521:MET:HB3	1:A:522:PRO:CD	2.22	0.67
1:A:556:THR:O	1:A:557:LEU:C	2.38	0.67
1:A:650:HIS:O	1:A:651:ILE:HB	1.94	0.67
1:B:200:VAL:HG12	1:B:201:ASP:N	2.08	0.67
1:B:700:ALA:HB1	1:B:827:LYS:HB2	1.75	0.67
1:B:771:VAL:HG12	1:B:772:ILE:N	2.09	0.67
1:A:252:PHE:CD2	1:A:684:LEU:HD21	2.30	0.66
2:L:62:ASP:CG	2:L:62:ASP:O	2.37	0.66
2:O:116:LEU:HD12	2:O:119:LEU:HB2	1.76	0.66
1:A:524:ASP:OD1	1:A:525:TYR:N	2.27	0.66
1:B:229:ARG:HD2	1:B:230:GLN:HE22	1.60	0.66
1:B:672:LEU:HB3	1:B:673:PRO:HD2	1.77	0.66
2:D:99:GLU:O	2:D:99:GLU:HG2	1.94	0.66
2:D:99:GLU:OE1	2:D:116:LEU:HD22	1.94	0.66
2:O:49:GLY:HA2	2:O:54:LEU:HD23	1.77	0.66
1:B:825:VAL:CG1	1:B:826:TYR:N	2.57	0.66
2:E:239:ASN:HD22	2:E:246:THR:HG22	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:HIS:CD2	1:A:248:ILE:H	2.14	0.66
1:A:508:GLU:HG2	1:A:512:GLN:NE2	2.10	0.66
1:B:508:GLU:CD	2:J:71:LEU:HB3	2.20	0.66
1:B:724:ALA:HB2	1:B:824:LYS:HE3	1.77	0.66
2:C:153:HIS:NE2	2:E:153:HIS:NE2	2.43	0.66
2:E:14:ALA:O	2:E:18:ILE:HD12	1.95	0.66
1:A:701:GLN:HG2	1:A:826:TYR:CD2	2.31	0.66
1:B:374:ALA:HB1	1:B:580:SER:CA	2.25	0.66
2:D:144:ARG:O	2:D:145:ARG:HB2	1.94	0.66
2:L:153:HIS:NE2	2:M:153:HIS:NE2	2.44	0.66
1:A:443:GLN:CD	1:A:521:MET:HG2	2.21	0.66
1:A:454:THR:HB	1:A:457:GLN:HB3	1.78	0.66
1:A:513:LEU:O	1:A:516:GLN:OE1	2.14	0.66
1:A:653:ASP:HB3	1:A:656:ARG:HB2	1.77	0.66
1:B:396:PHE:HB2	1:B:578:LEU:HD11	1.77	0.66
2:E:23:LEU:HD23	2:E:24:TYR:N	2.11	0.66
2:N:9:LYS:O	2:N:13:ASP:HB2	1.96	0.66
2:N:150:PHE:HB2	2:N:152:PHE:CE1	2.30	0.66
1:A:277:ARG:HD3	1:A:559:ALA:CB	2.25	0.66
1:B:594:ILE:HB	1:B:595:PRO:CD	2.26	0.66
1:B:825:VAL:CG1	1:B:826:TYR:H	2.08	0.66
1:B:349:MET:O	1:B:353:LEU:HB2	1.94	0.66
2:C:2:ASP:HB2	2:C:128:ASN:HD21	1.60	0.66
2:J:5:TYR:CE2	2:J:131:ASN:HA	2.31	0.66
2:M:9:LYS:O	2:M:13:ASP:HB2	1.96	0.66
2:N:4:LEU:HA	2:N:7:LEU:CD1	2.26	0.66
1:A:506:LEU:HD21	1:A:543:LEU:C	2.20	0.66
1:A:717:MET:HE1	1:A:830:PRO:O	1.95	0.66
1:B:140:LYS:O	1:B:142:LEU:N	2.29	0.66
1:B:445:MET:O	1:B:447:TYR:N	2.23	0.66
1:B:504:ASN:O	1:B:507:MET:N	2.29	0.66
2:C:22:THR:HG23	2:C:73:LEU:HD12	1.78	0.66
2:G:145:ARG:HH11	2:G:145:ARG:CB	2.00	0.66
2:I:110:ALA:HB1	2:I:111:PRO:HD2	1.77	0.66
1:B:170:TYR:HE1	1:B:681:ILE:HG23	1.60	0.66
1:B:194:ARG:NE	1:B:194:ARG:HA	2.11	0.66
2:O:4:LEU:HA	2:O:7:LEU:CD1	2.26	0.66
1:A:166:PHE:O	1:A:169:LEU:HB2	1.96	0.65
2:C:150:PHE:HB2	2:C:152:PHE:HE1	1.61	0.65
2:D:9:LYS:O	2:D:13:ASP:HB2	1.94	0.65
2:F:26:ASN:OD1	2:H:33:GLN:HB2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:109:ILE:HB	2:I:380:ASP:HB3	1.79	0.65
2:N:150:PHE:HB2	2:N:152:PHE:HE1	1.61	0.65
1:A:603:TYR:O	1:A:606:VAL:HG22	1.96	0.65
2:C:4:LEU:HA	2:C:7:LEU:CD1	2.27	0.65
2:C:54:LEU:HD12	2:C:55:PRO:HD2	1.77	0.65
2:G:128:ASN:O	2:H:22:THR:HB	1.95	0.65
2:L:135:TYR:CZ	2:L:342:MET:HE3	2.31	0.65
1:A:660:ASP:O	1:A:661:GLN:C	2.38	0.65
1:A:755:GLN:O	1:A:757:VAL:HG23	1.96	0.65
1:A:849:THR:HB	1:A:851:TYR:HE1	1.61	0.65
1:B:322:THR:HB	1:B:390:ARG:HH11	1.61	0.65
1:B:396:PHE:HE1	1:B:398:THR:HA	1.60	0.65
1:B:642:VAL:O	1:B:646:LEU:HG	1.96	0.65
2:D:109:ILE:HB	2:D:380:ASP:HB3	1.78	0.65
2:G:9:LYS:O	2:G:13:ASP:HB2	1.96	0.65
2:J:12:LYS:HG2	2:J:16:ASP:OD2	1.95	0.65
2:K:46:PHE:HE2	2:K:119:LEU:HD21	1.62	0.65
2:M:144:ARG:HD2	2:N:82:ARG:CZ	2.27	0.65
2:C:9:LYS:O	2:C:13:ASP:HB2	1.96	0.65
1:A:308:LEU:O	1:A:309:ASN:C	2.39	0.65
1:A:711:GLN:O	1:A:712:LEU:HD23	1.96	0.65
1:A:871:PHE:O	1:A:871:PHE:HD1	1.80	0.65
1:A:501:HIS:O	1:A:503:ILE:HG13	1.97	0.65
2:D:22:THR:O	2:D:72:ASN:HA	1.95	0.65
2:G:4:LEU:HA	2:G:7:LEU:CD1	2.26	0.65
2:I:150:PHE:HB2	2:I:152:PHE:CZ	2.32	0.65
1:A:516:GLN:OE1	1:A:516:GLN:N	2.28	0.65
1:A:622:VAL:HG11	1:A:673:PRO:O	1.97	0.65
1:A:642:VAL:O	1:A:646:LEU:HG	1.96	0.65
1:B:492:VAL:O	1:B:493:LEU:C	2.40	0.65
2:H:9:LYS:O	2:H:13:ASP:HB2	1.97	0.65
2:I:130:ASP:HA	2:J:17:LYS:HG2	1.78	0.65
2:I:153:HIS:NE2	2:K:153:HIS:NE2	2.45	0.65
2:N:12:LYS:C	2:N:14:ALA:N	2.54	0.65
1:A:142:LEU:O	1:A:144:ASN:N	2.28	0.65
1:A:658:PRO:CG	1:B:348:LYS:HG2	2.23	0.65
1:A:782:VAL:O	1:A:785:GLN:HG2	1.97	0.65
1:A:803:ASN:C	1:A:805:ASP:H	2.05	0.65
1:B:170:TYR:CE1	1:B:681:ILE:HG23	2.31	0.65
1:B:401:TYR:HA	1:B:404:LEU:HD13	1.79	0.65
1:A:779:ASP:CA	1:A:798:ILE:HD12	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:236:ARG:O	1:B:237:ASN:HB2	1.97	0.65
1:B:315:GLU:CB	1:B:571:LEU:HD11	2.25	0.65
1:B:745:ALA:O	1:B:746:GLN:C	2.40	0.65
1:A:271:PHE:HA	1:A:274:ILE:HD12	1.79	0.65
1:B:96:PRO:HG2	1:B:657:VAL:HG22	1.79	0.65
1:B:298:TYR:HD1	1:B:299:ILE:N	1.94	0.65
1:B:508:GLU:C	1:B:512:GLN:HE21	2.05	0.65
2:J:135:TYR:CZ	2:J:342:MET:HE3	2.32	0.65
2:N:12:LYS:HG2	2:N:16:ASP:OD2	1.96	0.65
1:B:180:TYR:C	1:B:180:TYR:CD1	2.75	0.64
1:B:378:CYS:HB2	1:B:580:SER:HB2	1.79	0.64
2:E:9:LYS:O	2:E:13:ASP:HB2	1.97	0.64
2:F:9:LYS:O	2:F:13:ASP:HB2	1.97	0.64
2:I:4:LEU:HA	2:I:7:LEU:CD1	2.27	0.64
2:J:57:ARG:HH11	2:J:94:ASN:HD21	1.46	0.64
1:B:314:PHE:CZ	1:B:664:ARG:HG2	2.32	0.64
1:B:603:TYR:O	1:B:606:VAL:HG22	1.97	0.64
2:D:4:LEU:HA	2:D:7:LEU:CD1	2.27	0.64
2:D:106:ARG:HG2	2:D:107:ASN:H	1.62	0.64
2:L:9:LYS:O	2:L:13:ASP:HB2	1.96	0.64
1:A:802:ILE:HA	1:A:807:ASN:ND2	2.12	0.64
2:O:104:SER:HB3	2:O:108:GLY:HA2	1.79	0.64
1:A:714:ARG:HA	1:A:720:TYR:HB3	1.78	0.64
1:A:863:VAL:HG12	1:A:864:GLU:H	1.61	0.64
2:D:110:ALA:HB1	2:D:111:PRO:CD	2.28	0.64
2:L:27:VAL:O	2:L:31:ILE:HG12	1.97	0.64
1:A:414:VAL:HB	1:A:419:PHE:HE1	1.62	0.64
1:A:834:ASP:O	1:A:838:SER:HB2	1.97	0.64
1:B:124:ARG:HB2	1:B:249:ASP:CG	2.22	0.64
1:B:182:LEU:CD2	1:B:183:LEU:H	2.08	0.64
1:B:491:GLN:NE2	1:B:566:GLN:HG2	2.12	0.64
1:B:606:VAL:HG23	1:B:607:ASN:N	2.11	0.64
2:J:144:ARG:NH2	2:J:146:GLN:HE22	1.96	0.64
1:A:246:HIS:O	1:A:249:ASP:N	2.31	0.64
1:A:548:ARG:HB3	1:A:876:ILE:HG23	1.78	0.64
1:B:371:ASN:C	1:B:373:GLN:N	2.52	0.64
1:B:645:PHE:HD2	1:B:646:LEU:HD23	1.62	0.64
1:B:718:TYR:HB3	1:B:721:VAL:CG2	2.18	0.64
2:F:109:ILE:HB	2:F:380:ASP:HB3	1.79	0.64
2:J:4:LEU:HA	2:J:7:LEU:CD1	2.28	0.64
2:J:9:LYS:O	2:J:13:ASP:HB2	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:12:LYS:HG2	2:K:16:ASP:OD2	1.97	0.64
2:M:139:TRP:NE1	2:M:143:ASN:ND2	2.46	0.64
1:A:246:HIS:HD2	1:A:248:ILE:HB	1.63	0.64
1:A:378:CYS:SG	1:A:584:LEU:HD13	2.38	0.64
1:A:770:SER:O	1:A:771:VAL:C	2.40	0.64
1:B:703:VAL:HG22	1:B:825:VAL:HG22	1.78	0.64
2:F:38:ILE:HG22	2:F:42:ASN:HD21	1.62	0.64
2:J:8:SER:C	2:J:10:THR:N	2.55	0.64
2:M:42:ASN:HA	2:M:61:PHE:HB3	1.80	0.64
2:N:128:ASN:O	2:N:129:PHE:HB3	1.98	0.64
1:A:606:VAL:HG23	1:A:607:ASN:N	2.13	0.64
1:B:182:LEU:HD11	1:B:847:THR:HA	1.78	0.64
1:B:389:GLN:HA	1:B:389:GLN:OE1	1.98	0.64
1:B:492:VAL:HG13	1:B:565:MET:SD	2.38	0.64
1:B:721:VAL:HG12	1:B:722:ASN:H	1.63	0.64
2:F:135:TYR:CZ	2:F:342:MET:HE3	2.33	0.64
2:M:12:LYS:HG2	2:M:16:ASP:OD2	1.98	0.64
1:A:360:ILE:HG23	1:A:363:GLU:HB2	1.78	0.64
1:A:563:MET:HE3	1:A:611:HIS:NE2	2.13	0.64
2:D:54:LEU:HD12	2:D:55:PRO:HD2	1.79	0.64
2:G:106:ARG:HG2	2:G:107:ASN:H	1.62	0.64
2:D:12:LYS:HG2	2:D:16:ASP:OD2	1.98	0.64
2:E:4:LEU:HA	2:E:7:LEU:CD1	2.28	0.64
2:H:57:ARG:HH11	2:H:94:ASN:HD21	1.44	0.64
2:K:4:LEU:HA	2:K:7:LEU:CD1	2.28	0.64
2:O:14:ALA:O	2:O:18:ILE:HD12	1.97	0.64
1:A:158:GLY:N	1:A:762:ALA:HB3	2.13	0.63
1:A:371:ASN:HB3	1:A:583:SER:HB2	1.80	0.63
1:A:784:ALA:O	1:A:785:GLN:C	2.41	0.63
1:B:491:GLN:HE22	1:B:566:GLN:HG2	1.63	0.63
1:B:498:ARG:CB	1:B:505:GLN:HE22	2.10	0.63
2:I:19:VAL:CG2	2:K:128:ASN:HB3	2.27	0.63
2:J:110:ALA:HB1	2:J:111:PRO:CD	2.28	0.63
2:L:12:LYS:HG2	2:L:16:ASP:OD2	1.98	0.63
2:M:27:VAL:O	2:M:31:ILE:HG12	1.97	0.63
1:A:772:ILE:O	1:A:775:ILE:HG13	1.98	0.63
1:B:346:ILE:O	1:B:349:MET:HB3	1.97	0.63
1:B:442:MET:HG2	1:B:443:GLN:H	1.63	0.63
1:B:645:PHE:CD2	1:B:646:LEU:HD23	2.33	0.63
2:F:4:LEU:HA	2:F:7:LEU:CD1	2.29	0.63
2:J:71:LEU:HG	2:J:72:ASN:OD1	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:8:SER:C	2:K:10:THR:N	2.55	0.63
2:M:4:LEU:HA	2:M:7:LEU:CD1	2.28	0.63
1:A:491:GLN:OE1	1:A:564:ASN:HB3	1.99	0.63
1:B:285:ILE:C	1:B:286:LEU:HD13	2.22	0.63
1:B:396:PHE:CE1	1:B:398:THR:HA	2.33	0.63
1:B:730:PHE:N	1:B:730:PHE:CD1	2.67	0.63
1:B:772:ILE:O	1:B:775:ILE:HB	1.98	0.63
2:F:110:ALA:HB1	2:F:111:PRO:HD2	1.80	0.63
2:I:145:ARG:HH11	2:I:145:ARG:CB	2.12	0.63
1:A:560:CYS:HB2	1:A:603:TYR:CD2	2.33	0.63
1:A:721:VAL:HG11	1:A:799:LEU:HD22	1.81	0.63
1:B:305:GLN:HG3	1:B:564:ASN:HD21	1.62	0.63
1:B:415:PRO:CB	1:B:480:PHE:HB2	2.28	0.63
1:B:503:ILE:HD11	1:B:548:ARG:CG	2.26	0.63
1:B:722:ASN:ND2	1:B:824:LYS:HA	2.10	0.63
2:D:109:ILE:HD12	2:D:109:ILE:O	1.99	0.63
2:F:12:LYS:HG2	2:F:16:ASP:OD2	1.99	0.63
2:O:141:LEU:HD12	2:O:148:THR:HG21	1.80	0.63
1:A:262:VAL:HG12	1:A:297:ARG:HB3	1.80	0.63
1:B:498:ARG:HD3	2:I:32:GLN:HE21	1.63	0.63
2:C:12:LYS:C	2:C:14:ALA:N	2.56	0.63
2:F:104:SER:O	2:F:105:GLN:HB2	1.98	0.63
2:L:346:VAL:HG21	2:L:385:VAL:HG13	1.81	0.63
1:A:197:GLY:O	1:A:198:LYS:C	2.42	0.63
1:A:521:MET:HA	1:A:521:MET:CE	2.26	0.63
1:B:231:ARG:HB3	1:B:240:ASN:HB2	1.80	0.63
1:B:422:GLU:HA	1:B:425:VAL:CG2	2.29	0.63
1:B:492:VAL:HG11	1:B:558:MET:SD	2.38	0.63
1:B:587:LEU:HG	1:B:587:LEU:O	1.97	0.63
1:B:701:GLN:HB2	1:B:826:TYR:CD2	2.29	0.63
1:B:735:LEU:HD21	1:B:759:LEU:HB3	1.80	0.63
1:A:513:LEU:HA	1:A:516:GLN:HE22	1.64	0.63
2:C:12:LYS:HG2	2:C:16:ASP:OD2	1.99	0.63
2:L:24:TYR:O	2:L:27:VAL:HG22	1.98	0.63
2:L:85:ILE:O	2:L:89:VAL:HG23	1.99	0.63
2:O:12:LYS:HG2	2:O:16:ASP:OD2	1.99	0.63
2:O:85:ILE:O	2:O:89:VAL:HG23	1.99	0.63
1:A:180:TYR:CD1	1:A:180:TYR:C	2.75	0.63
1:A:795:LEU:O	1:A:797:PRO:HD3	1.98	0.63
1:B:127:GLU:OE1	1:B:151:LYS:HE2	1.98	0.63
1:B:549:LEU:HD13	1:B:877:MET:CE	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:818:VAL:HG12	1:B:819:PRO:HD2	1.80	0.63
2:K:346:VAL:HG21	2:K:385:VAL:HG13	1.81	0.63
2:N:106:ARG:H	2:N:106:ARG:CD	1.99	0.63
2:O:147:ARG:HG2	2:O:148:THR:N	2.13	0.63
1:A:601:PHE:HD1	1:A:601:PHE:H	1.46	0.63
1:A:744:TYR:C	1:A:746:GLN:H	2.07	0.63
1:A:147:TYR:CE2	1:A:717:MET:HE2	2.34	0.62
1:A:328:LEU:HD11	1:A:606:VAL:HG21	1.80	0.62
1:A:416:ASN:HB3	1:A:424:LEU:CD2	2.29	0.62
1:B:274:ILE:HG23	1:B:278:ILE:CD1	2.24	0.62
1:B:457:GLN:CG	1:B:458:ILE:N	2.53	0.62
2:I:12:LYS:HG2	2:I:16:ASP:OD2	1.99	0.62
2:I:85:ILE:O	2:I:89:VAL:HG23	1.99	0.62
2:M:12:LYS:C	2:M:14:ALA:N	2.57	0.62
2:N:49:GLY:HA2	2:N:54:LEU:HD23	1.81	0.62
2:N:346:VAL:HG21	2:N:385:VAL:HG13	1.81	0.62
2:O:8:SER:C	2:O:10:THR:N	2.55	0.62
1:A:200:VAL:O	1:A:204:THR:OG1	2.17	0.62
1:A:721:VAL:HG13	1:A:800:TYR:O	1.98	0.62
1:A:810:TYR:O	1:A:812:VAL:N	2.32	0.62
1:B:95:ILE:HG22	1:B:97:THR:OG1	1.99	0.62
1:B:199:VAL:CG1	1:B:200:VAL:N	2.62	0.62
1:B:451:ASP:N	1:B:452:PRO:HD3	2.13	0.62
1:B:494:ASN:ND2	1:B:495:ASP:N	2.46	0.62
1:B:704:ILE:O	1:B:823:THR:OG1	2.17	0.62
1:B:812:VAL:HG22	1:B:813:ALA:N	2.13	0.62
2:D:68:THR:O	2:D:69:THR:C	2.41	0.62
2:J:346:VAL:HG21	2:J:385:VAL:HG13	1.81	0.62
2:O:135:TYR:CZ	2:O:342:MET:HE3	2.34	0.62
2:O:346:VAL:HG21	2:O:385:VAL:HG13	1.81	0.62
1:A:360:ILE:CG2	1:A:363:GLU:HB2	2.29	0.62
1:A:472:LEU:O	1:A:476:ASN:HB2	1.99	0.62
1:A:545:ASP:HA	1:A:548:ARG:HD2	1.80	0.62
1:A:839:MET:HE3	1:A:840:HIS:CA	2.29	0.62
1:B:596:SER:HB2	1:B:599:THR:OG1	1.99	0.62
2:C:135:TYR:CZ	2:C:342:MET:HE3	2.33	0.62
2:E:8:SER:C	2:E:10:THR:N	2.55	0.62
2:H:346:VAL:HG21	2:H:385:VAL:HG13	1.81	0.62
2:J:144:ARG:HD2	2:K:82:ARG:CZ	2.28	0.62
2:K:12:LYS:C	2:K:14:ALA:N	2.56	0.62
2:K:48:THR:HG22	2:K:115:SER:OG	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:135:TYR:OH	2:O:340:GLU:OE1	2.17	0.62
1:A:503:ILE:CD1	1:A:547:THR:HB	2.29	0.62
1:B:122:LEU:HD11	1:B:200:VAL:CG1	2.29	0.62
1:B:497:ILE:HG12	2:I:68:THR:HG23	1.82	0.62
1:B:681:ILE:O	1:B:684:LEU:HB3	1.99	0.62
1:B:723:ILE:O	1:B:824:LYS:HD2	2.00	0.62
2:C:21:GLY:O	2:C:22:THR:O	2.17	0.62
2:E:149:GLY:C	2:E:150:PHE:CD1	2.77	0.62
1:B:494:ASN:CG	1:B:495:ASP:H	2.07	0.62
2:C:8:SER:O	2:C:11:LEU:N	2.33	0.62
2:E:116:LEU:HA	2:E:119:LEU:HD12	1.81	0.62
2:H:109:ILE:O	2:H:109:ILE:CG1	2.48	0.62
2:I:346:VAL:HG21	2:I:385:VAL:HG13	1.81	0.62
2:L:4:LEU:HA	2:L:7:LEU:CD1	2.28	0.62
2:L:12:LYS:C	2:L:14:ALA:N	2.56	0.62
1:A:763:LEU:HD23	1:A:764:PRO:HD3	1.80	0.62
1:B:432:VAL:HA	1:B:436:ILE:CD1	2.12	0.62
1:B:692:ILE:HD12	1:B:692:ILE:H	1.63	0.62
1:B:717:MET:HE3	1:B:718:TYR:HE1	1.64	0.62
2:J:85:ILE:O	2:J:89:VAL:HG23	1.99	0.62
2:K:62:ASP:CG	2:K:62:ASP:O	2.42	0.62
1:A:366:PHE:C	1:A:368:THR:N	2.48	0.62
1:B:140:LYS:C	1:B:142:LEU:H	2.06	0.62
1:B:371:ASN:HA	1:B:374:ALA:HB3	1.82	0.62
1:B:435:ILE:O	1:B:436:ILE:HG12	2.00	0.62
2:D:12:LYS:C	2:D:14:ALA:N	2.56	0.62
2:F:8:SER:C	2:F:10:THR:N	2.55	0.62
1:A:596:SER:O	1:A:600:LEU:HD12	1.99	0.62
2:F:346:VAL:HG21	2:F:385:VAL:HG13	1.81	0.62
2:H:4:LEU:HA	2:H:7:LEU:CD1	2.28	0.62
2:H:76:ASN:CB	2:J:76:ASN:HB2	2.30	0.62
2:I:8:SER:C	2:I:10:THR:N	2.56	0.62
2:I:23:LEU:HD23	2:I:24:TYR:H	1.65	0.62
2:J:22:THR:HG22	2:J:73:LEU:HD12	1.81	0.62
2:L:38:ILE:HD12	2:L:65:LEU:CD2	2.29	0.62
2:N:8:SER:O	2:N:11:LEU:N	2.33	0.62
1:B:634:TYR:O	1:B:635:GLN:HG2	1.99	0.62
2:G:46:PHE:HE2	2:G:119:LEU:HD21	1.63	0.62
2:H:12:LYS:HG2	2:H:16:ASP:OD2	2.00	0.62
2:M:346:VAL:HG21	2:M:385:VAL:HG13	1.81	0.62
2:O:23:LEU:HD23	2:O:24:TYR:N	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:ARG:HH22	1:A:736:GLU:CD	2.07	0.62
1:A:587:LEU:C	1:A:588:ILE:HG13	2.24	0.62
1:A:692:ILE:H	1:A:692:ILE:HD12	1.64	0.62
1:B:240:ASN:HA	1:B:842:LEU:O	2.00	0.62
1:B:477:ASN:O	1:B:478:ASN:C	2.43	0.62
1:B:591:ALA:O	1:B:877:MET:HE3	1.98	0.62
1:B:722:ASN:O	1:B:824:LYS:HB2	1.99	0.62
2:D:27:VAL:O	2:D:31:ILE:HG12	1.99	0.62
2:L:109:ILE:HD12	2:L:109:ILE:O	1.99	0.62
1:B:503:ILE:HG21	1:B:544:VAL:HG13	1.80	0.61
1:B:839:MET:SD	1:B:839:MET:C	2.83	0.61
2:E:12:LYS:HG2	2:E:16:ASP:OD2	1.99	0.61
1:A:568:VAL:HG12	1:A:569:GLN:N	2.14	0.61
1:B:277:ARG:C	1:B:278:ILE:HG12	2.23	0.61
1:B:863:VAL:HG12	1:B:864:GLU:H	1.65	0.61
2:G:27:VAL:O	2:G:31:ILE:HG12	2.01	0.61
2:L:22:THR:HG23	2:L:73:LEU:CD1	2.23	0.61
2:M:116:LEU:HA	2:M:119:LEU:HD12	1.82	0.61
2:M:145:ARG:HB3	2:M:145:ARG:CZ	2.31	0.61
2:N:66:LEU:HD13	2:N:77:TYR:OH	2.00	0.61
1:A:362:SER:CB	1:A:365:GLN:NE2	2.63	0.61
1:A:447:TYR:OH	1:A:458:ILE:HG23	2.01	0.61
1:B:94:THR:O	1:B:316:SER:HB3	2.01	0.61
1:B:182:LEU:HD21	1:B:846:LEU:HA	1.82	0.61
1:B:194:ARG:HA	1:B:194:ARG:CZ	2.30	0.61
1:B:415:PRO:HG2	1:B:480:PHE:CD1	2.30	0.61
1:B:428:GLN:HB2	1:B:456:PHE:HD1	1.61	0.61
2:D:23:LEU:HD23	2:D:24:TYR:H	1.62	0.61
2:D:346:VAL:HG21	2:D:385:VAL:HG13	1.81	0.61
2:E:8:SER:O	2:E:11:LEU:N	2.34	0.61
2:E:346:VAL:HG21	2:E:385:VAL:HG13	1.81	0.61
2:J:12:LYS:C	2:J:14:ALA:N	2.55	0.61
2:G:12:LYS:HG2	2:G:16:ASP:OD2	1.99	0.61
2:J:116:LEU:HA	2:J:119:LEU:HD12	1.82	0.61
2:K:8:SER:O	2:K:11:LEU:N	2.34	0.61
2:O:38:ILE:HG22	2:O:42:ASN:HD21	1.64	0.61
1:A:389:GLN:HG3	1:A:389:GLN:O	2.00	0.61
1:A:765:PHE:CD1	1:A:765:PHE:C	2.79	0.61
1:B:521:MET:HB2	1:B:522:PRO:HD2	1.81	0.61
2:E:12:LYS:C	2:E:14:ALA:N	2.56	0.61
2:G:38:ILE:HG22	2:G:42:ASN:HD21	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:128:ASN:HB3	2:H:19:VAL:HG23	1.81	0.61
2:I:116:LEU:HA	2:I:119:LEU:HD12	1.82	0.61
2:L:8:SER:O	2:L:11:LEU:N	2.33	0.61
2:M:63:PHE:CD2	2:M:84:THR:HG23	2.35	0.61
2:O:8:SER:O	2:O:11:LEU:N	2.34	0.61
1:B:297:ARG:HG3	1:B:848:PHE:CD2	2.29	0.61
1:B:556:THR:O	1:B:557:LEU:C	2.44	0.61
2:D:85:ILE:O	2:D:89:VAL:HG23	2.01	0.61
1:A:135:ARG:O	1:A:136:ALA:C	2.44	0.61
1:B:545:ASP:HA	1:B:548:ARG:HD2	1.82	0.61
1:A:257:LEU:HD13	1:A:843:THR:O	2.01	0.61
1:A:282:VAL:O	1:A:284:TYR:N	2.34	0.61
1:A:443:GLN:O	1:A:445:MET:N	2.34	0.61
1:A:450:GLY:O	1:A:451:ASP:HB2	2.01	0.61
1:B:496:ASN:HB3	1:B:498:ARG:HB3	1.83	0.61
2:D:8:SER:C	2:D:10:THR:N	2.54	0.61
2:O:147:ARG:O	2:O:148:THR:HB	1.99	0.61
2:O:150:PHE:N	2:O:150:PHE:CD1	2.69	0.61
1:A:125:ILE:HD13	1:A:126:PHE:HE2	1.66	0.61
1:A:729:GLY:C	1:A:730:PHE:CD1	2.78	0.61
1:B:272:ASN:C	1:B:274:ILE:N	2.54	0.61
2:H:108:GLY:C	2:H:110:ALA:H	2.09	0.61
2:J:6:SER:OG	2:J:128:ASN:HA	2.00	0.61
2:L:72:ASN:ND2	2:N:126:ARG:HH11	1.99	0.61
2:O:116:LEU:HA	2:O:119:LEU:HD12	1.82	0.61
1:A:701:GLN:HB3	1:A:826:TYR:HD2	1.66	0.61
1:B:96:PRO:O	1:B:320:THR:HG21	1.99	0.61
1:B:523:VAL:O	1:B:525:TYR:N	2.34	0.61
1:B:744:TYR:O	1:B:745:ALA:HB3	2.00	0.61
1:B:870:ALA:C	1:B:872:ASP:N	2.56	0.61
2:G:346:VAL:HG21	2:G:385:VAL:HG13	1.81	0.61
2:I:19:VAL:HG23	2:K:128:ASN:HB3	1.83	0.61
2:J:8:SER:O	2:J:11:LEU:N	2.34	0.61
2:K:152:PHE:N	2:K:152:PHE:CD1	2.69	0.61
2:L:8:SER:C	2:L:10:THR:N	2.55	0.61
2:M:8:SER:C	2:M:10:THR:N	2.55	0.61
2:N:116:LEU:HA	2:N:119:LEU:HD12	1.82	0.61
1:A:434:THR:O	1:A:434:THR:HG22	2.00	0.60
1:A:570:THR:CG2	1:A:571:LEU:H	2.12	0.60
1:A:817:TRP:CG	1:A:818:VAL:N	2.65	0.60
1:B:133:ILE:CD1	1:B:145:ARG:HB2	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:ASP:CG	1:B:153:ASP:O	2.43	0.60
1:B:180:TYR:CD1	1:B:181:LEU:N	2.68	0.60
1:B:333:VAL:HG11	1:B:380:LYS:HA	1.83	0.60
1:B:482:GLN:CB	1:B:493:LEU:HD22	2.30	0.60
1:B:673:PRO:C	1:B:674:VAL:HG22	2.26	0.60
2:E:150:PHE:HB2	2:E:152:PHE:CZ	2.37	0.60
2:N:109:ILE:HB	2:N:380:ASP:HB3	1.82	0.60
1:A:319:ASP:OD2	1:A:571:LEU:HB3	2.00	0.60
1:A:403:SER:HA	1:A:582:THR:OG1	2.00	0.60
1:A:503:ILE:C	1:A:505:GLN:N	2.55	0.60
1:A:631:LEU:HB3	1:A:633:LEU:CD1	2.31	0.60
1:A:817:TRP:CH2	1:A:819:PRO:HA	2.36	0.60
1:B:156:PRO:HB2	1:B:161:ASP:CB	2.30	0.60
1:B:364:THR:HG21	3:W:622:ALA:HA	1.83	0.60
1:B:503:ILE:HD13	1:B:544:VAL:CG1	2.31	0.60
1:B:527:ARG:O	1:B:531:ARG:CG	2.49	0.60
1:B:779:ASP:HA	1:B:798:ILE:HD11	1.82	0.60
2:C:346:VAL:HG21	2:C:385:VAL:HG13	1.81	0.60
2:F:109:ILE:HD12	2:F:109:ILE:O	2.01	0.60
2:H:142:GLN:HE21	2:H:143:ASN:N	1.98	0.60
2:L:150:PHE:HB2	2:L:152:PHE:HE1	1.60	0.60
2:M:49:GLY:HA2	2:M:54:LEU:CD2	2.31	0.60
1:A:122:LEU:HD11	1:A:200:VAL:HG12	1.82	0.60
1:A:625:ILE:O	1:A:628:ALA:HB3	2.00	0.60
1:A:757:VAL:HG12	1:A:758:ALA:N	2.17	0.60
1:A:779:ASP:HA	1:A:798:ILE:HD11	1.80	0.60
1:B:118:LYS:CG	1:B:119:GLN:H	2.13	0.60
1:B:684:LEU:O	1:B:687:MET:HG2	2.02	0.60
2:D:133:SER:O	2:D:135:TYR:N	2.35	0.60
2:G:12:LYS:C	2:G:14:ALA:N	2.57	0.60
1:A:355:LEU:HD13	1:A:363:GLU:HG2	1.83	0.60
1:B:424:LEU:HD12	1:B:424:LEU:O	2.01	0.60
2:E:57:ARG:HH11	2:E:94:ASN:HD21	1.49	0.60
2:I:153:HIS:NE2	2:J:153:HIS:NE2	2.50	0.60
2:M:5:TYR:CE2	2:M:131:ASN:HA	2.37	0.60
2:M:8:SER:O	2:M:11:LEU:N	2.34	0.60
1:B:266:ASN:O	1:B:267:ASN:C	2.45	0.60
1:B:275:PRO:HD2	1:B:278:ILE:HD11	1.83	0.60
1:B:875:ARG:HD3	1:B:878:ASN:HD22	1.66	0.60
2:E:133:SER:O	2:E:135:TYR:N	2.35	0.60
2:F:12:LYS:C	2:F:14:ALA:N	2.56	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:116:LEU:HA	2:L:119:LEU:HD12	1.83	0.60
2:O:24:TYR:HB2	2:O:71:LEU:HD12	1.83	0.60
1:A:437:TYR:CD2	1:A:442:MET:HG3	2.36	0.60
1:B:389:GLN:NE2	1:B:567:HIS:HA	2.17	0.60
1:B:604:TYR:O	1:B:608:VAL:HG23	2.00	0.60
2:D:8:SER:O	2:D:11:LEU:N	2.34	0.60
2:E:129:PHE:CD1	2:E:129:PHE:C	2.80	0.60
2:H:8:SER:O	2:H:11:LEU:N	2.34	0.60
2:N:27:VAL:O	2:N:30:LEU:N	2.34	0.60
2:N:157:ILE:HG12	2:N:214:LEU:HD13	1.84	0.60
1:A:203:GLU:O	1:A:207:ILE:HG13	2.02	0.60
1:B:371:ASN:HD22	1:B:583:SER:CB	2.10	0.60
1:B:674:VAL:CG2	1:B:679:LEU:HD13	2.27	0.60
1:B:874:MET:O	1:B:875:ARG:CB	2.50	0.60
2:E:85:ILE:O	2:E:89:VAL:HG23	2.01	0.60
2:F:104:SER:HB3	2:F:108:GLY:HA3	1.84	0.60
2:H:23:LEU:H	2:H:26:ASN:ND2	2.00	0.60
2:I:68:THR:HG22	2:I:69:THR:N	2.16	0.60
2:L:73:LEU:HD22	2:L:77:TYR:CD2	2.36	0.60
2:M:145:ARG:HB3	2:M:145:ARG:NH1	2.16	0.60
1:A:237:ASN:OD1	1:A:237:ASN:O	2.20	0.60
1:A:326:TYR:CD1	1:A:384:ALA:HB1	2.36	0.60
1:A:492:VAL:CG1	1:A:558:MET:SD	2.90	0.60
1:A:546:LEU:CD1	1:A:584:LEU:HD23	2.32	0.60
1:A:727:LEU:HD12	1:A:727:LEU:O	2.02	0.60
1:B:274:ILE:CG2	1:B:278:ILE:HD11	2.25	0.60
1:B:387:LEU:HD23	1:B:554:TYR:CE1	2.36	0.60
1:B:743:ASP:OD2	1:B:745:ALA:HA	2.01	0.60
2:C:133:SER:O	2:C:135:TYR:N	2.34	0.60
2:D:116:LEU:HA	2:D:119:LEU:HD12	1.82	0.60
2:F:133:SER:O	2:F:135:TYR:N	2.35	0.60
2:G:157:ILE:HG12	2:G:214:LEU:HD13	1.84	0.60
2:J:110:ALA:HB1	2:J:111:PRO:HD2	1.83	0.60
2:K:5:TYR:CE2	2:K:131:ASN:HA	2.37	0.60
2:K:116:LEU:HA	2:K:119:LEU:HD12	1.84	0.60
2:M:274:GLN:N	2:M:274:GLN:HE21	2.00	0.60
1:A:666:ARG:HG3	1:A:667:ASP:N	2.14	0.60
1:A:822:THR:C	1:A:823:THR:HG23	2.26	0.60
1:B:435:ILE:CG2	1:B:436:ILE:H	2.09	0.60
1:B:502:VAL:O	1:B:504:ASN:N	2.35	0.60
1:B:723:ILE:O	1:B:724:ALA:HB2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:868:ALA:C	1:B:876:ILE:HG23	2.26	0.60
2:D:38:ILE:HG22	2:D:42:ASN:HD21	1.67	0.60
2:E:157:ILE:HG12	2:E:214:LEU:HD13	1.84	0.60
2:H:8:SER:C	2:H:10:THR:N	2.56	0.60
2:J:14:ALA:C	2:J:16:ASP:H	2.10	0.60
2:J:133:SER:O	2:J:135:TYR:N	2.35	0.60
2:J:274:GLN:N	2:J:274:GLN:HE21	2.00	0.60
1:A:535:LEU:O	1:A:539:ARG:HG2	2.02	0.60
1:B:555:GLU:OE2	1:B:871:PHE:HE2	1.85	0.60
1:B:601:PHE:H	1:B:601:PHE:HD1	1.47	0.60
1:B:675:GLU:O	1:B:676:VAL:C	2.44	0.60
2:F:157:ILE:HG12	2:F:214:LEU:HD13	1.84	0.60
2:G:73:LEU:HD22	2:G:77:TYR:CD2	2.37	0.60
2:H:5:TYR:CE2	2:H:131:ASN:HA	2.37	0.60
2:I:12:LYS:C	2:I:14:ALA:N	2.56	0.60
2:K:133:SER:O	2:K:135:TYR:N	2.35	0.60
2:M:152:PHE:N	2:M:152:PHE:CD1	2.70	0.60
1:A:604:TYR:O	1:A:608:VAL:HG23	2.01	0.59
1:B:482:GLN:HG3	1:B:482:GLN:O	2.02	0.59
1:B:508:GLU:OE2	2:J:71:LEU:HB3	2.02	0.59
1:B:535:LEU:O	1:B:539:ARG:HG2	2.01	0.59
2:C:85:ILE:O	2:C:89:VAL:HG23	2.01	0.59
2:C:274:GLN:N	2:C:274:GLN:HE21	2.00	0.59
2:D:128:ASN:ND2	2:E:19:VAL:HG21	2.17	0.59
2:G:111:PRO:HB3	2:G:116:LEU:HD23	1.83	0.59
2:G:135:TYR:CZ	2:G:342:MET:HE3	2.37	0.59
2:H:133:SER:O	2:H:135:TYR:N	2.35	0.59
2:N:8:SER:C	2:N:10:THR:N	2.55	0.59
1:A:577:GLN:O	1:A:581:VAL:HG23	2.01	0.59
1:B:122:LEU:HG	1:B:201:ASP:CG	2.27	0.59
1:B:513:LEU:HA	1:B:516:GLN:OE1	2.01	0.59
2:D:76:ASN:HB2	2:L:76:ASN:HB2	1.83	0.59
2:H:152:PHE:N	2:H:152:PHE:CD1	2.69	0.59
2:I:60:ASN:C	2:I:61:PHE:CD1	2.80	0.59
2:I:157:ILE:HG12	2:I:214:LEU:HD13	1.84	0.59
2:L:19:VAL:CG2	2:N:128:ASN:HB3	2.32	0.59
2:M:24:TYR:O	2:M:27:VAL:HG22	2.02	0.59
1:A:246:HIS:CD2	1:A:248:ILE:HB	2.36	0.59
1:A:548:ARG:HH11	1:A:877:MET:CA	2.14	0.59
1:A:643:GLU:CG	1:A:662:MET:HE1	2.26	0.59
1:A:744:TYR:O	1:A:746:GLN:N	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:747:ILE:HD11	1:A:786:ILE:HG21	1.85	0.59
1:B:363:GLU:HA	1:B:363:GLU:OE1	2.02	0.59
1:B:401:TYR:O	1:B:404:LEU:HB2	2.02	0.59
1:B:787:VAL:O	1:B:788:LYS:C	2.46	0.59
1:B:863:VAL:HG12	1:B:864:GLU:N	2.17	0.59
2:C:14:ALA:C	2:C:16:ASP:H	2.10	0.59
2:C:131:ASN:HD22	2:C:131:ASN:N	1.99	0.59
2:G:8:SER:C	2:G:10:THR:N	2.56	0.59
2:G:85:ILE:O	2:G:89:VAL:HG23	2.01	0.59
2:H:274:GLN:N	2:H:274:GLN:HE21	2.00	0.59
2:M:133:SER:O	2:M:135:TYR:N	2.35	0.59
2:N:85:ILE:O	2:N:89:VAL:HG23	2.02	0.59
2:N:274:GLN:N	2:N:274:GLN:HE21	2.00	0.59
1:A:703:VAL:HG21	1:A:797:PRO:HB3	1.84	0.59
1:B:543:LEU:HD23	1:B:546:LEU:HD12	1.84	0.59
2:F:23:LEU:HD11	2:H:36:GLN:HB2	1.85	0.59
1:A:415:PRO:HB3	1:A:479:GLN:HA	1.84	0.59
1:A:545:ASP:O	1:A:548:ARG:N	2.35	0.59
1:A:700:ALA:O	1:A:701:GLN:HB2	2.02	0.59
1:A:839:MET:HG2	1:A:840:HIS:N	2.16	0.59
1:B:383:ILE:HD11	1:B:550:LEU:CD2	2.32	0.59
2:D:70:LEU:HD12	2:D:71:LEU:N	2.17	0.59
2:L:53:ASN:HD22	2:L:354:ALA:HB3	1.66	0.59
2:L:157:ILE:HG12	2:L:214:LEU:HD13	1.84	0.59
1:A:371:ASN:O	1:A:373:GLN:N	2.36	0.59
1:A:548:ARG:NH1	1:A:877:MET:HA	2.17	0.59
1:A:744:TYR:C	1:A:746:GLN:N	2.60	0.59
1:B:141:GLU:O	1:B:142:LEU:HB2	2.03	0.59
1:B:368:THR:O	1:B:371:ASN:ND2	2.36	0.59
1:B:393:SER:HB3	1:B:573:THR:HG21	1.84	0.59
2:D:104:SER:O	2:D:108:GLY:HA3	2.02	0.59
2:M:74:ASP:OD2	2:M:76:ASN:HB3	2.03	0.59
2:M:135:TYR:OH	2:M:340:GLU:OE1	2.20	0.59
2:O:274:GLN:HE21	2:O:274:GLN:N	2.00	0.59
1:A:160:TYR:CZ	1:A:635:GLN:HB2	2.38	0.59
1:A:803:ASN:H	1:A:807:ASN:ND2	2.00	0.59
1:B:190:ASN:HD21	1:B:193:SER:CB	2.10	0.59
1:B:498:ARG:HH22	2:J:25:SER:H	1.49	0.59
2:C:5:TYR:CE2	2:C:131:ASN:HA	2.36	0.59
2:D:157:ILE:HG12	2:D:214:LEU:HD13	1.84	0.59
2:J:157:ILE:HG12	2:J:214:LEU:HD13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:157:ILE:HG12	2:K:214:LEU:HD13	1.84	0.59
2:L:130:ASP:HA	2:M:17:LYS:HG2	1.83	0.59
1:A:368:THR:HG21	1:A:582:THR:HB	1.83	0.59
1:A:413:VAL:HG12	1:A:414:VAL:N	2.17	0.59
1:A:464:GLN:HG3	2:F:39:ILE:HD11	1.84	0.59
1:B:506:LEU:HD21	1:B:543:LEU:C	2.27	0.59
2:D:76:ASN:H	2:L:76:ASN:HB2	1.67	0.59
2:E:274:GLN:N	2:E:274:GLN:HE21	2.00	0.59
2:H:157:ILE:HG12	2:H:214:LEU:HD13	1.84	0.59
2:J:124:PHE:O	2:J:127:ILE:HG13	2.03	0.59
1:A:322:THR:HG21	1:A:390:ARG:HA	1.83	0.59
1:A:467:GLN:HE21	1:A:511:MET:HG2	1.67	0.59
1:A:520:THR:HG21	1:A:526:LYS:HD3	1.85	0.59
1:A:545:ASP:HA	1:A:548:ARG:CD	2.33	0.59
1:A:633:LEU:C	1:A:635:GLN:H	2.11	0.59
1:A:771:VAL:HG22	1:A:772:ILE:N	2.18	0.59
1:B:833:PHE:CZ	1:B:835:PHE:HA	2.38	0.59
2:F:8:SER:O	2:F:11:LEU:N	2.36	0.59
2:F:274:GLN:N	2:F:274:GLN:HE21	2.00	0.59
2:G:71:LEU:HG	2:G:72:ASN:N	2.17	0.59
2:G:152:PHE:CD1	2:G:152:PHE:N	2.71	0.59
2:H:85:ILE:O	2:H:89:VAL:HG23	2.03	0.59
2:L:274:GLN:HE21	2:L:274:GLN:N	2.00	0.59
2:O:4:LEU:HG	2:O:391:ILE:HG21	1.85	0.59
2:O:12:LYS:C	2:O:14:ALA:N	2.57	0.59
1:A:242:PRO:HA	1:A:841:MET:SD	2.42	0.59
1:A:401:TYR:O	1:A:404:LEU:HB2	2.02	0.59
1:A:546:LEU:HD11	1:A:588:ILE:HD12	1.83	0.59
1:A:722:ASN:HD22	1:A:824:LYS:HA	1.68	0.59
1:A:810:TYR:CD1	1:A:811:LEU:N	2.71	0.59
1:B:803:ASN:N	1:B:807:ASN:ND2	2.48	0.59
2:I:152:PHE:N	2:I:152:PHE:CD1	2.70	0.59
2:M:38:ILE:HG22	2:M:42:ASN:HD21	1.67	0.59
2:N:14:ALA:C	2:N:16:ASP:H	2.10	0.59
2:N:109:ILE:HD12	2:N:109:ILE:O	2.03	0.59
2:O:100:MET:HG3	2:O:388:VAL:HG11	1.85	0.59
1:A:437:TYR:CE2	1:A:442:MET:HG3	2.37	0.58
1:A:484:VAL:HG12	1:A:485:ILE:H	1.68	0.58
1:A:501:HIS:C	1:A:503:ILE:H	2.09	0.58
1:A:571:LEU:HD23	1:B:531:ARG:NH2	2.17	0.58
1:A:803:ASN:O	1:A:805:ASP:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:326:TYR:CD1	1:B:384:ALA:HB1	2.37	0.58
1:B:745:ALA:HB1	1:B:748:THR:CB	2.31	0.58
2:F:14:ALA:C	2:F:16:ASP:H	2.11	0.58
2:F:116:LEU:HA	2:F:119:LEU:HD12	1.85	0.58
2:G:153:HIS:NE2	2:H:153:HIS:NE2	2.51	0.58
2:H:116:LEU:HA	2:H:119:LEU:HD12	1.84	0.58
1:A:428:GLN:NE2	1:A:455:PRO:CB	2.59	0.58
1:A:508:GLU:O	1:A:512:GLN:HG3	2.02	0.58
1:A:571:LEU:HD23	1:B:531:ARG:CZ	2.32	0.58
1:B:437:TYR:CD2	1:B:443:GLN:HB3	2.38	0.58
1:B:463:ILE:HG21	1:B:468:VAL:HG11	1.84	0.58
1:B:717:MET:HE3	1:B:718:TYR:CE1	2.37	0.58
1:B:875:ARG:HD3	1:B:878:ASN:ND2	2.18	0.58
2:C:157:ILE:HG12	2:C:214:LEU:HD13	1.84	0.58
2:D:14:ALA:C	2:D:16:ASP:H	2.11	0.58
2:G:274:GLN:HE21	2:G:274:GLN:N	2.00	0.58
2:H:22:THR:HG23	2:H:73:LEU:HD12	1.83	0.58
1:A:420:ILE:CD1	1:A:422:GLU:HG3	2.33	0.58
1:A:661:GLN:HG3	1:B:348:LYS:HZ1	1.67	0.58
1:B:111:ILE:HG22	1:B:113:PRO:HD3	1.84	0.58
1:B:112:LYS:N	1:B:113:PRO:HD3	2.18	0.58
1:B:190:ASN:O	1:B:192:ASN:N	2.37	0.58
1:B:223:ARG:O	1:B:226:ALA:HB3	2.03	0.58
1:B:421:ARG:O	1:B:425:VAL:HG23	2.02	0.58
1:B:501:HIS:C	1:B:503:ILE:N	2.60	0.58
2:C:67:GLY:C	2:C:69:THR:H	2.09	0.58
2:D:274:GLN:HE21	2:D:274:GLN:N	2.00	0.58
2:E:152:PHE:N	2:E:152:PHE:CD1	2.71	0.58
2:K:14:ALA:C	2:K:16:ASP:H	2.11	0.58
2:K:260:GLU:HG2	2:K:274:GLN:HG3	1.85	0.58
2:L:5:TYR:CE2	2:L:131:ASN:HA	2.37	0.58
2:M:85:ILE:O	2:M:89:VAL:HG23	2.02	0.58
2:M:157:ILE:HG12	2:M:214:LEU:HD13	1.84	0.58
1:B:653:ASP:O	1:B:654:VAL:C	2.46	0.58
2:C:8:SER:C	2:C:10:THR:N	2.55	0.58
2:D:130:ASP:HA	2:E:17:LYS:HG2	1.84	0.58
2:F:5:TYR:CE2	2:F:131:ASN:HA	2.38	0.58
2:G:133:SER:O	2:G:135:TYR:N	2.35	0.58
2:I:10:THR:O	2:I:14:ALA:HB2	2.04	0.58
2:K:145:ARG:O	2:K:146:GLN:HG2	2.02	0.58
2:L:17:LYS:HG2	2:N:130:ASP:HA	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ILE:O	1:A:245:LEU:HD23	2.03	0.58
1:A:259:HIS:CD2	1:A:677:ARG:HG3	2.38	0.58
1:B:218:GLU:O	1:B:221:VAL:HG23	2.03	0.58
2:F:130:ASP:HA	2:G:17:LYS:HG2	1.85	0.58
2:G:116:LEU:HA	2:G:119:LEU:HD12	1.84	0.58
2:L:74:ASP:OD2	2:L:76:ASN:HB3	2.03	0.58
2:O:157:ILE:HG12	2:O:214:LEU:HD13	1.84	0.58
1:A:160:TYR:OH	1:A:635:GLN:HB2	2.04	0.58
1:A:188:VAL:HG12	1:A:189:GLU:N	2.17	0.58
1:A:306:ASP:C	1:A:308:LEU:N	2.56	0.58
1:B:508:GLU:O	1:B:512:GLN:HG3	2.04	0.58
2:E:22:THR:HG23	2:E:73:LEU:HD12	1.86	0.58
2:K:49:GLY:HA3	2:K:55:PRO:O	2.03	0.58
2:M:128:ASN:O	2:N:22:THR:HB	2.03	0.58
2:N:133:SER:O	2:N:135:TYR:N	2.36	0.58
1:A:839:MET:HE3	1:A:840:HIS:N	2.18	0.58
1:B:371:ASN:HB3	1:B:583:SER:HB2	1.86	0.58
1:B:772:ILE:CG2	1:B:773:SER:N	2.66	0.58
2:C:116:LEU:HA	2:C:119:LEU:HD12	1.84	0.58
2:D:99:GLU:CD	2:D:116:LEU:HD22	2.28	0.58
2:F:85:ILE:O	2:F:89:VAL:HG23	2.04	0.58
2:I:260:GLU:HG2	2:I:274:GLN:HG3	1.86	0.58
2:J:5:TYR:HE2	2:J:131:ASN:HA	1.69	0.58
2:K:85:ILE:O	2:K:89:VAL:HG23	2.02	0.58
2:O:260:GLU:HG2	2:O:274:GLN:HG3	1.86	0.58
1:A:467:GLN:HE22	1:A:511:MET:HE3	1.69	0.58
1:A:613:ASN:HD22	1:A:649:LEU:HD23	1.69	0.58
1:B:340:VAL:HB	1:B:587:LEU:HD12	1.84	0.58
1:B:416:ASN:O	1:B:418:MET:N	2.36	0.58
2:F:260:GLU:HG2	2:F:274:GLN:HG3	1.86	0.58
2:G:8:SER:O	2:G:11:LEU:N	2.36	0.58
2:J:116:LEU:HD12	2:J:119:LEU:HD12	1.86	0.58
2:L:133:SER:O	2:L:135:TYR:N	2.36	0.58
2:L:150:PHE:HA	2:M:397:LYS:HZ1	1.68	0.58
2:N:116:LEU:HD12	2:N:119:LEU:HD12	1.86	0.58
1:A:303:LEU:HA	1:A:615:ASN:HD22	1.67	0.58
1:A:304:LEU:N	1:A:615:ASN:HD21	2.02	0.58
1:A:365:GLN:HB2	1:A:366:PHE:CZ	2.39	0.58
1:A:420:ILE:CG1	1:A:423:SER:HB2	2.32	0.58
1:A:568:VAL:HG12	1:A:569:GLN:H	1.68	0.58
1:A:771:VAL:O	1:A:772:ILE:C	2.46	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:140:LYS:C	1:B:142:LEU:N	2.60	0.58
1:B:190:ASN:HB2	1:B:199:VAL:HG23	1.85	0.58
1:B:459:ALA:O	1:B:463:ILE:HG13	2.03	0.58
1:B:492:VAL:HG21	1:B:558:MET:HE3	1.84	0.58
1:B:696:SER:O	1:B:827:LYS:HE3	2.04	0.58
2:C:7:LEU:O	2:C:11:LEU:HG	2.04	0.58
2:C:260:GLU:HG2	2:C:274:GLN:HG3	1.86	0.58
2:J:10:THR:O	2:J:14:ALA:HB2	2.04	0.58
2:O:14:ALA:C	2:O:16:ASP:H	2.11	0.58
2:O:133:SER:O	2:O:135:TYR:N	2.36	0.58
1:A:390:ARG:HD2	1:A:570:THR:HG21	1.84	0.58
1:A:803:ASN:H	1:A:807:ASN:HD22	1.50	0.58
1:B:491:GLN:HE22	1:B:566:GLN:CG	2.16	0.58
2:I:38:ILE:HG22	2:I:42:ASN:ND2	2.16	0.57
2:I:274:GLN:N	2:I:274:GLN:HE21	2.00	0.57
2:K:53:ASN:HD22	2:K:354:ALA:CB	2.17	0.57
2:K:274:GLN:N	2:K:274:GLN:HE21	2.01	0.57
2:L:104:SER:HB3	2:L:108:GLY:HA2	1.86	0.57
1:A:527:ARG:O	1:A:531:ARG:CG	2.51	0.57
1:A:681:ILE:O	1:A:684:LEU:HB3	2.03	0.57
1:B:199:VAL:CG1	1:B:200:VAL:H	2.17	0.57
1:B:458:ILE:HD12	1:B:458:ILE:C	2.29	0.57
1:B:577:GLN:C	1:B:579:THR:N	2.60	0.57
2:D:260:GLU:HG2	2:D:274:GLN:HG3	1.86	0.57
2:I:8:SER:O	2:I:11:LEU:N	2.36	0.57
2:I:133:SER:O	2:I:135:TYR:N	2.36	0.57
2:K:65:LEU:C	2:K:66:LEU:HG	2.29	0.57
2:M:260:GLU:HG2	2:M:274:GLN:HG3	1.86	0.57
1:A:548:ARG:NH1	1:A:878:ASN:H	2.01	0.57
1:A:550:LEU:O	1:A:551:ALA:C	2.47	0.57
1:B:254:GLU:HG2	2:N:69:THR:CB	2.34	0.57
1:B:415:PRO:HB2	1:B:480:PHE:HB2	1.86	0.57
1:B:434:THR:HG22	1:B:434:THR:O	2.04	0.57
1:B:472:LEU:O	1:B:476:ASN:HB2	2.04	0.57
2:E:260:GLU:HG2	2:E:274:GLN:HG3	1.86	0.57
2:F:144:ARG:HD2	2:G:82:ARG:NH1	2.19	0.57
2:G:10:THR:O	2:G:14:ALA:HB2	2.05	0.57
2:K:8:SER:O	2:K:10:THR:N	2.38	0.57
2:K:10:THR:O	2:K:14:ALA:HB2	2.05	0.57
2:N:76:ASN:HB2	2:O:76:ASN:H	1.69	0.57
1:A:647:LYS:C	1:A:649:LEU:H	2.12	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:139:TRP:C	2:J:139:TRP:CD1	2.83	0.57
2:L:144:ARG:O	2:L:145:ARG:CB	2.48	0.57
1:A:127:GLU:OE2	1:A:151:LYS:HG2	2.03	0.57
1:A:342:THR:HG21	3:W:967:ILE:HG22	1.87	0.57
1:A:428:GLN:CD	1:A:456:PHE:HB2	2.27	0.57
1:A:503:ILE:HG22	1:A:506:LEU:HB2	1.86	0.57
1:A:738:LEU:O	1:A:740:ARG:N	2.37	0.57
1:A:771:VAL:CG1	1:A:809:PHE:HB3	2.34	0.57
1:B:504:ASN:O	1:B:505:GLN:C	2.46	0.57
2:C:116:LEU:HD12	2:C:119:LEU:HD12	1.86	0.57
2:H:12:LYS:C	2:H:14:ALA:N	2.56	0.57
2:J:129:PHE:CD1	2:J:129:PHE:C	2.82	0.57
2:K:7:LEU:O	2:K:11:LEU:HG	2.04	0.57
2:L:7:LEU:O	2:L:11:LEU:HG	2.05	0.57
2:L:145:ARG:O	2:L:146:GLN:HG3	2.04	0.57
1:A:783:PHE:O	1:A:786:ILE:HD12	2.05	0.57
1:B:117:LYS:HB2	1:B:179:ASP:OD2	2.04	0.57
1:B:371:ASN:C	1:B:373:GLN:H	2.11	0.57
1:B:466:PHE:O	1:B:467:GLN:C	2.47	0.57
1:B:786:ILE:HG13	1:B:787:VAL:HG23	1.87	0.57
1:B:817:TRP:CD1	1:B:818:VAL:N	2.73	0.57
2:N:5:TYR:CE2	2:N:131:ASN:HA	2.39	0.57
1:A:131:LEU:HD12	1:A:132:PRO:CD	2.35	0.57
1:A:259:HIS:ND1	1:A:260:GLN:N	2.52	0.57
1:A:722:ASN:C	1:A:723:ILE:HG13	2.29	0.57
1:B:246:HIS:HB3	1:B:249:ASP:OD2	2.05	0.57
1:B:518:PHE:N	1:B:518:PHE:CD1	2.72	0.57
1:B:535:LEU:O	1:B:539:ARG:CG	2.52	0.57
1:B:703:VAL:HG12	1:B:704:ILE:N	2.20	0.57
2:C:128:ASN:HB3	2:D:19:VAL:CG2	2.35	0.57
2:E:14:ALA:C	2:E:16:ASP:H	2.11	0.57
2:G:116:LEU:HD12	2:G:119:LEU:HD12	1.87	0.57
2:G:260:GLU:HG2	2:G:274:GLN:HG3	1.86	0.57
2:I:14:ALA:C	2:I:16:ASP:H	2.11	0.57
1:A:314:PHE:O	1:A:315:GLU:C	2.48	0.57
1:B:340:VAL:HB	1:B:587:LEU:CD1	2.35	0.57
1:B:473:HIS:CB	2:I:126:ARG:HH22	2.08	0.57
1:B:701:GLN:O	1:B:702:GLY:O	2.23	0.57
2:I:116:LEU:HD12	2:I:119:LEU:HD12	1.86	0.57
2:I:145:ARG:O	2:I:146:GLN:HG3	2.04	0.57
2:L:8:SER:C	2:L:10:THR:H	2.13	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:106:ARG:H	2:M:106:ARG:CD	2.14	0.57
2:O:150:PHE:HB2	2:O:152:PHE:HE1	1.70	0.57
1:A:122:LEU:HD11	1:A:201:ASP:HB2	1.85	0.57
1:A:187:ALA:O	1:A:188:VAL:HG23	2.04	0.57
1:A:420:ILE:CD1	1:A:423:SER:HB2	2.35	0.57
1:A:512:GLN:O	1:A:516:GLN:HG3	2.05	0.57
1:A:710:MET:CE	1:A:824:LYS:HE2	2.35	0.57
1:B:492:VAL:CG1	1:B:558:MET:SD	2.93	0.57
1:B:752:LEU:C	1:B:754:ASN:N	2.63	0.57
2:J:260:GLU:HG2	2:J:274:GLN:HG3	1.86	0.57
2:N:260:GLU:HG2	2:N:274:GLN:HG3	1.85	0.57
1:A:370:ILE:H	3:W:933:LEU:HD11	1.70	0.57
1:B:271:PHE:O	1:B:274:ILE:HB	2.05	0.57
1:B:312:ASP:O	1:B:313:ASN:HB2	2.05	0.57
1:B:396:PHE:CD1	1:B:396:PHE:C	2.83	0.57
2:C:150:PHE:HB2	2:C:152:PHE:CZ	2.40	0.57
2:E:27:VAL:O	2:E:31:ILE:HG12	2.05	0.57
2:E:35:ASN:HA	2:E:38:ILE:HD12	1.87	0.57
2:G:5:TYR:CE2	2:G:131:ASN:HA	2.40	0.57
2:G:24:TYR:O	2:G:27:VAL:HG22	2.03	0.57
2:H:7:LEU:O	2:H:11:LEU:HG	2.05	0.57
2:L:144:ARG:HD2	2:M:82:ARG:NH1	2.20	0.57
2:O:107:ASN:CG	2:O:107:ASN:O	2.48	0.57
1:A:180:TYR:HD1	1:A:181:LEU:N	2.03	0.56
1:A:597:PRO:HB3	1:A:860:ALA:CB	2.35	0.56
1:B:137:ASN:O	1:B:137:ASN:OD1	2.22	0.56
1:B:211:ILE:O	1:B:212:PHE:C	2.48	0.56
1:B:254:GLU:CG	2:N:69:THR:HB	2.35	0.56
1:B:775:ILE:N	1:B:775:ILE:HD12	2.20	0.56
1:B:790:ARG:CA	1:B:790:ARG:NE	2.47	0.56
2:D:41:MET:O	2:D:42:ASN:C	2.47	0.56
2:D:116:LEU:HD12	2:D:119:LEU:HD12	1.85	0.56
2:D:128:ASN:HB3	2:E:19:VAL:HG23	1.87	0.56
2:F:129:PHE:CD1	2:F:129:PHE:C	2.83	0.56
2:G:61:PHE:HA	2:G:63:PHE:HE1	1.70	0.56
2:G:135:TYR:OH	2:G:340:GLU:OE1	2.23	0.56
2:H:42:ASN:OD1	2:H:62:ASP:HA	2.05	0.56
2:K:14:ALA:O	2:K:18:ILE:HD12	2.05	0.56
2:N:74:ASP:OD2	2:N:76:ASN:HB3	2.05	0.56
1:A:226:ALA:O	1:A:228:MET:N	2.32	0.56
1:A:332:VAL:HG13	1:A:599:THR:CG2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:703:VAL:HG22	1:A:825:VAL:HG22	1.87	0.56
1:A:721:VAL:HG13	1:A:800:TYR:C	2.29	0.56
1:B:97:THR:HA	1:B:320:THR:HG23	1.86	0.56
1:B:550:LEU:O	1:B:551:ALA:C	2.49	0.56
2:D:8:SER:C	2:D:10:THR:H	2.13	0.56
2:M:139:TRP:HE1	2:M:143:ASN:HD21	1.52	0.56
2:O:110:ALA:HB1	2:O:111:PRO:CD	2.35	0.56
1:A:275:PRO:O	1:A:278:ILE:HG13	2.05	0.56
1:A:305:GLN:O	1:A:307:ARG:N	2.38	0.56
1:A:420:ILE:HD12	1:A:422:GLU:HG3	1.87	0.56
1:A:649:LEU:O	1:A:650:HIS:O	2.24	0.56
1:B:322:THR:O	1:B:323:THR:C	2.48	0.56
1:B:368:THR:O	1:B:369:GLY:O	2.23	0.56
1:B:390:ARG:HG3	1:B:391:THR:H	1.69	0.56
1:B:393:SER:N	1:B:573:THR:CG2	2.68	0.56
1:B:409:TRP:CH2	1:B:413:VAL:HG21	2.40	0.56
2:D:8:SER:O	2:D:10:THR:N	2.38	0.56
2:D:10:THR:O	2:D:14:ALA:HB2	2.05	0.56
2:H:139:TRP:CD1	2:H:139:TRP:C	2.83	0.56
2:H:260:GLU:HG2	2:H:274:GLN:HG3	1.85	0.56
2:I:116:LEU:CD1	2:I:119:LEU:HD12	2.36	0.56
2:J:152:PHE:CD1	2:J:152:PHE:N	2.71	0.56
2:K:35:ASN:HA	2:K:38:ILE:HD12	1.87	0.56
2:L:14:ALA:C	2:L:16:ASP:H	2.12	0.56
2:N:24:TYR:O	2:N:26:ASN:N	2.38	0.56
1:A:209:ASP:O	1:A:213:GLN:HG3	2.05	0.56
1:A:308:LEU:HB2	1:A:614:TYR:OH	2.06	0.56
1:A:410:LEU:O	1:A:413:VAL:HB	2.05	0.56
1:B:153:ASP:O	1:B:153:ASP:OD1	2.22	0.56
1:B:606:VAL:O	1:B:607:ASN:C	2.47	0.56
2:G:2:ASP:HB2	2:G:128:ASN:HD21	1.71	0.56
2:H:10:THR:O	2:H:14:ALA:HB2	2.06	0.56
2:H:27:VAL:CG2	2:H:31:ILE:HD11	2.35	0.56
2:J:74:ASP:OD2	2:J:76:ASN:HB3	2.04	0.56
2:M:110:ALA:HB1	2:M:111:PRO:CD	2.36	0.56
2:M:150:PHE:N	2:M:150:PHE:CD1	2.74	0.56
1:A:190:ASN:OD1	1:A:192:ASN:N	2.38	0.56
1:B:303:LEU:HD13	1:B:562:THR:HG21	1.88	0.56
1:B:618:ILE:O	1:B:622:VAL:HG23	2.06	0.56
2:H:14:ALA:C	2:H:16:ASP:H	2.11	0.56
2:I:139:TRP:CD1	2:I:139:TRP:C	2.84	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:38:ILE:HD12	2:L:65:LEU:HD23	1.86	0.56
2:M:7:LEU:O	2:M:11:LEU:HG	2.06	0.56
2:M:10:THR:O	2:M:14:ALA:HB2	2.05	0.56
2:M:14:ALA:C	2:M:16:ASP:H	2.11	0.56
2:N:144:ARG:O	2:N:145:ARG:CB	2.52	0.56
2:O:116:LEU:HD12	2:O:119:LEU:HD12	1.87	0.56
1:A:245:LEU:HB3	1:A:249:ASP:CB	2.34	0.56
1:A:516:GLN:CD	1:A:516:GLN:H	2.11	0.56
1:A:540:LEU:HD23	1:A:540:LEU:C	2.30	0.56
1:B:203:GLU:O	1:B:207:ILE:HG13	2.05	0.56
1:B:246:HIS:ND1	1:B:247:PRO:HD2	2.20	0.56
2:E:5:TYR:HE2	2:E:131:ASN:HA	1.69	0.56
2:E:109:ILE:HD12	2:E:109:ILE:O	2.05	0.56
2:F:150:PHE:HB2	2:F:152:PHE:HE1	1.70	0.56
2:I:76:ASN:H	2:M:76:ASN:CB	2.13	0.56
2:K:41:MET:O	2:K:42:ASN:C	2.49	0.56
2:L:260:GLU:HG2	2:L:274:GLN:HG3	1.86	0.56
2:M:8:SER:C	2:M:10:THR:H	2.13	0.56
1:B:392:MET:HA	1:B:573:THR:HG23	1.87	0.56
2:C:35:ASN:HA	2:C:38:ILE:HD12	1.88	0.56
2:D:38:ILE:HD12	2:D:65:LEU:CD2	2.35	0.56
2:E:8:SER:O	2:E:10:THR:N	2.39	0.56
2:F:7:LEU:O	2:F:11:LEU:HG	2.06	0.56
2:F:116:LEU:HD12	2:F:119:LEU:HD12	1.88	0.56
2:K:99:GLU:O	2:K:384:ARG:NH1	2.39	0.56
2:M:150:PHE:HB2	2:M:152:PHE:CZ	2.41	0.56
2:N:10:THR:O	2:N:14:ALA:HB2	2.06	0.56
1:A:319:ASP:OD2	1:A:571:LEU:CB	2.53	0.56
1:A:857:PHE:HD1	1:A:857:PHE:H	1.52	0.56
1:B:305:GLN:HE21	1:B:564:ASN:ND2	2.04	0.56
1:B:496:ASN:HB3	1:B:498:ARG:CB	2.35	0.56
2:D:139:TRP:C	2:D:139:TRP:CD1	2.84	0.56
2:K:57:ARG:NH1	2:K:94:ASN:HD21	2.03	0.56
2:M:35:ASN:HA	2:M:38:ILE:HD12	1.86	0.56
2:M:116:LEU:HD12	2:M:119:LEU:HD12	1.86	0.56
2:N:8:SER:C	2:N:10:THR:H	2.14	0.56
2:N:41:MET:O	2:N:42:ASN:C	2.49	0.56
2:O:7:LEU:O	2:O:11:LEU:HG	2.06	0.56
2:O:35:ASN:HA	2:O:38:ILE:HD12	1.88	0.56
1:A:389:GLN:NE2	1:A:568:VAL:H	2.04	0.56
1:A:404:LEU:CD2	1:A:435:ILE:HD11	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:461:GLN:HB3	2:F:32:GLN:NE2	2.20	0.56
1:A:496:ASN:O	1:A:497:ILE:C	2.49	0.56
1:A:852:SER:O	1:A:853:ASP:HB3	2.04	0.56
1:B:364:THR:HG23	3:W:622:ALA:HA	1.87	0.56
2:D:128:ASN:HB3	2:E:19:VAL:CG2	2.36	0.56
2:E:38:ILE:HG22	2:E:42:ASN:ND2	2.19	0.56
2:J:8:SER:O	2:J:10:THR:N	2.39	0.56
2:J:35:ASN:HA	2:J:38:ILE:HD12	1.87	0.56
2:J:50:GLY:O	2:J:51:ILE:HB	2.05	0.56
1:A:503:ILE:CG2	1:A:506:LEU:HB2	2.36	0.56
1:A:814:ASN:O	1:A:815:TYR:C	2.48	0.56
1:B:89:GLU:C	1:B:91:LEU:N	2.61	0.56
1:B:325:ASN:O	1:B:328:LEU:HB3	2.05	0.56
1:B:498:ARG:HG3	1:B:505:GLN:OE1	2.05	0.56
1:B:516:GLN:O	1:B:517:GLN:NE2	2.39	0.56
2:D:7:LEU:O	2:D:11:LEU:HG	2.06	0.56
2:N:7:LEU:O	2:N:11:LEU:HG	2.06	0.56
1:A:332:VAL:HG13	1:A:599:THR:HG22	1.87	0.55
1:A:440:PHE:O	1:A:442:MET:N	2.38	0.55
1:A:490:ASN:HB3	1:A:492:VAL:HG23	1.88	0.55
1:B:563:MET:SD	1:B:611:HIS:CD2	2.99	0.55
1:B:707:TYR:HE2	1:B:754:ASN:OD1	1.89	0.55
1:B:712:LEU:CB	1:B:819:PRO:HB2	2.36	0.55
1:B:763:LEU:HD22	1:B:764:PRO:CD	2.36	0.55
2:C:139:TRP:CD1	2:C:139:TRP:C	2.83	0.55
2:D:152:PHE:N	2:D:152:PHE:CD1	2.73	0.55
2:F:8:SER:C	2:F:10:THR:H	2.14	0.55
2:F:10:THR:O	2:F:14:ALA:HB2	2.05	0.55
2:G:14:ALA:C	2:G:16:ASP:H	2.11	0.55
2:I:57:ARG:NH1	2:I:94:ASN:HD21	2.02	0.55
2:I:145:ARG:HB3	2:I:145:ARG:CZ	2.35	0.55
2:O:41:MET:O	2:O:42:ASN:C	2.49	0.55
1:A:314:PHE:O	1:A:316:SER:N	2.38	0.55
1:A:346:ILE:O	1:A:349:MET:HB3	2.06	0.55
1:A:414:VAL:O	1:A:416:ASN:N	2.38	0.55
1:A:738:LEU:HA	1:A:741:THR:HG22	1.88	0.55
1:B:260:GLN:O	1:B:262:VAL:N	2.39	0.55
1:B:363:GLU:O	1:B:363:GLU:HG3	2.05	0.55
2:F:53:ASN:HD22	2:F:354:ALA:HB3	1.71	0.55
2:L:139:TRP:CD1	2:L:139:TRP:C	2.84	0.55
1:A:396:PHE:CB	1:A:578:LEU:HD12	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:535:LEU:O	1:A:539:ARG:CG	2.55	0.55
1:B:127:GLU:HB3	1:B:151:LYS:HE3	1.87	0.55
1:B:433:ASN:HD21	1:B:446:HIS:HB3	1.71	0.55
2:C:153:HIS:CD2	2:E:153:HIS:NE2	2.75	0.55
2:F:144:ARG:O	2:F:145:ARG:HB2	2.06	0.55
2:N:60:ASN:C	2:N:61:PHE:CD1	2.84	0.55
2:N:99:GLU:HG3	2:N:99:GLU:O	2.06	0.55
2:N:116:LEU:CD1	2:N:119:LEU:HD12	2.36	0.55
2:O:8:SER:O	2:O:10:THR:N	2.40	0.55
1:A:275:PRO:HB2	1:A:278:ILE:HG13	1.87	0.55
1:A:606:VAL:O	1:A:607:ASN:C	2.46	0.55
1:A:725:ARG:HB3	1:A:828:GLN:OE1	2.06	0.55
1:A:804:SER:HB2	1:A:810:TYR:CB	2.35	0.55
1:B:428:GLN:HG3	1:B:456:PHE:HD1	1.70	0.55
1:B:577:GLN:C	1:B:579:THR:H	2.14	0.55
2:C:99:GLU:HG3	2:C:99:GLU:O	2.07	0.55
2:C:129:PHE:C	2:C:129:PHE:CD1	2.85	0.55
2:I:35:ASN:HA	2:I:38:ILE:HD12	1.87	0.55
2:J:116:LEU:CD1	2:J:119:LEU:HD12	2.36	0.55
2:O:8:SER:C	2:O:10:THR:H	2.14	0.55
1:A:150:LEU:HD12	1:A:696:SER:CB	2.34	0.55
1:B:392:MET:C	1:B:573:THR:HG23	2.32	0.55
1:B:413:VAL:HG12	1:B:414:VAL:H	1.69	0.55
2:G:106:ARG:HD3	2:G:106:ARG:N	2.22	0.55
2:H:105:GLN:C	2:H:107:ASN:N	2.58	0.55
2:J:128:ASN:HB3	2:K:19:VAL:CG2	2.36	0.55
2:N:6:SER:OG	2:N:128:ASN:HA	2.05	0.55
2:O:23:LEU:HD23	2:O:23:LEU:C	2.31	0.55
1:A:383:ILE:HD11	1:A:550:LEU:HD23	1.89	0.55
1:B:508:GLU:HG2	1:B:512:GLN:HE21	1.71	0.55
1:B:625:ILE:O	1:B:628:ALA:HB3	2.06	0.55
1:B:650:HIS:O	1:B:652:PHE:N	2.39	0.55
1:B:675:GLU:HB3	1:B:678:ARG:HG3	1.88	0.55
1:B:723:ILE:HG22	1:B:724:ALA:N	2.16	0.55
1:B:804:SER:HA	1:B:810:TYR:CZ	2.42	0.55
2:C:144:ARG:HD2	2:D:82:ARG:NH1	2.20	0.55
2:C:145:ARG:O	2:C:146:GLN:HG3	2.06	0.55
2:D:116:LEU:CD1	2:D:119:LEU:HD12	2.36	0.55
2:F:8:SER:O	2:F:10:THR:N	2.39	0.55
2:G:8:SER:C	2:G:10:THR:H	2.14	0.55
2:G:63:PHE:N	2:G:63:PHE:CD1	2.74	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:116:LEU:HD12	2:H:119:LEU:HD12	1.89	0.55
2:J:8:SER:C	2:J:10:THR:H	2.14	0.55
2:K:60:ASN:C	2:K:61:PHE:CD1	2.85	0.55
2:L:35:ASN:HA	2:L:38:ILE:HD12	1.87	0.55
2:L:116:LEU:HD12	2:L:119:LEU:HD12	1.87	0.55
2:O:10:THR:O	2:O:14:ALA:HB2	2.06	0.55
2:O:144:ARG:O	2:O:145:ARG:HG2	2.07	0.55
1:A:732:GLN:O	1:A:733:ILE:HG23	2.06	0.55
1:B:371:ASN:O	1:B:373:GLN:N	2.39	0.55
1:B:457:GLN:C	1:B:458:ILE:HG13	2.31	0.55
1:B:784:ALA:O	1:B:785:GLN:O	2.25	0.55
1:B:805:ASP:C	1:B:807:ASN:N	2.65	0.55
2:C:10:THR:O	2:C:14:ALA:HB2	2.06	0.55
2:C:82:ARG:NH1	2:E:144:ARG:HD2	2.21	0.55
2:E:8:SER:C	2:E:10:THR:H	2.14	0.55
2:H:99:GLU:HG3	2:H:99:GLU:O	2.07	0.55
2:I:89:VAL:O	2:I:91:PHE:N	2.40	0.55
2:L:8:SER:O	2:L:10:THR:N	2.39	0.55
2:N:139:TRP:CD1	2:N:139:TRP:C	2.84	0.55
2:O:49:GLY:HA2	2:O:54:LEU:CD2	2.37	0.55
1:A:389:GLN:O	1:A:389:GLN:CG	2.54	0.55
1:A:510:LEU:HD22	1:A:540:LEU:CD1	2.26	0.55
1:A:563:MET:O	1:A:565:MET:N	2.40	0.55
1:B:113:PRO:HG2	1:B:609:ASN:HB3	1.89	0.55
1:B:160:TYR:OH	1:B:635:GLN:HG3	2.07	0.55
1:B:710:MET:HE1	1:B:824:LYS:NZ	2.22	0.55
1:B:763:LEU:O	1:B:764:PRO:O	2.25	0.55
1:B:826:TYR:O	1:B:827:LYS:C	2.50	0.55
2:C:152:PHE:N	2:C:152:PHE:CD1	2.74	0.55
2:E:99:GLU:HG3	2:E:99:GLU:O	2.05	0.55
2:F:139:TRP:CD1	2:F:139:TRP:C	2.85	0.55
2:H:8:SER:O	2:H:10:THR:N	2.40	0.55
2:I:101:VAL:HB	2:I:355:ILE:HG21	1.88	0.55
2:I:153:HIS:NE2	2:J:153:HIS:CD2	2.75	0.55
2:J:38:ILE:HG22	2:J:42:ASN:ND2	2.22	0.55
2:K:35:ASN:HA	2:K:38:ILE:CD1	2.37	0.55
1:A:214:ASP:O	1:A:215:GLU:C	2.50	0.55
1:A:675:GLU:O	1:A:676:VAL:C	2.50	0.55
1:B:594:ILE:C	1:B:594:ILE:CD1	2.79	0.55
2:E:139:TRP:CD1	2:E:139:TRP:C	2.84	0.55
2:E:151:THR:C	2:E:152:PHE:CD1	2.84	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:8:SER:O	2:G:10:THR:N	2.40	0.55
2:G:139:TRP:C	2:G:139:TRP:CD1	2.85	0.55
2:I:124:PHE:C	2:I:126:ARG:H	2.14	0.55
2:L:10:THR:O	2:L:14:ALA:HB2	2.06	0.55
2:L:116:LEU:CD1	2:L:119:LEU:HD12	2.37	0.55
2:M:99:GLU:HG3	2:M:99:GLU:O	2.07	0.55
1:A:500:GLY:O	1:A:502:VAL:N	2.36	0.55
1:B:360:ILE:N	1:B:360:ILE:HD12	2.22	0.55
1:B:654:VAL:O	1:B:656:ARG:N	2.39	0.55
1:B:698:LYS:O	1:B:699:ILE:CB	2.53	0.55
2:C:109:ILE:HG23	2:C:110:ALA:H	1.70	0.55
2:C:116:LEU:CD1	2:C:119:LEU:HD12	2.36	0.55
2:C:167:ASN:ND2	2:C:178:GLY:HA2	2.23	0.55
2:E:7:LEU:O	2:E:11:LEU:HG	2.07	0.55
2:F:144:ARG:O	2:F:145:ARG:CB	2.55	0.55
2:F:152:PHE:N	2:F:152:PHE:CD1	2.74	0.55
2:L:35:ASN:O	2:L:36:GLN:C	2.50	0.55
2:N:35:ASN:HA	2:N:38:ILE:HD12	1.89	0.55
1:A:142:LEU:O	1:A:143:ARG:HG2	2.08	0.54
1:A:289:ASP:C	1:A:290:ARG:HG2	2.32	0.54
1:A:369:GLY:O	1:A:370:ILE:C	2.49	0.54
1:A:501:HIS:C	1:A:503:ILE:N	2.62	0.54
1:A:525:TYR:O	1:A:529:ILE:HG13	2.05	0.54
1:A:705:ILE:HG22	1:A:757:VAL:O	2.07	0.54
1:A:793:ASP:C	1:A:795:LEU:N	2.63	0.54
1:B:195:ASP:O	1:B:197:GLY:N	2.39	0.54
1:B:245:LEU:HD12	1:B:250:TYR:HA	1.89	0.54
2:E:116:LEU:HD12	2:E:119:LEU:HD12	1.88	0.54
2:J:131:ASN:N	2:J:131:ASN:HD22	2.04	0.54
2:L:82:ARG:NH1	2:N:144:ARG:HD2	2.22	0.54
2:N:8:SER:O	2:N:10:THR:N	2.40	0.54
1:A:742:GLY:HA3	1:B:285:ILE:HD11	1.89	0.54
1:B:306:ASP:C	1:B:308:LEU:H	2.08	0.54
1:B:388:SER:O	1:B:389:GLN:HB2	2.07	0.54
1:B:779:ASP:HA	1:B:798:ILE:HG13	1.89	0.54
2:C:22:THR:HB	2:E:128:ASN:O	2.08	0.54
2:C:135:TYR:OH	2:C:340:GLU:OE1	2.24	0.54
2:D:144:ARG:HD2	2:E:82:ARG:CZ	2.36	0.54
2:G:35:ASN:HA	2:G:38:ILE:HD12	1.89	0.54
2:I:8:SER:C	2:I:10:THR:H	2.14	0.54
2:I:8:SER:O	2:I:10:THR:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:124:PHE:O	2:I:126:ARG:N	2.39	0.54
2:I:153:HIS:CD2	2:K:153:HIS:NE2	2.75	0.54
2:J:35:ASN:HA	2:J:38:ILE:CD1	2.37	0.54
2:O:30:LEU:O	2:O:31:ILE:C	2.51	0.54
2:O:35:ASN:HA	2:O:38:ILE:CD1	2.37	0.54
1:A:151:LYS:O	1:A:152:LYS:HB2	2.06	0.54
1:A:166:PHE:CE2	1:A:689:MET:HG3	2.42	0.54
1:A:393:SER:HB2	1:A:573:THR:HG21	1.90	0.54
1:A:717:MET:SD	1:A:829:VAL:HG22	2.47	0.54
1:A:730:PHE:CD1	1:A:730:PHE:N	2.75	0.54
1:A:863:VAL:HG12	1:A:864:GLU:N	2.22	0.54
1:A:871:PHE:O	1:A:871:PHE:CD1	2.60	0.54
2:E:35:ASN:HA	2:E:38:ILE:CD1	2.37	0.54
2:H:116:LEU:CD1	2:H:119:LEU:HD12	2.38	0.54
2:H:150:PHE:HB2	2:H:152:PHE:CE1	2.43	0.54
2:I:49:GLY:HA2	2:I:54:LEU:HD21	1.90	0.54
2:M:8:SER:O	2:M:10:THR:N	2.40	0.54
2:O:116:LEU:CD1	2:O:119:LEU:HD12	2.37	0.54
2:O:144:ARG:O	2:O:146:GLN:N	2.41	0.54
1:A:111:ILE:O	1:A:111:ILE:HG23	2.07	0.54
1:A:404:LEU:O	1:A:405:ILE:C	2.50	0.54
1:A:549:LEU:HD13	1:A:877:MET:HE3	1.89	0.54
1:B:305:GLN:NE2	1:B:564:ASN:CG	2.65	0.54
1:B:404:LEU:O	1:B:407:GLY:N	2.40	0.54
2:C:8:SER:O	2:C:10:THR:N	2.40	0.54
2:C:16:ASP:HB3	2:E:131:ASN:O	2.06	0.54
2:D:110:ALA:HB1	2:D:111:PRO:HD2	1.89	0.54
2:F:65:LEU:O	2:F:66:LEU:HD23	2.08	0.54
2:M:139:TRP:CD1	2:M:139:TRP:C	2.84	0.54
2:N:42:ASN:HA	2:N:61:PHE:HB2	1.88	0.54
1:A:386:MET:HE2	1:A:480:PHE:HZ	1.73	0.54
1:A:530:GLN:HA	1:A:533:ILE:CD1	2.37	0.54
1:A:663:TYR:O	1:A:666:ARG:HG2	2.08	0.54
1:B:323:THR:O	1:B:326:TYR:HB3	2.08	0.54
1:B:326:TYR:CD1	1:B:384:ALA:CB	2.91	0.54
1:B:370:ILE:O	1:B:373:GLN:HB3	2.08	0.54
1:B:394:LEU:C	1:B:396:PHE:N	2.65	0.54
1:B:480:PHE:O	1:B:481:ARG:C	2.49	0.54
1:B:481:ARG:HG2	2:I:65:LEU:HD12	1.89	0.54
2:E:10:THR:O	2:E:14:ALA:HB2	2.07	0.54
2:F:35:ASN:HA	2:F:38:ILE:HD12	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:74:ASP:OD2	2:H:76:ASN:HB3	2.07	0.54
2:J:14:ALA:C	2:J:16:ASP:N	2.65	0.54
2:K:8:SER:C	2:K:10:THR:H	2.14	0.54
1:A:688:ASN:O	1:A:689:MET:C	2.51	0.54
1:B:666:ARG:HG3	1:B:667:ASP:N	2.20	0.54
1:B:698:LYS:C	1:B:699:ILE:HD13	2.33	0.54
2:E:116:LEU:CD1	2:E:119:LEU:HD12	2.38	0.54
2:E:167:ASN:ND2	2:E:178:GLY:HA2	2.22	0.54
2:G:14:ALA:C	2:G:16:ASP:N	2.66	0.54
2:I:167:ASN:ND2	2:I:178:GLY:HA2	2.22	0.54
2:J:7:LEU:O	2:J:11:LEU:HG	2.06	0.54
2:N:110:ALA:HB1	2:N:111:PRO:CD	2.37	0.54
2:O:139:TRP:C	2:O:139:TRP:CD1	2.85	0.54
2:O:158:PHE:HE2	2:O:214:LEU:HD22	1.73	0.54
1:A:120:THR:HA	1:A:186:MET:HE1	1.88	0.54
1:A:217:THR:HG22	1:A:217:THR:O	2.07	0.54
1:B:428:GLN:HG2	1:B:429:LEU:H	1.71	0.54
1:B:501:HIS:C	1:B:503:ILE:H	2.15	0.54
1:B:875:ARG:CD	1:B:878:ASN:HD22	2.20	0.54
2:C:35:ASN:HA	2:C:38:ILE:CD1	2.38	0.54
2:H:35:ASN:HA	2:H:38:ILE:HD12	1.89	0.54
2:I:106:ARG:H	2:I:106:ARG:HD3	1.72	0.54
2:J:30:LEU:O	2:J:31:ILE:C	2.51	0.54
2:J:99:GLU:HG3	2:J:99:GLU:O	2.08	0.54
2:M:139:TRP:HE1	2:M:143:ASN:ND2	2.04	0.54
1:A:311:HIS:HB3	1:A:318:TRP:NE1	2.23	0.54
1:A:645:PHE:HD2	1:A:646:LEU:HD23	1.72	0.54
1:A:650:HIS:O	1:A:651:ILE:CB	2.56	0.54
1:A:701:GLN:HG2	1:A:826:TYR:CE2	2.43	0.54
2:C:8:SER:C	2:C:10:THR:H	2.14	0.54
2:C:35:ASN:O	2:C:36:GLN:C	2.51	0.54
2:C:60:ASN:C	2:C:61:PHE:CD1	2.85	0.54
2:F:158:PHE:HE2	2:F:214:LEU:HD22	1.73	0.54
2:H:8:SER:C	2:H:10:THR:H	2.14	0.54
2:M:167:ASN:ND2	2:M:178:GLY:HA2	2.23	0.54
1:A:178:PRO:HD2	1:A:256:PHE:CE2	2.43	0.54
1:A:642:VAL:HB	1:A:662:MET:HE2	1.90	0.54
1:B:427:CYS:O	1:B:431:ILE:HG13	2.08	0.54
2:C:153:HIS:O	2:C:154:LYS:C	2.50	0.54
2:D:167:ASN:ND2	2:D:178:GLY:HA2	2.23	0.54
2:G:116:LEU:CD1	2:G:119:LEU:HD12	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:14:ALA:C	2:K:16:ASP:N	2.65	0.54
2:K:158:PHE:HE2	2:K:214:LEU:HD22	1.73	0.54
2:L:72:ASN:ND2	2:N:126:ARG:NH1	2.56	0.54
2:L:128:ASN:O	2:M:22:THR:HB	2.08	0.54
1:A:273:TYR:O	1:A:273:TYR:CD2	2.61	0.54
1:A:298:TYR:O	1:A:299:ILE:HB	2.06	0.54
1:B:457:GLN:CB	1:B:476:ASN:ND2	2.63	0.54
1:B:580:SER:O	1:B:581:VAL:C	2.51	0.54
1:B:856:ALA:C	1:B:858:VAL:H	2.14	0.54
2:D:35:ASN:HA	2:D:38:ILE:HD12	1.89	0.54
2:I:7:LEU:O	2:I:11:LEU:HG	2.08	0.54
2:J:27:VAL:O	2:J:30:LEU:N	2.40	0.54
2:M:116:LEU:CD1	2:M:119:LEU:HD12	2.37	0.54
2:N:167:ASN:ND2	2:N:178:GLY:HA2	2.22	0.54
1:A:804:SER:HB2	1:A:810:TYR:HA	1.89	0.53
1:B:125:ILE:N	1:B:125:ILE:CD1	2.71	0.53
1:B:125:ILE:HB	1:B:126:PHE:CD2	2.43	0.53
1:B:184:LYS:C	1:B:186:MET:H	2.15	0.53
1:B:393:SER:CB	1:B:573:THR:HG21	2.38	0.53
1:B:457:GLN:O	1:B:458:ILE:HG13	2.08	0.53
1:B:503:ILE:HD13	1:B:544:VAL:HG12	1.88	0.53
1:B:862:THR:HG22	1:B:863:VAL:O	2.09	0.53
2:D:35:ASN:O	2:D:36:GLN:C	2.51	0.53
2:E:74:ASP:OD2	2:E:76:ASN:HB3	2.08	0.53
2:F:116:LEU:CD1	2:F:119:LEU:HD12	2.38	0.53
2:G:22:THR:OG1	2:G:26:ASN:ND2	2.41	0.53
2:G:150:PHE:HB2	2:G:152:PHE:CE1	2.43	0.53
2:H:23:LEU:N	2:H:26:ASN:ND2	2.57	0.53
2:H:135:TYR:OH	2:H:340:GLU:OE1	2.25	0.53
2:I:158:PHE:HE2	2:I:214:LEU:HD22	1.73	0.53
2:J:35:ASN:O	2:J:36:GLN:C	2.51	0.53
2:K:116:LEU:HD12	2:K:119:LEU:HD12	1.89	0.53
2:K:139:TRP:CD1	2:K:139:TRP:C	2.85	0.53
2:M:35:ASN:HA	2:M:38:ILE:CD1	2.38	0.53
1:B:252:PHE:O	1:B:254:GLU:N	2.40	0.53
1:B:467:GLN:HB3	1:B:512:GLN:HG2	1.90	0.53
2:G:46:PHE:CE2	2:G:119:LEU:HD21	2.43	0.53
2:G:128:ASN:HB3	2:H:19:VAL:CG2	2.37	0.53
2:K:150:PHE:HB2	2:K:152:PHE:CZ	2.42	0.53
2:K:167:ASN:ND2	2:K:178:GLY:HA2	2.22	0.53
2:L:153:HIS:NE2	2:N:153:HIS:NE2	2.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:89:VAL:O	2:N:91:PHE:N	2.41	0.53
1:B:449:ASN:HD21	1:B:455:PRO:CG	2.21	0.53
2:C:158:PHE:HE2	2:C:214:LEU:HD22	1.73	0.53
2:D:70:LEU:HD12	2:D:71:LEU:H	1.74	0.53
2:G:129:PHE:CD1	2:G:129:PHE:C	2.86	0.53
2:G:130:ASP:HA	2:H:17:LYS:HG2	1.90	0.53
2:K:215:ARG:HG3	2:K:371:ILE:O	2.09	0.53
2:L:41:MET:O	2:L:42:ASN:C	2.51	0.53
2:N:49:GLY:HA2	2:N:54:LEU:CD2	2.39	0.53
2:N:158:PHE:HE2	2:N:214:LEU:HD22	1.73	0.53
2:O:24:TYR:O	2:O:27:VAL:HG22	2.09	0.53
2:O:144:ARG:C	2:O:145:ARG:HG2	2.33	0.53
1:A:322:THR:O	1:A:323:THR:C	2.50	0.53
1:A:503:ILE:HG22	1:A:506:LEU:H	1.73	0.53
1:A:705:ILE:O	1:A:705:ILE:HG12	2.07	0.53
1:B:211:ILE:O	1:B:213:GLN:N	2.41	0.53
1:B:436:ILE:O	1:B:437:TYR:C	2.51	0.53
1:B:789:LEU:O	1:B:790:ARG:C	2.51	0.53
2:E:116:LEU:HA	2:E:119:LEU:CD1	2.38	0.53
2:I:35:ASN:HA	2:I:38:ILE:CD1	2.38	0.53
2:J:150:PHE:HB2	2:J:152:PHE:CZ	2.42	0.53
2:K:30:LEU:O	2:K:31:ILE:C	2.52	0.53
2:L:38:ILE:O	2:L:42:ASN:OD1	2.27	0.53
2:O:215:ARG:HG3	2:O:371:ILE:O	2.09	0.53
1:A:542:GLN:O	1:A:545:ASP:HB2	2.08	0.53
1:B:94:THR:HG23	1:B:658:PRO:HG3	1.90	0.53
1:B:122:LEU:HD11	1:B:200:VAL:HG12	1.88	0.53
1:B:170:TYR:CE1	1:B:681:ILE:CG2	2.92	0.53
1:B:182:LEU:HD23	1:B:183:LEU:N	2.15	0.53
1:B:199:VAL:HG12	1:B:200:VAL:H	1.70	0.53
1:B:246:HIS:CE1	1:B:247:PRO:HD2	2.44	0.53
1:B:293:PRO:C	1:B:295:THR:N	2.60	0.53
1:B:361:GLN:HE22	3:W:624:LYS:HZ1	1.56	0.53
1:B:361:GLN:NE2	3:W:624:LYS:NZ	2.54	0.53
1:B:457:GLN:C	1:B:459:ALA:N	2.57	0.53
1:B:497:ILE:HG23	2:I:68:THR:HG23	1.89	0.53
2:C:130:ASP:C	2:C:131:ASN:HD22	2.17	0.53
2:D:144:ARG:HD2	2:E:82:ARG:NH1	2.23	0.53
2:G:99:GLU:O	2:G:99:GLU:HG3	2.09	0.53
2:H:14:ALA:C	2:H:16:ASP:N	2.66	0.53
2:H:149:GLY:C	2:H:150:PHE:CD1	2.87	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:158:PHE:HE2	2:H:214:LEU:HD22	1.73	0.53
2:I:215:ARG:HG3	2:I:371:ILE:O	2.09	0.53
2:J:116:LEU:HA	2:J:119:LEU:CD1	2.38	0.53
2:K:35:ASN:O	2:K:36:GLN:C	2.51	0.53
2:L:63:PHE:N	2:L:63:PHE:CD1	2.75	0.53
2:L:158:PHE:HE2	2:L:214:LEU:HD22	1.73	0.53
2:N:215:ARG:HG3	2:N:371:ILE:O	2.09	0.53
1:A:311:HIS:NE2	1:A:566:GLN:NE2	2.54	0.53
1:A:384:ALA:O	1:A:385:ALA:C	2.50	0.53
1:A:546:LEU:HD22	1:A:584:LEU:HD21	1.90	0.53
1:A:560:CYS:CB	1:A:603:TYR:HD2	2.21	0.53
1:B:133:ILE:HD11	1:B:147:TYR:CE1	2.43	0.53
1:B:200:VAL:HB	1:B:204:THR:HG21	1.89	0.53
1:B:298:TYR:CD1	1:B:299:ILE:N	2.75	0.53
1:B:428:GLN:CG	1:B:456:PHE:HD1	2.21	0.53
1:B:442:MET:O	1:B:443:GLN:C	2.50	0.53
1:B:498:ARG:HG3	1:B:505:GLN:HE22	1.73	0.53
1:B:770:SER:HB3	1:B:772:ILE:HG22	1.90	0.53
2:F:99:GLU:HG3	2:F:99:GLU:O	2.08	0.53
1:A:226:ALA:C	1:A:228:MET:H	2.15	0.53
1:A:545:ASP:O	1:A:546:LEU:C	2.51	0.53
1:A:642:VAL:HG13	1:A:665:LEU:HD23	1.90	0.53
1:A:750:MET:HE2	1:A:757:VAL:HG21	1.91	0.53
2:D:116:LEU:HA	2:D:119:LEU:CD1	2.39	0.53
2:E:158:PHE:HE2	2:E:214:LEU:HD22	1.73	0.53
2:G:158:PHE:HE2	2:G:214:LEU:HD22	1.73	0.53
2:H:35:ASN:O	2:H:36:GLN:C	2.51	0.53
2:J:158:PHE:HE2	2:J:214:LEU:HD22	1.73	0.53
2:K:131:ASN:HD22	2:K:131:ASN:N	2.05	0.53
2:L:215:ARG:HG3	2:L:371:ILE:O	2.09	0.53
2:N:35:ASN:HA	2:N:38:ILE:CD1	2.38	0.53
2:O:167:ASN:ND2	2:O:178:GLY:HA2	2.22	0.53
1:A:238:VAL:HG12	1:A:239:VAL:N	2.24	0.53
1:A:487:GLY:O	1:A:488:VAL:HG23	2.08	0.53
1:A:491:GLN:HB3	1:A:564:ASN:HB3	1.90	0.53
1:A:629:ASN:C	1:A:631:LEU:N	2.61	0.53
1:B:400:ASN:ND2	1:B:403:SER:OG	2.41	0.53
1:B:415:PRO:O	1:B:416:ASN:C	2.52	0.53
1:B:436:ILE:O	1:B:438:PRO:N	2.42	0.53
1:B:498:ARG:CB	2:I:32:GLN:NE2	2.66	0.53
2:C:30:LEU:O	2:C:31:ILE:C	2.52	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:35:ASN:O	2:E:36:GLN:C	2.52	0.53
2:E:110:ALA:HB1	2:E:111:PRO:CD	2.39	0.53
2:F:144:ARG:HD2	2:G:82:ARG:CZ	2.38	0.53
2:I:99:GLU:HG3	2:I:99:GLU:O	2.09	0.53
2:I:116:LEU:HA	2:I:119:LEU:CD1	2.38	0.53
2:I:144:ARG:HD2	2:J:82:ARG:NH1	2.24	0.53
2:N:35:ASN:O	2:N:36:GLN:C	2.51	0.53
2:O:74:ASP:OD2	2:O:76:ASN:HB3	2.09	0.53
1:A:271:PHE:O	1:A:274:ILE:HD12	2.08	0.53
1:A:325:ASN:O	1:A:328:LEU:HB3	2.09	0.53
1:A:460:GLU:C	1:A:462:GLN:H	2.16	0.53
1:A:771:VAL:HA	1:A:802:ILE:HD11	1.91	0.53
1:A:853:ASP:O	1:A:854:LEU:CB	2.56	0.53
1:A:876:ILE:HG22	1:A:877:MET:HG2	1.89	0.53
1:B:190:ASN:O	1:B:190:ASN:CG	2.52	0.53
1:B:548:ARG:HD3	1:B:877:MET:H	1.73	0.53
1:B:755:GLN:O	1:B:757:VAL:HG23	2.08	0.53
1:B:785:GLN:O	1:B:786:ILE:C	2.51	0.53
1:B:786:ILE:O	1:B:788:LYS:N	2.41	0.53
2:C:215:ARG:HG3	2:C:371:ILE:O	2.09	0.53
2:H:167:ASN:ND2	2:H:178:GLY:HA2	2.23	0.53
2:H:215:ARG:HG3	2:H:371:ILE:O	2.09	0.53
2:I:45:GLU:C	2:I:46:PHE:CD1	2.87	0.53
2:K:46:PHE:CE2	2:K:119:LEU:HD21	2.41	0.53
2:K:116:LEU:CD1	2:K:119:LEU:HD12	2.39	0.53
2:L:30:LEU:O	2:L:31:ILE:C	2.52	0.53
2:M:145:ARG:NH1	2:M:145:ARG:CB	2.71	0.53
2:M:158:PHE:HE2	2:M:214:LEU:HD22	1.74	0.53
2:N:31:ILE:O	2:N:34:PHE:HB3	2.09	0.53
2:O:32:GLN:O	2:O:33:GLN:C	2.52	0.53
2:O:89:VAL:O	2:O:91:PHE:N	2.42	0.53
1:A:363:GLU:C	1:A:366:PHE:HE1	2.16	0.53
1:A:661:GLN:NE2	1:B:348:LYS:HZ2	2.06	0.53
1:A:769:SER:O	1:A:770:SER:C	2.51	0.53
1:B:182:LEU:CD2	1:B:183:LEU:N	2.71	0.53
1:B:387:LEU:O	1:B:389:GLN:N	2.42	0.53
1:B:501:HIS:ND1	1:B:548:ARG:HG2	2.24	0.53
1:B:508:GLU:OE2	2:J:70:LEU:HD23	2.09	0.53
1:B:642:VAL:O	1:B:645:PHE:HB3	2.09	0.53
1:B:654:VAL:HG12	1:B:655:ALA:N	2.24	0.53
1:B:655:ALA:C	1:B:657:VAL:H	2.17	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:708:ARG:O	1:B:710:MET:N	2.42	0.53
2:D:35:ASN:HA	2:D:38:ILE:CD1	2.39	0.53
2:F:167:ASN:ND2	2:F:178:GLY:HA2	2.22	0.53
2:G:215:ARG:HG3	2:G:371:ILE:O	2.09	0.53
2:J:215:ARG:HG3	2:J:371:ILE:O	2.09	0.53
2:M:215:ARG:HG3	2:M:371:ILE:O	2.09	0.53
2:O:99:GLU:O	2:O:99:GLU:HG3	2.09	0.53
1:A:297:ARG:HG3	1:A:848:PHE:CE2	2.43	0.52
1:A:323:THR:O	1:A:326:TYR:HB3	2.08	0.52
1:A:401:TYR:CD1	1:A:401:TYR:N	2.75	0.52
1:A:660:ASP:C	1:A:662:MET:N	2.66	0.52
1:A:721:VAL:CG1	1:A:799:LEU:HD22	2.39	0.52
1:A:794:THR:O	1:A:794:THR:HG22	2.08	0.52
1:B:437:TYR:HD2	1:B:443:GLN:HB3	1.73	0.52
1:B:442:MET:CE	1:B:463:ILE:HG12	2.19	0.52
1:B:499:ASN:O	1:B:500:GLY:O	2.27	0.52
1:B:654:VAL:O	1:B:657:VAL:HG23	2.08	0.52
1:B:742:GLY:O	1:B:744:TYR:CE2	2.62	0.52
2:C:150:PHE:HA	2:D:397:LYS:HZ1	1.74	0.52
2:I:37:MET:O	2:I:38:ILE:C	2.53	0.52
2:K:89:VAL:O	2:K:91:PHE:N	2.43	0.52
2:L:152:PHE:N	2:L:152:PHE:CD1	2.77	0.52
2:N:14:ALA:C	2:N:16:ASP:N	2.65	0.52
1:A:255:TYR:O	1:A:259:HIS:HB3	2.08	0.52
1:A:365:GLN:C	1:A:366:PHE:CG	2.88	0.52
1:A:424:LEU:HD12	1:A:424:LEU:O	2.08	0.52
1:A:618:ILE:HD13	1:A:645:PHE:CZ	2.44	0.52
1:B:135:ARG:O	1:B:138:GLY:N	2.43	0.52
1:B:326:TYR:CE1	1:B:384:ALA:HB3	2.44	0.52
1:B:384:ALA:O	1:B:385:ALA:C	2.50	0.52
1:B:478:ASN:C	1:B:480:PHE:H	2.17	0.52
1:B:540:LEU:HD23	1:B:540:LEU:C	2.34	0.52
1:B:663:TYR:O	1:B:666:ARG:HG2	2.09	0.52
2:I:35:ASN:O	2:I:36:GLN:C	2.52	0.52
2:I:41:MET:O	2:I:42:ASN:C	2.52	0.52
2:L:61:PHE:O	2:L:62:ASP:HB3	2.07	0.52
2:M:14:ALA:C	2:M:16:ASP:N	2.66	0.52
2:M:30:LEU:O	2:M:31:ILE:C	2.52	0.52
2:M:48:THR:O	2:M:56:ILE:HA	2.10	0.52
2:O:35:ASN:O	2:O:36:GLN:C	2.52	0.52
1:A:225:ILE:HA	1:A:228:MET:CE	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:ALA:O	1:A:333:VAL:HG23	2.10	0.52
1:A:340:VAL:HB	1:A:587:LEU:CD2	2.39	0.52
1:A:658:PRO:HB2	1:A:660:ASP:OD1	2.09	0.52
1:B:311:HIS:CD2	1:B:566:GLN:OE1	2.62	0.52
1:B:525:TYR:O	1:B:529:ILE:HG13	2.08	0.52
1:B:807:ASN:C	1:B:809:PHE:N	2.66	0.52
2:C:381:ASN:O	2:C:385:VAL:HB	2.10	0.52
2:D:42:ASN:HA	2:D:61:PHE:HB2	1.92	0.52
2:D:158:PHE:HE2	2:D:214:LEU:HD22	1.74	0.52
2:D:215:ARG:HG3	2:D:371:ILE:O	2.09	0.52
2:G:35:ASN:O	2:G:36:GLN:C	2.52	0.52
2:H:150:PHE:HB2	2:H:152:PHE:CZ	2.44	0.52
2:M:41:MET:O	2:M:42:ASN:C	2.52	0.52
2:M:101:VAL:HG23	2:M:102:ARG:N	2.24	0.52
2:M:116:LEU:HA	2:M:119:LEU:CD1	2.38	0.52
2:O:110:ALA:HB1	2:O:111:PRO:HD2	1.90	0.52
2:O:116:LEU:HA	2:O:119:LEU:CD1	2.39	0.52
1:A:326:TYR:CD1	1:A:384:ALA:CB	2.92	0.52
1:A:361:GLN:HG3	1:A:362:SER:H	1.75	0.52
1:A:555:GLU:OE2	1:A:871:PHE:CE2	2.63	0.52
1:B:89:GLU:C	1:B:91:LEU:H	2.16	0.52
1:B:296:ALA:C	1:B:297:ARG:HG2	2.35	0.52
1:B:418:MET:HB3	1:B:567:HIS:NE2	2.24	0.52
1:B:431:ILE:O	1:B:435:ILE:HB	2.09	0.52
1:B:689:MET:HA	1:B:692:ILE:HD13	1.91	0.52
2:C:14:ALA:C	2:C:16:ASP:N	2.65	0.52
2:D:24:TYR:CZ	2:D:68:THR:HG22	2.44	0.52
2:E:14:ALA:C	2:E:16:ASP:N	2.66	0.52
2:E:135:TYR:OH	2:E:342:MET:HE3	2.09	0.52
2:F:30:LEU:O	2:F:31:ILE:C	2.53	0.52
2:F:35:ASN:O	2:F:36:GLN:C	2.53	0.52
2:G:35:ASN:HA	2:G:38:ILE:CD1	2.39	0.52
2:I:74:ASP:OD2	2:I:76:ASN:HB3	2.08	0.52
2:J:150:PHE:HB2	2:J:152:PHE:HE1	1.73	0.52
2:L:167:ASN:ND2	2:L:178:GLY:HA2	2.22	0.52
2:M:31:ILE:O	2:M:34:PHE:HB3	2.09	0.52
2:M:35:ASN:O	2:M:36:GLN:C	2.51	0.52
2:O:23:LEU:HB3	2:O:26:ASN:HD21	1.73	0.52
1:A:383:ILE:O	1:A:384:ALA:C	2.53	0.52
1:A:421:ARG:O	1:A:425:VAL:HG23	2.10	0.52
1:A:636:LYS:O	1:A:637:LYS:C	2.52	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:742:GLY:O	1:A:743:ASP:O	2.28	0.52
1:A:872:ASP:OD2	1:A:874:MET:HB2	2.10	0.52
1:B:277:ARG:NH1	1:B:559:ALA:HB2	2.25	0.52
1:B:340:VAL:O	1:B:587:LEU:HD11	2.09	0.52
1:B:563:MET:HE3	1:B:563:MET:CA	2.35	0.52
2:D:32:GLN:O	2:D:33:GLN:C	2.52	0.52
2:D:74:ASP:OD2	2:D:76:ASN:HB3	2.09	0.52
2:F:150:PHE:HB2	2:F:152:PHE:CZ	2.44	0.52
2:F:381:ASN:O	2:F:385:VAL:HB	2.10	0.52
2:G:381:ASN:O	2:G:385:VAL:HB	2.10	0.52
2:K:53:ASN:ND2	2:K:354:ALA:HB3	2.25	0.52
2:N:116:LEU:HA	2:N:119:LEU:CD1	2.39	0.52
1:A:464:GLN:O	1:A:465:ASN:HB2	2.08	0.52
1:B:527:ARG:O	1:B:531:ARG:HG2	2.08	0.52
1:B:527:ARG:HG3	1:B:527:ARG:HH11	1.74	0.52
1:B:558:MET:O	1:B:561:VAL:HG23	2.09	0.52
1:B:763:LEU:HD22	1:B:764:PRO:HD2	1.92	0.52
1:B:811:LEU:N	1:B:811:LEU:HD23	2.24	0.52
2:E:30:LEU:O	2:E:31:ILE:C	2.51	0.52
2:E:215:ARG:HG3	2:E:371:ILE:O	2.09	0.52
2:F:215:ARG:HG3	2:F:371:ILE:O	2.09	0.52
2:G:7:LEU:O	2:G:11:LEU:HG	2.09	0.52
2:H:57:ARG:NH1	2:H:94:ASN:HD21	2.07	0.52
2:M:21:GLY:O	2:M:22:THR:O	2.28	0.52
2:M:37:MET:O	2:M:38:ILE:C	2.53	0.52
2:N:32:GLN:O	2:N:33:GLN:C	2.53	0.52
2:O:153:HIS:O	2:O:154:LYS:C	2.52	0.52
1:B:326:TYR:HD1	1:B:384:ALA:HB1	1.75	0.52
1:B:570:THR:HG22	1:B:571:LEU:H	1.75	0.52
1:B:632:ASN:O	1:B:634:TYR:N	2.38	0.52
1:B:639:LYS:O	1:B:640:ALA:C	2.52	0.52
1:B:771:VAL:CG1	1:B:772:ILE:N	2.71	0.52
2:E:32:GLN:O	2:E:33:GLN:C	2.52	0.52
2:F:5:TYR:HE2	2:F:131:ASN:HA	1.75	0.52
2:I:14:ALA:O	2:I:18:ILE:HD12	2.10	0.52
2:J:167:ASN:ND2	2:J:178:GLY:HA2	2.23	0.52
2:J:381:ASN:O	2:J:385:VAL:HB	2.10	0.52
2:K:381:ASN:O	2:K:385:VAL:HB	2.10	0.52
2:L:381:ASN:O	2:L:385:VAL:HB	2.10	0.52
2:N:12:LYS:O	2:N:14:ALA:N	2.43	0.52
2:N:381:ASN:O	2:N:385:VAL:HB	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:381:ASN:O	2:O:385:VAL:HB	2.10	0.52
1:A:786:ILE:O	1:A:789:LEU:N	2.43	0.52
1:B:812:VAL:HG23	1:B:817:TRP:CZ3	2.45	0.52
2:D:23:LEU:HD22	2:D:25:SER:OG	2.10	0.52
2:G:153:HIS:O	2:G:154:LYS:C	2.53	0.52
2:L:31:ILE:O	2:L:34:PHE:HB3	2.10	0.52
2:M:89:VAL:O	2:M:91:PHE:N	2.43	0.52
1:A:163:ARG:NH2	1:A:736:GLU:OE2	2.42	0.52
1:A:323:THR:OG1	1:A:390:ARG:NH1	2.43	0.52
1:A:467:GLN:HB3	1:A:512:GLN:HG2	1.92	0.52
1:B:314:PHE:N	1:B:314:PHE:CD1	2.77	0.52
1:B:444:ARG:HH22	1:B:520:THR:HA	1.75	0.52
1:B:540:LEU:HA	1:B:543:LEU:HB2	1.92	0.52
1:B:583:SER:O	1:B:584:LEU:C	2.53	0.52
1:B:723:ILE:CG2	1:B:724:ALA:H	2.13	0.52
2:I:135:TYR:OH	2:I:342:MET:HE3	2.09	0.52
2:K:32:GLN:O	2:K:33:GLN:C	2.53	0.52
2:K:99:GLU:O	2:K:99:GLU:HG3	2.10	0.52
2:L:35:ASN:HA	2:L:38:ILE:CD1	2.39	0.52
2:L:37:MET:O	2:L:38:ILE:C	2.53	0.52
2:L:106:ARG:HD3	2:L:106:ARG:N	2.17	0.52
2:L:110:ALA:HB1	2:L:111:PRO:HD2	1.92	0.52
1:A:205:ALA:O	1:A:206:SER:C	2.52	0.52
1:A:428:GLN:CD	1:A:456:PHE:N	2.67	0.52
1:A:494:ASN:CG	1:A:495:ASP:N	2.67	0.52
1:A:516:GLN:C	1:A:518:PHE:H	2.18	0.52
2:F:35:ASN:HA	2:F:38:ILE:CD1	2.40	0.52
2:F:135:TYR:OH	2:F:340:GLU:OE1	2.28	0.52
2:H:128:ASN:O	2:H:129:PHE:HB3	2.09	0.52
2:H:151:THR:C	2:H:152:PHE:CD1	2.88	0.52
2:L:32:GLN:O	2:L:33:GLN:C	2.52	0.52
2:M:131:ASN:HD22	2:M:131:ASN:N	2.07	0.52
1:A:310:LEU:O	1:A:318:TRP:CD1	2.62	0.51
1:A:647:LYS:C	1:A:649:LEU:N	2.68	0.51
1:A:769:SER:O	1:A:771:VAL:N	2.43	0.51
1:B:235:ASP:O	1:B:236:ARG:HB2	2.10	0.51
1:B:286:LEU:HD22	1:B:286:LEU:N	2.25	0.51
1:B:530:GLN:HA	1:B:533:ILE:CD1	2.40	0.51
1:B:563:MET:HA	1:B:563:MET:CE	2.39	0.51
2:C:116:LEU:HA	2:C:119:LEU:CD1	2.40	0.51
2:G:30:LEU:O	2:G:31:ILE:C	2.52	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:124:PHE:C	2:I:126:ARG:N	2.68	0.51
2:J:89:VAL:O	2:J:91:PHE:N	2.43	0.51
2:M:27:VAL:CG2	2:M:31:ILE:HD11	2.40	0.51
2:O:133:SER:O	2:O:136:ILE:HG22	2.10	0.51
1:A:125:ILE:N	1:A:125:ILE:CD1	2.63	0.51
1:A:269:ILE:HG21	1:A:298:TYR:HE2	1.76	0.51
1:A:286:LEU:O	1:A:287:ASN:HB2	2.09	0.51
1:A:431:ILE:HG23	1:A:435:ILE:HD12	1.91	0.51
1:B:378:CYS:SG	1:B:581:VAL:HA	2.50	0.51
1:B:422:GLU:O	1:B:425:VAL:N	2.43	0.51
1:B:653:ASP:O	1:B:653:ASP:CG	2.52	0.51
2:C:27:VAL:O	2:C:30:LEU:N	2.38	0.51
2:D:105:GLN:NE2	2:D:359:PRO:O	2.43	0.51
2:H:145:ARG:O	2:H:146:GLN:HG3	2.10	0.51
2:J:11:LEU:O	2:J:15:ARG:N	2.39	0.51
2:K:74:ASP:OD2	2:K:76:ASN:HB3	2.10	0.51
2:M:32:GLN:O	2:M:33:GLN:C	2.52	0.51
1:A:259:HIS:HD1	1:A:260:GLN:N	2.07	0.51
1:A:326:TYR:CE1	1:A:384:ALA:HB3	2.45	0.51
1:A:332:VAL:O	1:A:333:VAL:C	2.53	0.51
1:A:647:LYS:O	1:A:649:LEU:N	2.43	0.51
1:A:803:ASN:C	1:A:805:ASP:N	2.63	0.51
1:B:133:ILE:HD11	1:B:147:TYR:HE1	1.76	0.51
1:B:503:ILE:O	1:B:504:ASN:C	2.54	0.51
2:C:24:TYR:OH	2:C:68:THR:HG22	2.10	0.51
2:D:6:SER:O	2:D:8:SER:N	2.44	0.51
2:E:135:TYR:OH	2:E:340:GLU:OE1	2.28	0.51
2:G:32:GLN:O	2:G:33:GLN:C	2.53	0.51
2:H:76:ASN:N	2:J:76:ASN:HB2	2.24	0.51
2:H:148:THR:OG1	2:H:332:GLU:HG2	2.10	0.51
2:I:128:ASN:HD22	2:J:19:VAL:CB	2.21	0.51
2:L:116:LEU:HA	2:L:119:LEU:CD1	2.40	0.51
2:M:381:ASN:O	2:M:385:VAL:HB	2.10	0.51
2:N:37:MET:O	2:N:38:ILE:C	2.53	0.51
1:A:420:ILE:HG12	1:A:423:SER:CB	2.38	0.51
1:A:519:PRO:O	1:A:520:THR:HG23	2.10	0.51
1:A:645:PHE:CD2	1:A:646:LEU:HD23	2.44	0.51
1:B:442:MET:SD	1:B:463:ILE:HA	2.49	0.51
1:B:460:GLU:HG3	1:B:473:HIS:HD2	1.76	0.51
1:B:498:ARG:HG3	1:B:505:GLN:NE2	2.26	0.51
1:B:498:ARG:CG	1:B:505:GLN:HE22	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:639:LYS:O	1:B:642:VAL:HG23	2.10	0.51
1:B:699:ILE:HG13	1:B:763:LEU:O	2.10	0.51
1:B:779:ASP:HA	1:B:798:ILE:CG1	2.39	0.51
2:C:74:ASP:OD2	2:C:76:ASN:HB3	2.11	0.51
2:D:381:ASN:O	2:D:385:VAL:HB	2.10	0.51
2:E:6:SER:O	2:E:8:SER:N	2.44	0.51
2:E:89:VAL:O	2:E:91:PHE:N	2.44	0.51
2:G:89:VAL:O	2:G:91:PHE:N	2.44	0.51
2:H:5:TYR:HE2	2:H:131:ASN:HA	1.75	0.51
2:N:30:LEU:O	2:N:31:ILE:C	2.54	0.51
1:A:631:LEU:O	1:A:633:LEU:HD12	2.10	0.51
1:A:661:GLN:HG3	1:B:348:LYS:NZ	2.26	0.51
1:A:773:SER:HB3	1:A:778:LEU:HD12	1.91	0.51
1:B:104:ILE:HD12	1:B:327:ILE:HD12	1.92	0.51
1:B:548:ARG:HH11	1:B:878:ASN:N	2.04	0.51
1:B:705:ILE:HG22	1:B:707:TYR:CE1	2.45	0.51
2:D:89:VAL:O	2:D:91:PHE:N	2.43	0.51
2:H:31:ILE:O	2:H:34:PHE:HB3	2.11	0.51
2:K:155:PRO:O	2:K:186:SER:HB3	2.10	0.51
2:M:253:ILE:HD13	2:M:319:THR:HB	1.93	0.51
2:N:133:SER:O	2:N:136:ILE:HG22	2.11	0.51
2:O:106:ARG:HD3	2:O:106:ARG:N	2.23	0.51
1:A:252:PHE:O	1:A:254:GLU:N	2.44	0.51
1:A:427:CYS:O	1:A:431:ILE:HG13	2.11	0.51
1:A:443:GLN:NE2	1:A:521:MET:HB3	2.25	0.51
1:A:817:TRP:CD1	1:A:818:VAL:H	2.28	0.51
1:B:178:PRO:HD2	1:B:256:PHE:CE2	2.45	0.51
1:B:272:ASN:O	1:B:274:ILE:N	2.43	0.51
1:B:431:ILE:HG23	1:B:435:ILE:HD12	1.93	0.51
1:B:481:ARG:NH2	1:B:496:ASN:HD21	2.08	0.51
2:E:31:ILE:O	2:E:34:PHE:HB3	2.09	0.51
2:I:32:GLN:O	2:I:33:GLN:C	2.54	0.51
2:K:116:LEU:HA	2:K:119:LEU:CD1	2.41	0.51
2:L:89:VAL:O	2:L:91:PHE:N	2.43	0.51
2:L:153:HIS:O	2:L:154:LYS:C	2.54	0.51
2:N:66:LEU:O	2:N:67:GLY:C	2.53	0.51
2:O:60:ASN:C	2:O:61:PHE:CD1	2.89	0.51
1:A:158:GLY:O	1:A:162:VAL:HG23	2.09	0.51
1:A:159:ASP:O	1:A:162:VAL:HB	2.11	0.51
1:B:302:ASN:O	1:B:303:LEU:HD23	2.11	0.51
1:B:305:GLN:NE2	1:B:564:ASN:ND2	2.58	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:110:ALA:HB1	2:C:111:PRO:CD	2.41	0.51
2:D:360:VAL:O	2:D:378:ARG:HD3	2.11	0.51
2:E:41:MET:O	2:E:42:ASN:C	2.52	0.51
2:F:109:ILE:CB	2:F:380:ASP:HB3	2.40	0.51
2:H:381:ASN:O	2:H:385:VAL:HB	2.10	0.51
2:I:1:MET:C	2:I:3:VAL:N	2.67	0.51
2:J:32:GLN:O	2:J:33:GLN:C	2.54	0.51
2:J:253:ILE:HD13	2:J:319:THR:HB	1.92	0.51
2:K:106:ARG:HD3	2:K:106:ARG:N	2.17	0.51
2:K:253:ILE:HD13	2:K:319:THR:HB	1.93	0.51
2:O:31:ILE:O	2:O:34:PHE:HB3	2.11	0.51
2:O:54:LEU:HD12	2:O:55:PRO:HD2	1.93	0.51
2:O:253:ILE:HD13	2:O:319:THR:HB	1.93	0.51
1:A:326:TYR:HD1	1:A:384:ALA:HB1	1.75	0.51
1:A:772:ILE:O	1:A:773:SER:C	2.54	0.51
1:B:298:TYR:CD1	1:B:298:TYR:C	2.88	0.51
1:B:481:ARG:CZ	1:B:496:ASN:OD1	2.59	0.51
1:B:491:GLN:HG3	1:B:491:GLN:O	2.10	0.51
1:B:658:PRO:HD2	1:B:661:GLN:HG3	1.93	0.51
2:C:42:ASN:HA	2:C:61:PHE:HB2	1.92	0.51
2:E:381:ASN:O	2:E:385:VAL:HB	2.10	0.51
2:F:23:LEU:HD11	2:H:36:GLN:OE1	2.10	0.51
2:F:360:VAL:O	2:F:378:ARG:HD3	2.11	0.51
2:G:111:PRO:HB3	2:G:116:LEU:CD2	2.41	0.51
2:H:35:ASN:HA	2:H:38:ILE:CD1	2.41	0.51
2:I:14:ALA:C	2:I:16:ASP:N	2.66	0.51
2:I:381:ASN:O	2:I:385:VAL:HB	2.10	0.51
2:J:12:LYS:O	2:J:14:ALA:N	2.43	0.51
2:J:360:VAL:O	2:J:378:ARG:HD3	2.11	0.51
2:M:24:TYR:O	2:M:26:ASN:N	2.44	0.51
2:M:106:ARG:HG2	2:M:107:ASN:H	1.75	0.51
2:M:109:ILE:HB	2:M:380:ASP:HB3	1.93	0.51
2:M:360:VAL:O	2:M:378:ARG:HD3	2.11	0.51
2:O:1:MET:O	2:O:2:ASP:C	2.53	0.51
1:A:130:GLN:O	1:A:131:LEU:HB3	2.10	0.51
1:A:368:THR:O	1:A:368:THR:HG22	2.09	0.51
1:A:631:LEU:CB	1:A:633:LEU:HD13	2.38	0.51
1:B:608:VAL:O	1:B:609:ASN:C	2.54	0.51
1:B:712:LEU:HD11	1:B:722:ASN:HB3	1.93	0.51
1:B:869:VAL:N	1:B:876:ILE:HG23	2.26	0.51
2:C:17:LYS:HG2	2:E:130:ASP:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:89:VAL:O	2:C:91:PHE:N	2.43	0.51
2:F:89:VAL:O	2:F:91:PHE:N	2.44	0.51
2:G:253:ILE:HD13	2:G:319:THR:HB	1.93	0.51
2:G:360:VAL:O	2:G:378:ARG:HD3	2.11	0.51
1:A:362:SER:HB2	1:A:365:GLN:HE22	1.72	0.51
1:A:527:ARG:O	1:A:531:ARG:HG2	2.10	0.51
1:A:546:LEU:HD11	1:A:584:LEU:HD23	1.93	0.51
1:A:601:PHE:O	1:A:602:HIS:C	2.54	0.51
1:A:618:ILE:O	1:A:622:VAL:HG23	2.11	0.51
1:A:701:GLN:O	1:A:761:GLY:O	2.29	0.51
1:B:140:LYS:HE2	1:B:805:ASP:OD2	2.10	0.51
2:C:41:MET:O	2:C:42:ASN:C	2.53	0.51
2:C:128:ASN:HB3	2:D:19:VAL:HG23	1.93	0.51
2:F:63:PHE:CD2	2:F:84:THR:HG23	2.46	0.51
2:F:74:ASP:OD2	2:F:76:ASN:HB3	2.11	0.51
2:G:41:MET:O	2:G:42:ASN:C	2.54	0.51
2:G:103:GLU:HG3	2:G:359:PRO:HD2	1.93	0.51
2:G:116:LEU:HA	2:G:119:LEU:CD1	2.40	0.51
2:J:153:HIS:NE2	2:K:153:HIS:NE2	2.59	0.51
2:K:129:PHE:C	2:K:129:PHE:CD1	2.89	0.51
1:A:508:GLU:O	1:A:512:GLN:NE2	2.45	0.50
1:A:555:GLU:OE1	1:A:871:PHE:HD2	1.93	0.50
1:A:676:VAL:O	1:A:680:ASP:HB2	2.10	0.50
1:A:706:ALA:C	1:A:708:ARG:H	2.19	0.50
1:A:775:ILE:C	1:A:777:LYS:H	2.19	0.50
1:B:178:PRO:HD2	1:B:256:PHE:CD2	2.45	0.50
1:B:509:ALA:O	1:B:513:LEU:CG	2.50	0.50
1:B:539:ARG:O	1:B:542:GLN:N	2.44	0.50
1:B:854:LEU:O	1:B:855:LEU:C	2.54	0.50
2:C:49:GLY:HA2	2:C:54:LEU:HD23	1.93	0.50
2:F:253:ILE:HD13	2:F:319:THR:HB	1.93	0.50
2:H:12:LYS:O	2:H:14:ALA:N	2.44	0.50
2:H:116:LEU:HA	2:H:119:LEU:CD1	2.40	0.50
2:K:11:LEU:O	2:K:15:ARG:N	2.38	0.50
2:L:99:GLU:O	2:L:99:GLU:HG3	2.10	0.50
2:N:135:TYR:OH	2:N:340:GLU:OE1	2.25	0.50
1:A:452:PRO:O	1:A:453:GLN:CB	2.58	0.50
1:A:467:GLN:NE2	1:A:511:MET:HG2	2.25	0.50
1:B:182:LEU:HD11	1:B:847:THR:CA	2.40	0.50
1:B:449:ASN:ND2	1:B:455:PRO:CG	2.75	0.50
1:B:527:ARG:O	1:B:531:ARG:HG3	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:671:LEU:O	1:B:672:LEU:HD23	2.10	0.50
1:B:783:PHE:O	1:B:784:ALA:C	2.54	0.50
2:C:133:SER:O	2:C:136:ILE:HG22	2.12	0.50
2:D:30:LEU:O	2:D:31:ILE:C	2.53	0.50
2:D:155:PRO:O	2:D:186:SER:HB3	2.11	0.50
2:I:133:SER:O	2:I:136:ILE:HG22	2.11	0.50
2:K:360:VAL:O	2:K:378:ARG:HD3	2.11	0.50
2:L:23:LEU:HD11	2:N:36:GLN:HB2	1.92	0.50
2:O:37:MET:O	2:O:38:ILE:C	2.54	0.50
1:B:298:TYR:HE1	1:B:300:ARG:HA	1.77	0.50
1:B:340:VAL:O	1:B:341:SER:C	2.54	0.50
1:B:518:PHE:CB	1:B:519:PRO:CD	2.89	0.50
1:B:739:MET:C	1:B:741:THR:H	2.19	0.50
1:B:878:ASN:OD1	1:B:878:ASN:O	2.29	0.50
2:D:253:ILE:HD13	2:D:319:THR:HB	1.93	0.50
2:E:56:ILE:O	2:E:56:ILE:HG22	2.11	0.50
2:F:61:PHE:N	2:F:61:PHE:CD1	2.79	0.50
2:H:89:VAL:O	2:H:91:PHE:N	2.44	0.50
2:J:37:MET:O	2:J:38:ILE:C	2.54	0.50
2:L:6:SER:O	2:L:8:SER:N	2.44	0.50
2:L:150:PHE:CD1	2:L:150:PHE:N	2.78	0.50
2:L:155:PRO:O	2:L:186:SER:HB3	2.11	0.50
2:N:23:LEU:O	2:N:26:ASN:ND2	2.43	0.50
1:A:199:VAL:CG1	1:A:200:VAL:H	2.07	0.50
1:A:436:ILE:CD1	1:A:437:TYR:CD1	2.94	0.50
1:A:545:ASP:OD1	1:A:877:MET:HA	2.11	0.50
1:A:822:THR:O	1:A:823:THR:HG23	2.12	0.50
1:B:498:ARG:HD3	2:I:32:GLN:NE2	2.26	0.50
1:B:596:SER:O	1:B:599:THR:HB	2.11	0.50
1:B:712:LEU:HB2	1:B:819:PRO:HB2	1.94	0.50
2:C:12:LYS:O	2:C:14:ALA:N	2.45	0.50
2:G:6:SER:O	2:G:8:SER:N	2.44	0.50
2:G:31:ILE:O	2:G:34:PHE:HB3	2.11	0.50
2:H:253:ILE:HD13	2:H:319:THR:HB	1.93	0.50
2:I:31:ILE:O	2:I:34:PHE:HB3	2.11	0.50
2:L:133:SER:O	2:L:136:ILE:HG22	2.12	0.50
2:L:253:ILE:HD13	2:L:319:THR:HB	1.93	0.50
2:N:1:MET:O	2:N:2:ASP:C	2.55	0.50
2:N:66:LEU:HD13	2:N:77:TYR:CZ	2.46	0.50
2:N:106:ARG:HG2	2:N:107:ASN:H	1.77	0.50
1:A:389:GLN:OE1	1:A:567:HIS:HA	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:TYR:HD1	1:A:635:GLN:HG3	1.76	0.50
1:B:402:MET:HE1	1:B:532:GLY:CA	2.42	0.50
1:B:428:GLN:NE2	1:B:455:PRO:HB2	2.26	0.50
1:B:710:MET:HE2	1:B:711:GLN:O	2.11	0.50
2:C:46:PHE:HE2	2:C:119:LEU:HD21	1.75	0.50
2:C:360:VAL:O	2:C:378:ARG:HD3	2.11	0.50
2:D:12:LYS:O	2:D:14:ALA:N	2.45	0.50
2:D:100:MET:HG3	2:D:388:VAL:HG11	1.93	0.50
2:D:124:PHE:O	2:D:127:ILE:HG13	2.11	0.50
2:F:14:ALA:C	2:F:16:ASP:N	2.66	0.50
2:G:124:PHE:O	2:G:127:ILE:HG13	2.11	0.50
2:I:1:MET:O	2:I:2:ASP:C	2.54	0.50
2:I:30:LEU:O	2:I:31:ILE:C	2.52	0.50
2:L:125:LYS:O	2:L:127:ILE:N	2.42	0.50
2:L:360:VAL:O	2:L:378:ARG:HD3	2.11	0.50
1:A:608:VAL:O	1:A:609:ASN:C	2.55	0.50
1:B:176:GLU:O	1:B:178:PRO:HD3	2.11	0.50
1:B:211:ILE:C	1:B:213:GLN:N	2.67	0.50
1:B:387:LEU:HD23	1:B:554:TYR:HE1	1.74	0.50
1:B:578:LEU:HA	1:B:581:VAL:CG2	2.42	0.50
1:B:872:ASP:CG	1:B:874:MET:H	2.20	0.50
2:E:150:PHE:CD1	2:E:150:PHE:N	2.80	0.50
2:E:253:ILE:HD13	2:E:319:THR:HB	1.93	0.50
2:F:32:GLN:O	2:F:33:GLN:C	2.54	0.50
2:F:73:LEU:HD22	2:F:77:TYR:CD2	2.46	0.50
2:G:167:ASN:ND2	2:G:178:GLY:HA2	2.22	0.50
2:I:6:SER:O	2:I:8:SER:N	2.44	0.50
2:J:6:SER:O	2:J:8:SER:N	2.45	0.50
2:L:11:LEU:O	2:L:15:ARG:N	2.39	0.50
2:L:89:VAL:C	2:L:91:PHE:H	2.20	0.50
2:O:11:LEU:O	2:O:15:ARG:N	2.40	0.50
1:A:229:ARG:O	1:A:242:PRO:CG	2.60	0.50
1:A:332:VAL:HG11	1:A:557:LEU:HD21	1.93	0.50
1:A:466:PHE:O	1:A:467:GLN:C	2.54	0.50
1:B:170:TYR:CE1	1:B:682:PHE:HB2	2.47	0.50
1:B:364:THR:HG22	1:B:364:THR:O	2.12	0.50
1:B:420:ILE:O	1:B:421:ARG:C	2.54	0.50
1:B:463:ILE:HG21	1:B:468:VAL:CG1	2.41	0.50
1:B:499:ASN:N	1:B:505:GLN:NE2	2.60	0.50
1:B:536:LEU:HD22	1:B:536:LEU:N	2.27	0.50
1:B:589:GLY:C	1:B:591:ALA:H	2.20	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:618:ILE:HD13	1:B:645:PHE:CZ	2.47	0.50
1:B:810:TYR:HA	1:B:812:VAL:HG12	1.92	0.50
2:C:31:ILE:O	2:C:34:PHE:HB3	2.12	0.50
2:C:37:MET:O	2:C:38:ILE:C	2.55	0.50
2:D:37:MET:O	2:D:38:ILE:C	2.55	0.50
2:D:133:SER:O	2:D:136:ILE:HG22	2.11	0.50
2:F:6:SER:O	2:F:8:SER:N	2.45	0.50
2:I:360:VAL:O	2:I:378:ARG:HD3	2.11	0.50
2:J:1:MET:C	2:J:3:VAL:N	2.68	0.50
2:K:124:PHE:O	2:K:126:ARG:N	2.45	0.50
2:N:104:SER:O	2:N:108:GLY:HA3	2.12	0.50
1:A:266:ASN:C	1:A:292:LEU:HD12	2.36	0.50
1:A:297:ARG:HG3	1:A:848:PHE:CD2	2.46	0.50
1:A:309:ASN:HA	1:A:311:HIS:CE1	2.47	0.50
1:A:554:TYR:CZ	1:A:558:MET:HE1	2.47	0.50
1:A:603:TYR:O	1:A:606:VAL:CG2	2.60	0.50
1:A:660:ASP:CA	1:B:539:ARG:HH11	2.24	0.50
1:A:704:ILE:HG23	1:A:758:ALA:HB2	1.94	0.50
1:B:113:PRO:HD2	1:B:609:ASN:HB3	1.94	0.50
1:B:141:GLU:O	1:B:142:LEU:CB	2.60	0.50
1:B:205:ALA:O	1:B:206:SER:C	2.55	0.50
1:B:392:MET:HB3	1:B:574:GLU:O	2.10	0.50
1:B:477:ASN:O	1:B:479:GLN:N	2.44	0.50
1:B:510:LEU:HD12	1:B:513:LEU:HD12	1.94	0.50
2:I:12:LYS:O	2:I:14:ALA:N	2.45	0.50
2:I:150:PHE:N	2:I:150:PHE:CD1	2.79	0.50
2:J:23:LEU:O	2:J:26:ASN:ND2	2.45	0.50
2:L:14:ALA:C	2:L:16:ASP:N	2.67	0.50
2:N:360:VAL:O	2:N:378:ARG:HD3	2.11	0.50
1:A:246:HIS:O	1:A:247:PRO:C	2.54	0.50
1:A:503:ILE:HG22	1:A:503:ILE:O	2.12	0.50
1:A:563:MET:HE2	1:A:563:MET:CA	2.31	0.50
1:A:613:ASN:HD22	1:A:649:LEU:HD21	1.75	0.50
1:B:436:ILE:CG1	1:B:437:TYR:H	2.21	0.50
1:B:444:ARG:HH21	1:B:520:THR:CG2	2.09	0.50
2:C:253:ILE:HD13	2:C:319:THR:HB	1.93	0.50
2:E:24:TYR:O	2:E:26:ASN:N	2.43	0.50
2:E:360:VAL:O	2:E:378:ARG:HD3	2.11	0.50
2:F:153:HIS:NE2	2:G:153:HIS:CD2	2.80	0.50
2:G:74:ASP:OD2	2:G:76:ASN:HB3	2.12	0.50
2:G:124:PHE:O	2:G:126:ARG:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:155:PRO:O	2:G:186:SER:HB3	2.12	0.50
2:G:273:TYR:C	2:G:274:GLN:HE21	2.20	0.50
2:H:32:GLN:O	2:H:33:GLN:C	2.54	0.50
2:J:63:PHE:N	2:J:63:PHE:CD1	2.80	0.50
2:J:153:HIS:O	2:J:154:LYS:C	2.53	0.50
2:N:253:ILE:HD13	2:N:319:THR:HB	1.93	0.50
1:A:284:TYR:OH	1:A:594:ILE:HG23	2.12	0.49
1:A:310:LEU:CD1	1:A:310:LEU:N	2.69	0.49
1:A:311:HIS:HA	1:A:318:TRP:CD1	2.47	0.49
1:A:392:MET:O	1:A:420:ILE:HG23	2.11	0.49
1:A:445:MET:C	1:A:447:TYR:N	2.54	0.49
1:A:465:ASN:HB3	1:A:468:VAL:HB	1.94	0.49
1:A:555:GLU:OE1	1:A:871:PHE:CD2	2.66	0.49
1:A:580:SER:O	1:A:581:VAL:C	2.55	0.49
1:A:674:VAL:HG12	1:A:678:ARG:HB2	1.93	0.49
1:A:774:LEU:HD12	1:A:774:LEU:O	2.11	0.49
1:B:85:GLU:O	1:B:86:ILE:C	2.54	0.49
1:B:108:LEU:C	1:B:110:ASP:N	2.67	0.49
1:B:402:MET:HE1	1:B:532:GLY:HA3	1.94	0.49
1:B:419:PHE:O	1:B:420:ILE:C	2.54	0.49
1:B:772:ILE:O	1:B:773:SER:C	2.54	0.49
2:E:101:VAL:HG23	2:E:102:ARG:N	2.27	0.49
2:H:135:TYR:OH	2:H:342:MET:HE3	2.10	0.49
2:J:60:ASN:C	2:J:61:PHE:CD1	2.90	0.49
2:K:133:SER:O	2:K:136:ILE:HG22	2.12	0.49
2:O:6:SER:O	2:O:8:SER:N	2.45	0.49
1:A:141:GLU:O	1:A:142:LEU:HB2	2.11	0.49
1:A:230:GLN:O	1:A:230:GLN:NE2	2.45	0.49
1:A:390:ARG:HG3	1:A:391:THR:N	2.26	0.49
1:A:416:ASN:C	1:A:418:MET:N	2.70	0.49
1:A:503:ILE:HG22	1:A:506:LEU:CB	2.42	0.49
1:A:779:ASP:OD1	1:A:779:ASP:N	2.43	0.49
1:B:134:TYR:CD2	1:B:803:ASN:HB2	2.47	0.49
1:B:267:ASN:N	1:B:292:LEU:HD12	2.27	0.49
1:B:322:THR:HG21	1:B:390:ARG:HA	1.94	0.49
1:B:601:PHE:O	1:B:602:HIS:C	2.53	0.49
1:B:639:LYS:O	1:B:642:VAL:N	2.44	0.49
2:C:106:ARG:HD3	2:C:106:ARG:N	2.10	0.49
2:D:14:ALA:C	2:D:16:ASP:N	2.66	0.49
2:E:37:MET:O	2:E:38:ILE:C	2.54	0.49
2:F:116:LEU:HA	2:F:119:LEU:CD1	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:133:SER:O	2:G:136:ILE:HG22	2.12	0.49
2:H:101:VAL:HB	2:H:355:ILE:HG21	1.94	0.49
2:H:360:VAL:O	2:H:378:ARG:HD3	2.11	0.49
2:J:41:MET:O	2:J:42:ASN:C	2.54	0.49
2:O:35:ASN:HD21	2:O:66:LEU:HD12	1.77	0.49
1:A:415:PRO:HD2	1:A:480:PHE:HE1	1.76	0.49
1:A:527:ARG:HH11	1:A:527:ARG:HG3	1.77	0.49
1:A:762:ALA:C	1:A:763:LEU:HG	2.37	0.49
1:A:867:ASN:CG	1:A:867:ASN:O	2.54	0.49
1:B:159:ASP:OD2	1:B:761:GLY:HA3	2.11	0.49
1:B:277:ARG:NH1	1:B:277:ARG:CB	2.75	0.49
1:B:287:ASN:O	1:B:288:MET:HE2	2.12	0.49
1:B:428:GLN:HE22	1:B:455:PRO:HB2	1.77	0.49
1:B:590:ASN:N	1:B:590:ASN:ND2	2.46	0.49
1:B:596:SER:O	1:B:597:PRO:C	2.55	0.49
1:B:735:LEU:CD2	1:B:759:LEU:HB3	2.42	0.49
2:C:32:GLN:O	2:C:33:GLN:C	2.54	0.49
2:E:12:LYS:O	2:E:14:ALA:N	2.45	0.49
2:E:22:THR:CG2	2:E:73:LEU:HD12	2.42	0.49
2:F:273:TYR:C	2:F:274:GLN:HE21	2.21	0.49
2:H:30:LEU:O	2:H:31:ILE:C	2.53	0.49
2:I:273:TYR:C	2:I:274:GLN:HE21	2.20	0.49
2:K:31:ILE:O	2:K:34:PHE:HB3	2.11	0.49
2:N:1:MET:C	2:N:3:VAL:N	2.69	0.49
2:O:14:ALA:C	2:O:16:ASP:N	2.66	0.49
2:O:273:TYR:C	2:O:274:GLN:HE21	2.21	0.49
1:A:149:LYS:NZ	1:A:697:ASP:OD1	2.45	0.49
1:A:224:PHE:O	1:A:225:ILE:C	2.55	0.49
1:A:771:VAL:HG12	1:A:809:PHE:HB3	1.93	0.49
1:B:428:GLN:CB	1:B:456:PHE:HD1	2.24	0.49
1:B:450:GLY:O	1:B:451:ASP:HB2	2.11	0.49
1:B:498:ARG:HH12	2:J:25:SER:CB	2.23	0.49
1:B:698:LYS:O	1:B:699:ILE:HD13	2.12	0.49
1:B:869:VAL:HG13	1:B:873:ASN:HA	1.92	0.49
2:J:89:VAL:C	2:J:91:PHE:H	2.21	0.49
2:J:144:ARG:O	2:J:145:ARG:HB2	2.12	0.49
2:K:37:MET:O	2:K:38:ILE:C	2.55	0.49
2:M:133:SER:O	2:M:136:ILE:HG22	2.13	0.49
1:A:117:LYS:HB2	1:A:179:ASP:CG	2.37	0.49
1:A:178:PRO:HD2	1:A:256:PHE:HE2	1.77	0.49
1:A:333:VAL:CG1	1:A:380:LYS:HA	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:415:PRO:HG2	1:A:480:PHE:HD1	1.73	0.49
1:A:718:TYR:N	1:A:718:TYR:CD1	2.80	0.49
1:B:122:LEU:O	1:B:123:PHE:HB3	2.12	0.49
1:B:174:LEU:O	1:B:177:MET:HB2	2.12	0.49
1:B:305:GLN:O	1:B:307:ARG:N	2.46	0.49
1:B:812:VAL:HA	1:B:817:TRP:HZ3	1.78	0.49
2:C:273:TYR:C	2:C:274:GLN:HE21	2.21	0.49
2:J:144:ARG:NH2	2:J:146:GLN:NE2	2.61	0.49
2:J:273:TYR:C	2:J:274:GLN:HE21	2.20	0.49
2:K:12:LYS:O	2:K:14:ALA:N	2.45	0.49
2:L:60:ASN:C	2:L:61:PHE:CD1	2.91	0.49
2:N:22:THR:OG1	2:N:26:ASN:ND2	2.40	0.49
2:N:89:VAL:C	2:N:91:PHE:H	2.21	0.49
2:O:63:PHE:N	2:O:63:PHE:CD1	2.81	0.49
1:A:101:LYS:C	1:A:103:SER:H	2.20	0.49
1:A:124:ARG:C	1:A:125:ILE:HD12	2.37	0.49
1:A:442:MET:HE3	1:A:463:ILE:CG2	2.43	0.49
1:B:150:LEU:HD12	1:B:696:SER:HA	1.93	0.49
1:B:603:TYR:O	1:B:606:VAL:CG2	2.61	0.49
2:C:6:SER:O	2:C:8:SER:N	2.45	0.49
2:C:89:VAL:C	2:C:91:PHE:H	2.21	0.49
2:C:153:HIS:CE1	2:D:153:HIS:CD2	3.01	0.49
2:F:12:LYS:O	2:F:14:ALA:N	2.45	0.49
2:H:126:ARG:C	2:H:127:ILE:HG13	2.37	0.49
2:H:155:PRO:O	2:H:186:SER:HB3	2.13	0.49
2:I:89:VAL:C	2:I:91:PHE:H	2.19	0.49
2:J:1:MET:O	2:J:2:ASP:C	2.54	0.49
2:J:31:ILE:O	2:J:34:PHE:HB3	2.13	0.49
2:J:115:SER:O	2:J:119:LEU:HG	2.13	0.49
2:O:360:VAL:O	2:O:378:ARG:HD3	2.11	0.49
1:A:147:TYR:N	1:A:147:TYR:CD1	2.80	0.49
1:A:389:GLN:HE22	1:A:568:VAL:H	1.60	0.49
1:A:452:PRO:O	1:A:453:GLN:HB3	2.13	0.49
1:A:457:GLN:O	1:A:459:ALA:N	2.45	0.49
1:A:524:ASP:C	1:A:526:LYS:N	2.71	0.49
1:A:548:ARG:O	1:A:551:ALA:HB3	2.12	0.49
1:A:854:LEU:O	1:A:856:ALA:N	2.46	0.49
1:B:447:TYR:C	1:B:448:ARG:HG2	2.38	0.49
1:B:544:VAL:HG11	1:B:548:ARG:HH21	1.78	0.49
1:B:674:VAL:O	1:B:675:GLU:C	2.54	0.49
2:E:115:SER:O	2:E:119:LEU:HG	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:150:PHE:N	2:F:150:PHE:CD1	2.80	0.49
2:G:153:HIS:NE2	2:H:153:HIS:CD2	2.81	0.49
2:I:5:TYR:CE2	2:I:131:ASN:HA	2.47	0.49
2:I:253:ILE:HD13	2:I:319:THR:HB	1.93	0.49
2:L:139:TRP:HE1	2:L:143:ASN:HD22	1.61	0.49
2:M:5:TYR:HE2	2:M:131:ASN:HA	1.77	0.49
1:A:539:ARG:O	1:A:542:GLN:N	2.44	0.49
1:A:557:LEU:O	1:A:558:MET:C	2.55	0.49
1:A:652:PHE:N	1:A:652:PHE:CD1	2.80	0.49
1:A:662:MET:O	1:A:665:LEU:CB	2.61	0.49
1:A:820:THR:HG22	1:A:820:THR:O	2.13	0.49
1:B:158:GLY:O	1:B:159:ASP:C	2.56	0.49
1:B:182:LEU:HD21	1:B:846:LEU:HD12	1.95	0.49
1:B:434:THR:C	1:B:435:ILE:HG13	2.37	0.49
1:B:487:GLY:O	1:B:488:VAL:HB	2.13	0.49
1:B:854:LEU:CD2	1:B:855:LEU:N	2.76	0.49
2:E:21:GLY:O	2:E:22:THR:O	2.31	0.49
2:E:110:ALA:HB1	2:E:111:PRO:HD2	1.95	0.49
2:F:72:ASN:ND2	2:H:126:ARG:NH1	2.60	0.49
2:H:37:MET:O	2:H:38:ILE:C	2.55	0.49
2:J:2:ASP:HB2	2:J:128:ASN:HD21	1.77	0.49
2:O:1:MET:C	2:O:3:VAL:N	2.68	0.49
2:O:89:VAL:C	2:O:91:PHE:H	2.21	0.49
2:O:109:ILE:HB	2:O:380:ASP:HB3	1.94	0.49
1:A:192:ASN:O	1:A:193:SER:CB	2.49	0.49
1:A:870:ALA:C	1:A:872:ASP:H	2.20	0.49
1:B:87:GLN:C	1:B:89:GLU:N	2.68	0.49
1:B:139:GLU:O	1:B:141:GLU:N	2.46	0.49
1:B:428:GLN:O	1:B:432:VAL:HG23	2.13	0.49
1:B:501:HIS:O	1:B:503:ILE:HG13	2.12	0.49
1:B:676:VAL:O	1:B:680:ASP:HB2	2.13	0.49
1:B:845:ASN:HB3	1:B:848:PHE:HE1	1.77	0.49
2:F:46:PHE:CE2	2:F:119:LEU:HD21	2.48	0.49
2:F:101:VAL:HG23	2:F:102:ARG:N	2.27	0.49
2:G:42:ASN:HA	2:G:61:PHE:HB2	1.94	0.49
2:H:6:SER:O	2:H:8:SER:N	2.46	0.49
2:I:144:ARG:NH2	2:I:146:GLN:HE22	2.10	0.49
2:J:101:VAL:HG23	2:J:102:ARG:N	2.27	0.49
2:J:150:PHE:N	2:J:150:PHE:CD1	2.81	0.49
2:L:12:LYS:O	2:L:14:ALA:N	2.45	0.49
2:L:273:TYR:C	2:L:274:GLN:HE21	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:HIS:HE2	1:A:566:GLN:HE22	1.59	0.49
1:A:597:PRO:HB3	1:A:860:ALA:HB3	1.94	0.49
1:A:646:LEU:HD23	1:A:646:LEU:N	2.28	0.49
1:A:666:ARG:HG2	1:A:667:ASP:H	1.78	0.49
1:B:277:ARG:NH1	1:B:277:ARG:HB2	2.28	0.49
1:B:422:GLU:OE1	1:B:422:GLU:N	2.46	0.49
1:B:473:HIS:CB	2:I:126:ARG:NH2	2.69	0.49
1:B:587:LEU:O	1:B:587:LEU:CG	2.60	0.49
2:C:106:ARG:HG2	2:C:107:ASN:H	1.77	0.49
2:D:273:TYR:C	2:D:274:GLN:HE21	2.21	0.49
2:E:1:MET:C	2:E:3:VAL:N	2.68	0.49
2:F:37:MET:O	2:F:38:ILE:C	2.56	0.49
2:F:41:MET:O	2:F:42:ASN:C	2.56	0.49
2:G:12:LYS:O	2:G:14:ALA:N	2.46	0.49
2:K:59:TRP:N	2:K:59:TRP:CD1	2.79	0.49
2:K:273:TYR:C	2:K:274:GLN:HE21	2.21	0.49
2:M:12:LYS:O	2:M:14:ALA:N	2.46	0.49
2:M:273:TYR:C	2:M:274:GLN:HE21	2.20	0.49
2:O:125:LYS:C	2:O:127:ILE:H	2.21	0.49
1:A:122:LEU:HD11	1:A:201:ASP:CB	2.43	0.48
1:A:179:ASP:HA	1:A:677:ARG:NH2	2.27	0.48
1:A:271:PHE:CA	1:A:274:ILE:HD12	2.43	0.48
1:A:404:LEU:O	1:A:407:GLY:N	2.46	0.48
1:B:302:ASN:ND2	1:B:615:ASN:HB3	2.27	0.48
1:B:404:LEU:O	1:B:405:ILE:C	2.55	0.48
1:B:643:GLU:HG2	1:B:662:MET:HE1	1.95	0.48
1:B:785:GLN:O	1:B:787:VAL:N	2.46	0.48
2:C:1:MET:C	2:C:3:VAL:N	2.70	0.48
2:C:3:VAL:O	2:C:4:LEU:C	2.56	0.48
2:E:273:TYR:C	2:E:274:GLN:HE21	2.21	0.48
2:G:23:LEU:C	2:G:23:LEU:HD23	2.38	0.48
2:G:115:SER:O	2:G:119:LEU:HG	2.13	0.48
2:G:295:MET:HE3	2:G:298:PRO:HD3	1.96	0.48
2:I:49:GLY:HA2	2:I:54:LEU:CD2	2.43	0.48
2:K:1:MET:O	2:K:2:ASP:C	2.54	0.48
2:K:1:MET:C	2:K:3:VAL:N	2.68	0.48
2:M:151:THR:C	2:M:152:PHE:CD1	2.91	0.48
2:O:69:THR:O	2:O:70:LEU:O	2.31	0.48
1:A:529:ILE:O	1:A:533:ILE:HG13	2.12	0.48
1:B:137:ASN:O	1:B:137:ASN:CG	2.55	0.48
1:B:473:HIS:O	1:B:477:ASN:ND2	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:583:SER:O	1:B:587:LEU:HB3	2.12	0.48
2:I:122:LEU:C	2:I:124:PHE:H	2.21	0.48
2:K:6:SER:O	2:K:8:SER:N	2.46	0.48
2:K:14:ALA:C	2:K:18:ILE:HD12	2.39	0.48
2:L:109:ILE:HB	2:L:380:ASP:HB3	1.94	0.48
2:L:135:TYR:OH	2:L:340:GLU:OE1	2.30	0.48
2:M:6:SER:O	2:M:8:SER:N	2.45	0.48
2:M:38:ILE:HG22	2:M:42:ASN:ND2	2.27	0.48
2:N:21:GLY:O	2:N:22:THR:C	2.56	0.48
2:N:53:ASN:ND2	2:N:354:ALA:HB3	2.28	0.48
2:O:48:THR:O	2:O:56:ILE:HA	2.12	0.48
1:A:434:THR:O	1:A:434:THR:CG2	2.61	0.48
1:B:477:ASN:HD21	2:I:39:ILE:HG21	1.77	0.48
1:B:486:ASP:O	1:B:488:VAL:N	2.46	0.48
1:B:522:PRO:O	1:B:525:TYR:HB2	2.14	0.48
1:B:765:PHE:CZ	1:B:767:THR:HG23	2.48	0.48
1:B:870:ALA:O	1:B:871:PHE:C	2.55	0.48
2:G:37:MET:O	2:G:38:ILE:C	2.55	0.48
2:G:144:ARG:O	2:G:145:ARG:HB2	2.14	0.48
2:H:41:MET:O	2:H:42:ASN:C	2.56	0.48
2:I:19:VAL:HG21	2:K:128:ASN:HB3	1.94	0.48
2:J:135:TYR:OH	2:J:340:GLU:OE1	2.30	0.48
2:M:123:LYS:HG3	2:M:124:PHE:CE1	2.49	0.48
2:M:131:ASN:O	2:N:16:ASP:HB3	2.13	0.48
2:O:3:VAL:O	2:O:4:LEU:C	2.56	0.48
1:A:122:LEU:HD23	1:A:122:LEU:N	2.28	0.48
1:A:390:ARG:HE	1:A:574:GLU:HG2	1.78	0.48
1:A:416:ASN:C	1:A:418:MET:H	2.21	0.48
1:A:704:ILE:O	1:A:823:THR:HB	2.14	0.48
1:B:228:MET:HG3	1:B:228:MET:O	2.12	0.48
1:B:231:ARG:CB	1:B:240:ASN:HB2	2.42	0.48
1:B:275:PRO:HD2	1:B:278:ILE:CD1	2.43	0.48
1:B:321:ILE:O	1:B:322:THR:C	2.57	0.48
1:B:329:ALA:HB3	1:B:384:ALA:CB	2.43	0.48
1:B:361:GLN:NE2	3:W:624:LYS:HZ2	2.11	0.48
1:B:422:GLU:O	1:B:425:VAL:HB	2.12	0.48
2:E:89:VAL:C	2:E:91:PHE:H	2.22	0.48
2:E:125:LYS:C	2:E:127:ILE:H	2.21	0.48
2:E:133:SER:O	2:E:136:ILE:HG22	2.13	0.48
2:J:36:GLN:OE1	2:K:23:LEU:HD21	2.13	0.48
2:L:3:VAL:O	2:L:4:LEU:C	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:5:TYR:HE2	2:L:130:ASP:O	1.97	0.48
2:N:151:THR:C	2:N:152:PHE:CD1	2.91	0.48
1:A:170:TYR:CE1	1:A:682:PHE:HB2	2.49	0.48
1:A:215:GLU:CD	1:A:215:GLU:H	2.21	0.48
1:A:305:GLN:OE1	1:A:564:ASN:ND2	2.44	0.48
1:A:339:LEU:O	1:A:340:VAL:C	2.55	0.48
1:A:484:VAL:CG1	1:A:485:ILE:H	2.25	0.48
1:A:486:ASP:OD2	1:A:490:ASN:HB2	2.13	0.48
1:A:545:ASP:OD1	1:A:548:ARG:NH1	2.46	0.48
1:A:810:TYR:C	1:A:812:VAL:N	2.71	0.48
1:A:854:LEU:O	1:A:855:LEU:C	2.56	0.48
1:A:855:LEU:O	1:A:856:ALA:C	2.56	0.48
1:B:113:PRO:CD	1:B:609:ASN:HB3	2.43	0.48
1:B:176:GLU:O	1:B:178:PRO:CD	2.61	0.48
1:B:341:SER:O	1:B:342:THR:C	2.57	0.48
1:B:392:MET:CA	1:B:573:THR:HG23	2.43	0.48
1:B:521:MET:CB	1:B:522:PRO:CD	2.90	0.48
1:B:635:GLN:C	1:B:636:LYS:O	2.50	0.48
2:D:125:LYS:O	2:D:127:ILE:N	2.46	0.48
2:E:1:MET:O	2:E:2:ASP:C	2.56	0.48
2:E:6:SER:OG	2:E:128:ASN:HA	2.13	0.48
2:H:22:THR:OG1	2:H:26:ASN:ND2	2.46	0.48
2:H:115:SER:O	2:H:119:LEU:HG	2.13	0.48
2:I:48:THR:O	2:I:56:ILE:HA	2.13	0.48
2:J:155:PRO:O	2:J:186:SER:HB3	2.14	0.48
2:M:89:VAL:C	2:M:91:PHE:H	2.21	0.48
2:O:14:ALA:O	2:O:18:ILE:CD1	2.61	0.48
2:O:42:ASN:HA	2:O:61:PHE:HB2	1.95	0.48
1:A:118:LYS:CG	1:A:119:GLN:N	2.73	0.48
1:A:296:ALA:C	1:A:297:ARG:HG2	2.38	0.48
1:A:404:LEU:CB	1:A:435:ILE:HD11	2.43	0.48
1:A:428:GLN:CB	1:A:456:PHE:HD1	2.22	0.48
1:A:659:ASP:O	1:A:660:ASP:O	2.32	0.48
1:A:822:THR:O	1:A:823:THR:OG1	2.22	0.48
1:A:865:PRO:O	1:A:867:ASN:N	2.47	0.48
1:B:104:ILE:HD12	1:B:327:ILE:CD1	2.44	0.48
1:B:782:VAL:O	1:B:785:GLN:HB2	2.14	0.48
2:C:150:PHE:N	2:C:150:PHE:CD1	2.82	0.48
2:D:24:TYR:CE1	2:D:68:THR:HG22	2.48	0.48
2:D:31:ILE:O	2:D:34:PHE:HB3	2.13	0.48
2:D:150:PHE:HB2	2:D:152:PHE:HE1	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:53:ASN:ND2	2:F:354:ALA:HB3	2.28	0.48
2:G:54:LEU:HD12	2:G:55:PRO:HD2	1.96	0.48
2:J:3:VAL:O	2:J:4:LEU:C	2.56	0.48
2:K:3:VAL:O	2:K:4:LEU:C	2.56	0.48
2:K:295:MET:HE3	2:K:298:PRO:HD3	1.96	0.48
2:M:128:ASN:HD22	2:N:19:VAL:HB	1.79	0.48
1:A:216:GLU:CD	1:A:216:GLU:N	2.55	0.48
1:A:458:ILE:O	1:A:462:GLN:HG2	2.13	0.48
1:A:627:ALA:O	1:A:631:LEU:HG	2.13	0.48
1:B:220:ALA:O	1:B:223:ARG:HB2	2.14	0.48
1:B:305:GLN:CG	1:B:564:ASN:HD21	2.26	0.48
1:B:312:ASP:O	1:B:312:ASP:CG	2.56	0.48
1:B:459:ALA:HB1	1:B:463:ILE:CD1	2.36	0.48
1:B:542:GLN:O	1:B:543:LEU:C	2.57	0.48
1:B:701:GLN:CD	1:B:701:GLN:N	2.72	0.48
1:B:723:ILE:O	1:B:724:ALA:CB	2.61	0.48
2:C:1:MET:O	2:C:2:ASP:C	2.56	0.48
2:C:63:PHE:CD1	2:C:63:PHE:N	2.81	0.48
2:E:23:LEU:O	2:E:26:ASN:ND2	2.47	0.48
2:F:144:ARG:O	2:F:145:ARG:HG3	2.14	0.48
2:G:23:LEU:HD23	2:G:24:TYR:N	2.28	0.48
2:H:273:TYR:C	2:H:274:GLN:HE21	2.21	0.48
2:I:89:VAL:C	2:I:91:PHE:N	2.70	0.48
2:K:150:PHE:N	2:K:150:PHE:CD1	2.82	0.48
2:N:6:SER:O	2:N:8:SER:N	2.47	0.48
2:N:153:HIS:O	2:N:154:LYS:C	2.57	0.48
2:N:295:MET:HE3	2:N:298:PRO:HD3	1.96	0.48
1:A:145:ARG:HB3	1:A:147:TYR:CE1	2.49	0.48
1:A:583:SER:O	1:A:584:LEU:C	2.56	0.48
1:B:233:GLN:HB2	1:B:238:VAL:HB	1.96	0.48
1:B:319:ASP:OD2	1:B:572:THR:N	2.46	0.48
1:B:452:PRO:O	1:B:453:GLN:OE1	2.32	0.48
1:B:594:ILE:HB	1:B:595:PRO:HD2	1.94	0.48
1:B:745:ALA:HA	1:B:748:THR:OG1	2.13	0.48
1:B:775:ILE:N	1:B:775:ILE:CD1	2.76	0.48
2:D:70:LEU:CG	2:D:71:LEU:N	2.76	0.48
2:F:3:VAL:O	2:F:4:LEU:C	2.56	0.48
2:H:1:MET:O	2:H:2:ASP:C	2.57	0.48
2:I:128:ASN:O	2:J:22:THR:HB	2.14	0.48
2:L:89:VAL:C	2:L:91:PHE:N	2.71	0.48
2:M:22:THR:HG23	2:M:73:LEU:CD1	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:VAL:HG21	1:A:845:ASN:O	2.13	0.48
1:A:298:TYR:C	1:A:298:TYR:CD1	2.91	0.48
1:A:328:LEU:HG	1:A:603:TYR:HE1	1.79	0.48
1:A:484:VAL:HG12	1:A:485:ILE:N	2.28	0.48
1:A:563:MET:O	1:A:564:ASN:C	2.56	0.48
1:A:817:TRP:CZ3	1:A:819:PRO:HA	2.49	0.48
1:B:214:ASP:O	1:B:216:GLU:N	2.47	0.48
1:B:283:ASN:O	1:B:863:VAL:HG23	2.13	0.48
1:B:466:PHE:CD1	2:H:80:THR:HG22	2.48	0.48
1:B:517:GLN:N	1:B:518:PHE:CE1	2.79	0.48
1:B:536:LEU:N	1:B:536:LEU:CD2	2.77	0.48
1:B:712:LEU:HB3	1:B:819:PRO:HB2	1.96	0.48
1:B:811:LEU:HA	1:B:814:ASN:HD22	1.79	0.48
2:C:145:ARG:HB3	2:C:145:ARG:CZ	2.43	0.48
2:D:89:VAL:C	2:D:91:PHE:H	2.22	0.48
2:F:31:ILE:O	2:F:34:PHE:HB3	2.13	0.48
2:G:89:VAL:C	2:G:91:PHE:H	2.22	0.48
2:G:151:THR:C	2:G:152:PHE:CD1	2.92	0.48
2:J:346:VAL:CG2	2:J:385:VAL:HG13	2.44	0.48
2:K:89:VAL:C	2:K:91:PHE:H	2.21	0.48
2:K:89:VAL:C	2:K:91:PHE:N	2.71	0.48
2:L:50:GLY:HA2	2:L:56:ILE:HD11	1.95	0.48
2:L:106:ARG:HG2	2:L:107:ASN:H	1.78	0.48
2:O:295:MET:HE3	2:O:298:PRO:HD3	1.96	0.48
1:A:314:PHE:N	1:A:314:PHE:CD1	2.82	0.48
1:A:356:GLU:O	3:W:982:SER:HB2	2.14	0.48
1:A:436:ILE:HD11	1:A:437:TYR:CE1	2.49	0.48
1:A:527:ARG:O	1:A:531:ARG:HG3	2.13	0.48
1:A:694:ARG:HD2	1:A:828:GLN:HG3	1.96	0.48
1:A:785:GLN:O	1:A:786:ILE:C	2.57	0.48
1:B:126:PHE:HB3	1:B:149:LYS:O	2.14	0.48
1:B:236:ARG:O	1:B:237:ASN:CB	2.61	0.48
1:B:447:TYR:OH	1:B:458:ILE:HD11	2.13	0.48
1:B:449:ASN:HD21	1:B:455:PRO:HG3	1.78	0.48
1:B:533:ILE:O	1:B:536:LEU:HB2	2.14	0.48
1:B:743:ASP:CG	1:B:744:TYR:N	2.72	0.48
1:B:770:SER:O	1:B:771:VAL:C	2.57	0.48
2:E:60:ASN:C	2:E:61:PHE:CD1	2.91	0.48
2:F:38:ILE:HG22	2:F:42:ASN:ND2	2.27	0.48
2:I:4:LEU:O	2:I:5:TYR:C	2.57	0.48
2:I:346:VAL:CG2	2:I:385:VAL:HG13	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:19:VAL:O	2:J:21:GLY:N	2.47	0.48
2:J:133:SER:O	2:J:136:ILE:HG22	2.13	0.48
2:K:115:SER:O	2:K:119:LEU:HG	2.14	0.48
2:L:139:TRP:HE1	2:L:143:ASN:ND2	2.11	0.48
2:O:63:PHE:CD2	2:O:84:THR:HG23	2.49	0.48
2:O:346:VAL:CG2	2:O:385:VAL:HG13	2.44	0.48
1:A:393:SER:C	1:A:394:LEU:HG	2.38	0.47
1:B:122:LEU:HD11	1:B:200:VAL:HG11	1.94	0.47
1:B:405:ILE:O	1:B:408:MET:HB2	2.14	0.47
1:B:433:ASN:C	1:B:435:ILE:H	2.22	0.47
1:B:521:MET:H	1:B:521:MET:HE2	1.79	0.47
2:C:131:ASN:N	2:C:131:ASN:ND2	2.62	0.47
2:D:66:LEU:O	2:D:67:GLY:O	2.31	0.47
2:E:131:ASN:HD22	2:E:131:ASN:N	2.11	0.47
2:H:295:MET:HE3	2:H:298:PRO:HD3	1.96	0.47
2:I:48:THR:HG21	2:I:94:ASN:HB3	1.96	0.47
2:J:48:THR:O	2:J:56:ILE:HA	2.13	0.47
2:L:346:VAL:CG2	2:L:385:VAL:HG13	2.44	0.47
2:M:74:ASP:O	2:M:75:ALA:C	2.57	0.47
2:N:3:VAL:O	2:N:4:LEU:C	2.56	0.47
2:N:42:ASN:HA	2:N:61:PHE:CB	2.44	0.47
2:N:99:GLU:OE2	2:N:112:GLN:HG2	2.13	0.47
2:N:125:LYS:C	2:N:127:ILE:H	2.22	0.47
2:N:152:PHE:CD1	2:N:152:PHE:N	2.82	0.47
2:O:12:LYS:O	2:O:14:ALA:N	2.46	0.47
1:A:540:LEU:HA	1:A:543:LEU:HB2	1.96	0.47
2:C:5:TYR:HE2	2:C:131:ASN:HA	1.80	0.47
2:C:89:VAL:C	2:C:91:PHE:N	2.72	0.47
2:D:1:MET:C	2:D:3:VAL:N	2.70	0.47
2:D:99:GLU:CD	2:D:116:LEU:CD2	2.86	0.47
2:G:3:VAL:O	2:G:4:LEU:C	2.56	0.47
2:H:22:THR:HG23	2:H:73:LEU:CD1	2.43	0.47
2:H:51:ILE:HG23	2:H:51:ILE:O	2.14	0.47
2:H:89:VAL:C	2:H:91:PHE:H	2.22	0.47
2:H:89:VAL:C	2:H:91:PHE:N	2.73	0.47
2:M:1:MET:C	2:M:3:VAL:N	2.71	0.47
2:M:115:SER:O	2:M:119:LEU:HG	2.14	0.47
2:O:89:VAL:C	2:O:91:PHE:N	2.71	0.47
1:A:306:ASP:HB3	1:A:310:LEU:HD11	1.95	0.47
1:A:437:TYR:N	1:A:438:PRO:CD	2.73	0.47
1:A:503:ILE:HG12	1:A:547:THR:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:ARG:NH2	1:A:588:ILE:O	2.47	0.47
1:A:660:ASP:O	1:A:663:TYR:N	2.47	0.47
1:A:701:GLN:HB3	1:A:826:TYR:CD2	2.46	0.47
1:B:295:THR:O	1:B:297:ARG:HG2	2.14	0.47
1:B:493:LEU:HD11	1:B:567:HIS:HB2	1.95	0.47
1:B:810:TYR:C	1:B:812:VAL:HG12	2.38	0.47
1:B:822:THR:HG22	1:B:822:THR:O	2.14	0.47
2:H:133:SER:O	2:H:136:ILE:HG22	2.14	0.47
2:I:33:GLN:HA	2:J:23:LEU:HD12	1.95	0.47
2:I:149:GLY:C	2:I:150:PHE:CD1	2.92	0.47
2:M:11:LEU:O	2:M:15:ARG:N	2.41	0.47
2:M:89:VAL:C	2:M:91:PHE:N	2.72	0.47
1:A:714:ARG:HG2	1:A:720:TYR:HD2	1.79	0.47
1:A:827:LYS:O	1:A:828:GLN:O	2.32	0.47
1:B:249:ASP:O	1:B:250:TYR:C	2.58	0.47
1:B:355:LEU:HG	1:B:356:GLU:H	1.76	0.47
1:B:369:GLY:C	1:B:371:ASN:N	2.69	0.47
1:B:460:GLU:HG3	1:B:473:HIS:CD2	2.49	0.47
1:B:513:LEU:HA	1:B:516:GLN:HE22	1.71	0.47
2:D:48:THR:O	2:D:56:ILE:HA	2.14	0.47
2:D:295:MET:HE3	2:D:298:PRO:HD3	1.96	0.47
2:F:89:VAL:C	2:F:91:PHE:N	2.72	0.47
2:G:346:VAL:CG2	2:G:385:VAL:HG13	2.45	0.47
2:K:125:LYS:C	2:K:127:ILE:H	2.22	0.47
2:L:295:MET:HE3	2:L:298:PRO:HD3	1.96	0.47
2:N:27:VAL:O	2:N:28:SER:C	2.58	0.47
1:A:148:TRP:CH2	1:A:246:HIS:HB2	2.49	0.47
1:A:311:HIS:ND1	1:A:311:HIS:N	2.63	0.47
1:A:353:LEU:C	1:A:354:GLN:HG2	2.37	0.47
1:A:587:LEU:C	1:A:587:LEU:HD22	2.39	0.47
1:A:742:GLY:CA	1:B:285:ILE:HD11	2.44	0.47
1:B:95:ILE:O	1:B:97:THR:N	2.46	0.47
1:B:413:VAL:O	1:B:414:VAL:C	2.58	0.47
1:B:481:ARG:HG2	2:I:65:LEU:CD1	2.44	0.47
1:B:513:LEU:O	1:B:516:GLN:OE1	2.32	0.47
1:B:666:ARG:HG2	1:B:667:ASP:H	1.79	0.47
1:B:735:LEU:HD21	1:B:759:LEU:CB	2.45	0.47
2:C:4:LEU:O	2:C:5:TYR:C	2.58	0.47
2:C:115:SER:O	2:C:119:LEU:HG	2.15	0.47
2:C:295:MET:HE3	2:C:298:PRO:HD3	1.96	0.47
2:D:3:VAL:O	2:D:4:LEU:C	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:133:SER:O	2:F:136:ILE:HG22	2.14	0.47
2:F:295:MET:HE3	2:F:298:PRO:HD3	1.96	0.47
2:I:14:ALA:C	2:I:18:ILE:HD12	2.39	0.47
2:I:295:MET:HE3	2:I:298:PRO:HD3	1.96	0.47
2:J:129:PHE:O	2:J:131:ASN:ND2	2.47	0.47
2:K:125:LYS:O	2:K:127:ILE:N	2.45	0.47
2:N:23:LEU:HD23	2:N:24:TYR:N	2.29	0.47
2:O:115:SER:O	2:O:119:LEU:HG	2.14	0.47
1:A:338:GLU:HG3	1:A:338:GLU:O	2.14	0.47
1:A:527:ARG:HH11	1:A:531:ARG:HH21	1.63	0.47
1:A:596:SER:HB3	1:A:599:THR:OG1	2.15	0.47
1:A:723:ILE:O	1:A:824:LYS:HD2	2.14	0.47
1:A:864:GLU:CD	1:A:865:PRO:HD2	2.40	0.47
1:B:593:VAL:HG12	1:B:594:ILE:N	2.30	0.47
1:B:698:LYS:C	1:B:699:ILE:CD1	2.87	0.47
2:E:346:VAL:CG2	2:E:385:VAL:HG13	2.44	0.47
2:F:69:THR:O	2:F:70:LEU:C	2.56	0.47
2:F:78:VAL:O	2:F:81:ALA:HB3	2.14	0.47
2:F:89:VAL:C	2:F:91:PHE:H	2.22	0.47
2:I:144:ARG:O	2:I:145:ARG:HB2	2.15	0.47
2:K:100:MET:HG3	2:K:388:VAL:HG11	1.95	0.47
2:M:53:ASN:O	2:M:353:TYR:HD2	1.97	0.47
2:N:152:PHE:HD2	2:N:337:ASP:HB3	1.78	0.47
2:N:273:TYR:C	2:N:274:GLN:HE21	2.21	0.47
1:A:133:ILE:O	1:A:134:TYR:HD2	1.97	0.47
1:A:248:ILE:O	1:A:251:ALA:HB3	2.14	0.47
1:A:321:ILE:O	1:A:322:THR:C	2.58	0.47
1:A:450:GLY:O	1:A:451:ASP:CB	2.62	0.47
1:A:454:THR:HB	1:A:457:GLN:CB	2.44	0.47
1:A:508:GLU:HG2	1:A:512:GLN:HE21	1.75	0.47
1:A:699:ILE:HA	1:A:763:LEU:O	2.14	0.47
1:A:738:LEU:C	1:A:740:ARG:N	2.62	0.47
1:A:772:ILE:HA	1:A:775:ILE:CD1	2.45	0.47
1:A:775:ILE:C	1:A:777:LYS:N	2.71	0.47
1:B:122:LEU:O	1:B:253:ASN:OD1	2.32	0.47
1:B:308:LEU:HD23	1:B:308:LEU:HA	1.73	0.47
1:B:548:ARG:O	1:B:551:ALA:HB3	2.15	0.47
1:B:557:LEU:O	1:B:558:MET:C	2.58	0.47
1:B:721:VAL:CG1	1:B:722:ASN:N	2.77	0.47
1:B:725:ARG:H	1:B:725:ARG:CD	2.22	0.47
1:B:817:TRP:CD1	1:B:818:VAL:H	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:852:SER:O	1:B:854:LEU:N	2.46	0.47
2:D:135:TYR:CZ	2:D:342:MET:HE3	2.49	0.47
2:E:4:LEU:O	2:E:5:TYR:C	2.57	0.47
2:E:295:MET:HE3	2:E:298:PRO:HD3	1.96	0.47
2:F:72:ASN:ND2	2:H:126:ARG:HH11	2.12	0.47
2:F:142:GLN:HE21	2:F:143:ASN:N	2.12	0.47
2:H:23:LEU:N	2:H:26:ASN:HD22	2.12	0.47
2:I:102:ARG:HG2	2:I:102:ARG:HH11	1.80	0.47
2:I:139:TRP:HE1	2:I:143:ASN:HD22	1.62	0.47
2:J:63:PHE:CD2	2:J:84:THR:HG23	2.50	0.47
2:J:89:VAL:C	2:J:91:PHE:N	2.71	0.47
2:L:128:ASN:ND2	2:M:19:VAL:HG21	2.30	0.47
2:M:3:VAL:O	2:M:4:LEU:C	2.57	0.47
2:M:27:VAL:HG21	2:M:31:ILE:HD11	1.97	0.47
2:N:11:LEU:O	2:N:15:ARG:N	2.39	0.47
2:N:115:SER:O	2:N:119:LEU:HG	2.15	0.47
2:N:124:PHE:O	2:N:127:ILE:HG13	2.15	0.47
1:A:259:HIS:O	1:A:260:GLN:C	2.56	0.47
1:A:510:LEU:HD12	1:A:513:LEU:HD12	1.96	0.47
1:A:510:LEU:CD2	1:A:540:LEU:HD13	2.29	0.47
1:A:578:LEU:HA	1:A:581:VAL:CG2	2.44	0.47
1:A:594:ILE:HG12	1:A:595:PRO:HD2	1.95	0.47
1:A:763:LEU:HD23	1:A:764:PRO:CD	2.44	0.47
1:B:73:LEU:HB2	3:W:509:PHE:O	2.15	0.47
1:B:195:ASP:O	1:B:196:ALA:C	2.58	0.47
1:B:443:GLN:C	1:B:445:MET:H	2.21	0.47
1:B:458:ILE:HD12	1:B:459:ALA:CA	2.45	0.47
1:B:480:PHE:CE2	1:B:493:LEU:CB	2.96	0.47
1:B:549:LEU:HD12	1:B:549:LEU:HA	1.64	0.47
2:D:115:SER:O	2:D:119:LEU:HG	2.15	0.47
2:D:346:VAL:CG2	2:D:385:VAL:HG13	2.44	0.47
2:F:46:PHE:HE2	2:F:119:LEU:HD21	1.80	0.47
2:I:115:SER:O	2:I:119:LEU:HG	2.14	0.47
2:J:74:ASP:O	2:J:75:ALA:C	2.57	0.47
2:K:103:GLU:HG3	2:K:359:PRO:HD2	1.95	0.47
2:L:100:MET:HG3	2:L:388:VAL:HG11	1.95	0.47
2:N:346:VAL:CG2	2:N:385:VAL:HG13	2.44	0.47
2:O:73:LEU:HD22	2:O:77:TYR:CD2	2.50	0.47
2:O:104:SER:O	2:O:108:GLY:HA3	2.15	0.47
1:A:211:ILE:C	1:A:213:GLN:H	2.23	0.47
1:A:217:THR:O	1:A:218:GLU:HB2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:ARG:CD	1:A:559:ALA:HB2	2.43	0.47
1:A:663:TYR:O	1:A:666:ARG:N	2.47	0.47
1:A:803:ASN:ND2	1:A:806:SER:H	2.13	0.47
1:A:850:VAL:C	1:A:851:TYR:CD1	2.93	0.47
1:B:845:ASN:HB3	1:B:848:PHE:CE1	2.49	0.47
1:B:854:LEU:O	1:B:856:ALA:N	2.47	0.47
2:C:106:ARG:H	2:C:106:ARG:CD	2.10	0.47
2:E:5:TYR:HE2	2:E:130:ASP:O	1.98	0.47
2:F:53:ASN:HD22	2:F:354:ALA:CB	2.26	0.47
2:I:23:LEU:HD22	2:I:25:SER:OG	2.14	0.47
2:J:27:VAL:HG21	2:J:31:ILE:HD11	1.96	0.47
2:K:27:VAL:O	2:K:31:ILE:HG12	2.15	0.47
1:A:122:LEU:CD1	1:A:201:ASP:HB2	2.45	0.47
1:A:356:GLU:HB3	1:A:357:ALA:H	1.30	0.47
1:A:440:PHE:O	1:A:441:GLY:C	2.58	0.47
1:A:461:GLN:CA	2:F:32:GLN:NE2	2.75	0.47
1:B:112:LYS:N	1:B:113:PRO:CD	2.78	0.47
1:B:354:GLN:HA	1:B:354:GLN:OE1	2.15	0.47
1:B:383:ILE:HD11	1:B:550:LEU:HD23	1.97	0.47
1:B:519:PRO:O	1:B:520:THR:OG1	2.32	0.47
1:B:645:PHE:HD2	1:B:646:LEU:CD2	2.25	0.47
2:C:150:PHE:HA	2:D:397:LYS:NZ	2.30	0.47
2:E:3:VAL:O	2:E:4:LEU:C	2.57	0.47
2:F:145:ARG:C	2:F:146:GLN:HG2	2.40	0.47
2:H:11:LEU:O	2:H:15:ARG:N	2.39	0.47
2:H:346:VAL:CG2	2:H:385:VAL:HG13	2.44	0.47
2:J:295:MET:HE3	2:J:298:PRO:HD3	1.96	0.47
2:K:109:ILE:HG13	2:K:110:ALA:N	2.29	0.47
2:L:125:LYS:C	2:L:127:ILE:H	2.22	0.47
2:O:65:LEU:O	2:O:66:LEU:HD23	2.15	0.47
1:A:134:TYR:CE1	1:A:803:ASN:CG	2.93	0.46
1:A:169:LEU:HD12	1:A:169:LEU:HA	1.62	0.46
1:A:180:TYR:CD1	1:A:181:LEU:N	2.83	0.46
1:A:286:LEU:H	1:A:286:LEU:CD2	2.10	0.46
1:B:183:LEU:O	1:B:184:LYS:C	2.57	0.46
1:B:380:LYS:O	1:B:381:THR:C	2.58	0.46
1:B:409:TRP:O	1:B:412:THR:HB	2.16	0.46
1:B:479:GLN:O	1:B:480:PHE:HB3	2.16	0.46
1:B:501:HIS:HD1	1:B:548:ARG:HG2	1.80	0.46
2:C:129:PHE:CE1	2:C:130:ASP:HB2	2.50	0.46
2:D:128:ASN:HD22	2:E:19:VAL:HG21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:27:VAL:O	2:F:30:LEU:N	2.47	0.46
2:F:106:ARG:HB2	2:F:106:ARG:NH1	2.30	0.46
2:H:3:VAL:O	2:H:4:LEU:C	2.58	0.46
2:I:36:GLN:HE22	2:I:126:ARG:HD3	1.80	0.46
2:I:42:ASN:OD1	2:I:62:ASP:N	2.48	0.46
2:L:27:VAL:CG2	2:L:31:ILE:HD11	2.45	0.46
2:L:57:ARG:HB3	2:L:59:TRP:CZ2	2.49	0.46
2:N:4:LEU:O	2:N:5:TYR:C	2.58	0.46
2:N:124:PHE:O	2:N:126:ARG:N	2.49	0.46
2:O:153:HIS:C	2:O:155:PRO:N	2.71	0.46
1:A:419:PHE:N	1:A:419:PHE:CD1	2.82	0.46
1:A:746:GLN:O	1:A:750:MET:HG3	2.14	0.46
2:D:150:PHE:CD1	2:D:150:PHE:N	2.83	0.46
2:E:54:LEU:HD12	2:E:55:PRO:CD	2.42	0.46
2:I:74:ASP:O	2:I:75:ALA:C	2.57	0.46
2:I:128:ASN:HB3	2:J:19:VAL:CG2	2.44	0.46
2:I:144:ARG:O	2:I:145:ARG:CB	2.64	0.46
2:K:4:LEU:O	2:K:5:TYR:C	2.58	0.46
2:M:14:ALA:C	2:M:18:ILE:HD12	2.40	0.46
2:M:14:ALA:O	2:M:18:ILE:HD12	2.16	0.46
2:M:295:MET:HE3	2:M:298:PRO:HD3	1.96	0.46
1:A:250:TYR:HB2	1:A:840:HIS:CD2	2.50	0.46
1:A:253:ASN:O	1:A:256:PHE:HB2	2.14	0.46
1:A:499:ASN:CA	1:A:505:GLN:NE2	2.77	0.46
1:A:854:LEU:CD2	1:A:855:LEU:N	2.78	0.46
1:A:856:ALA:O	1:A:858:VAL:N	2.41	0.46
1:B:75:VAL:O	1:B:75:VAL:HG12	2.16	0.46
1:B:282:VAL:O	1:B:284:TYR:N	2.48	0.46
1:B:420:ILE:O	1:B:422:GLU:N	2.48	0.46
1:B:467:GLN:HE22	1:B:511:MET:HE3	1.80	0.46
1:B:820:THR:HG22	1:B:820:THR:O	2.15	0.46
2:C:62:ASP:H	2:C:63:PHE:HD1	1.62	0.46
2:C:110:ALA:HB1	2:C:111:PRO:HD2	1.97	0.46
2:E:73:LEU:HD22	2:E:77:TYR:CD2	2.50	0.46
2:F:100:MET:HG3	2:F:388:VAL:HG11	1.97	0.46
2:N:76:ASN:HB2	2:O:76:ASN:HB2	1.97	0.46
2:N:89:VAL:C	2:N:91:PHE:N	2.71	0.46
1:A:275:PRO:C	1:A:277:ARG:H	2.23	0.46
1:A:363:GLU:HA	1:A:366:PHE:HE1	1.80	0.46
1:A:428:GLN:HG3	1:A:456:PHE:HA	1.97	0.46
1:A:722:ASN:HB3	1:A:824:LYS:HA	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:848:PHE:C	1:A:849:THR:OG1	2.58	0.46
1:B:371:ASN:O	1:B:372:SER:C	2.58	0.46
1:B:383:ILE:O	1:B:384:ALA:C	2.57	0.46
1:B:500:GLY:HA3	1:B:871:PHE:HZ	1.80	0.46
1:B:818:VAL:HA	1:B:819:PRO:HD3	1.75	0.46
2:C:19:VAL:HG23	2:E:128:ASN:HB3	1.98	0.46
2:D:1:MET:O	2:D:2:ASP:C	2.56	0.46
2:D:4:LEU:O	2:D:5:TYR:C	2.58	0.46
2:D:38:ILE:HG22	2:D:42:ASN:ND2	2.30	0.46
2:D:89:VAL:C	2:D:91:PHE:N	2.72	0.46
2:F:115:SER:O	2:F:119:LEU:HG	2.14	0.46
2:G:125:LYS:C	2:G:127:ILE:H	2.24	0.46
2:H:27:VAL:HG21	2:H:31:ILE:HD11	1.96	0.46
2:H:150:PHE:CD1	2:H:150:PHE:N	2.84	0.46
2:I:397:LYS:HZ1	2:K:150:PHE:HA	1.79	0.46
2:K:63:PHE:CD1	2:K:63:PHE:N	2.82	0.46
2:L:153:HIS:NE2	2:M:153:HIS:CD2	2.84	0.46
2:M:128:ASN:HB3	2:N:19:VAL:HG23	1.97	0.46
2:O:4:LEU:O	2:O:5:TYR:C	2.58	0.46
1:A:145:ARG:HB3	1:A:147:TYR:HE1	1.79	0.46
1:A:151:LYS:O	1:A:152:LYS:CB	2.63	0.46
1:A:405:ILE:HG21	1:A:536:LEU:CG	2.43	0.46
1:A:633:LEU:C	1:A:635:GLN:N	2.72	0.46
1:B:360:ILE:O	1:B:361:GLN:HB2	2.15	0.46
2:D:14:ALA:O	2:D:18:ILE:HD12	2.16	0.46
2:I:6:SER:C	2:I:8:SER:N	2.73	0.46
2:J:148:THR:OG1	2:J:332:GLU:HG2	2.15	0.46
2:K:54:LEU:HD12	2:K:55:PRO:CD	2.41	0.46
2:L:6:SER:C	2:L:8:SER:N	2.73	0.46
2:L:151:THR:C	2:L:152:PHE:CD1	2.94	0.46
2:M:6:SER:C	2:M:8:SER:N	2.73	0.46
2:N:150:PHE:N	2:N:150:PHE:CD1	2.84	0.46
2:O:141:LEU:CD1	2:O:148:THR:HG21	2.46	0.46
1:A:122:LEU:CG	1:A:201:ASP:HB2	2.46	0.46
1:A:197:GLY:O	1:A:198:LYS:O	2.34	0.46
1:A:386:MET:HE3	1:A:414:VAL:HG13	1.98	0.46
1:A:414:VAL:C	1:A:416:ASN:H	2.22	0.46
1:A:454:THR:HG22	1:A:457:GLN:H	1.80	0.46
1:A:639:LYS:HE3	1:A:659:ASP:OD1	2.15	0.46
1:A:807:ASN:C	1:A:809:PHE:N	2.73	0.46
1:B:366:PHE:O	1:B:368:THR:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:490:ASN:O	1:B:492:VAL:HG23	2.15	0.46
1:B:605:ASN:ND2	1:B:855:LEU:HD12	2.30	0.46
2:D:14:ALA:C	2:D:18:ILE:HD12	2.41	0.46
2:I:61:PHE:CD1	2:I:61:PHE:N	2.83	0.46
2:O:74:ASP:O	2:O:75:ALA:C	2.58	0.46
2:O:139:TRP:NE1	2:O:143:ASN:ND2	2.63	0.46
1:A:299:ILE:O	1:A:301:PRO:HD3	2.15	0.46
1:A:314:PHE:CZ	1:A:664:ARG:HG2	2.51	0.46
1:A:329:ALA:HB3	1:A:384:ALA:CB	2.46	0.46
1:A:620:ASP:O	1:A:624:ILE:HG13	2.15	0.46
1:B:122:LEU:HD23	1:B:186:MET:HE1	1.98	0.46
1:B:413:VAL:CG1	1:B:414:VAL:H	2.26	0.46
1:B:807:ASN:C	1:B:809:PHE:H	2.23	0.46
1:B:857:PHE:N	1:B:857:PHE:CD1	2.72	0.46
2:D:61:PHE:N	2:D:61:PHE:CD1	2.84	0.46
2:D:74:ASP:O	2:D:75:ALA:C	2.59	0.46
2:D:123:LYS:HG3	2:D:124:PHE:CE1	2.50	0.46
2:F:22:THR:CG2	2:F:73:LEU:HD12	2.45	0.46
2:F:346:VAL:CG2	2:F:385:VAL:HG13	2.44	0.46
2:J:149:GLY:C	2:J:150:PHE:CD1	2.94	0.46
2:L:49:GLY:HA2	2:L:54:LEU:HD23	1.98	0.46
2:N:74:ASP:O	2:N:75:ALA:C	2.58	0.46
1:A:404:LEU:HB3	1:A:435:ILE:HD11	1.98	0.46
1:A:506:LEU:HD23	1:A:544:VAL:CA	2.29	0.46
1:A:660:ASP:HB3	1:B:539:ARG:NH1	2.20	0.46
1:A:708:ARG:HD2	1:A:708:ARG:HA	1.80	0.46
1:B:373:GLN:O	1:B:376:ASN:N	2.49	0.46
1:B:478:ASN:O	1:B:480:PHE:N	2.45	0.46
1:B:601:PHE:HB3	1:B:855:LEU:HD13	1.98	0.46
1:B:770:SER:O	1:B:773:SER:HB2	2.15	0.46
1:B:786:ILE:O	1:B:787:VAL:C	2.59	0.46
1:B:812:VAL:C	1:B:814:ASN:H	2.23	0.46
2:C:346:VAL:CG2	2:C:385:VAL:HG13	2.44	0.46
2:F:22:THR:HG23	2:F:73:LEU:HD12	1.98	0.46
2:I:3:VAL:O	2:I:4:LEU:C	2.57	0.46
2:L:153:HIS:CD2	2:N:153:HIS:NE2	2.83	0.46
2:M:346:VAL:CG2	2:M:385:VAL:HG13	2.45	0.46
2:N:61:PHE:CD1	2:N:61:PHE:N	2.84	0.46
1:A:461:GLN:CB	2:F:32:GLN:NE2	2.79	0.46
1:A:779:ASP:OD2	1:A:822:THR:O	2.34	0.46
1:A:846:LEU:HD23	1:A:846:LEU:HA	1.65	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:LYS:CG	1:B:119:GLN:N	2.73	0.46
1:B:239:VAL:CG2	1:B:845:ASN:O	2.63	0.46
1:B:252:PHE:O	1:B:253:ASN:C	2.59	0.46
1:B:314:PHE:HZ	1:B:664:ARG:HG2	1.78	0.46
1:B:345:GLN:HG3	1:B:349:MET:CE	2.46	0.46
1:B:383:ILE:HD11	1:B:550:LEU:HD22	1.97	0.46
1:B:465:ASN:O	1:B:466:PHE:C	2.58	0.46
1:B:510:LEU:HD13	1:B:540:LEU:HB2	1.98	0.46
1:B:552:TYR:O	1:B:553:ASN:C	2.58	0.46
1:B:727:LEU:HG	1:B:727:LEU:O	2.15	0.46
1:B:848:PHE:O	1:B:849:THR:OG1	2.28	0.46
1:B:856:ALA:C	1:B:858:VAL:N	2.72	0.46
2:I:72:ASN:CG	2:K:126:ARG:NH1	2.74	0.46
2:I:155:PRO:O	2:I:186:SER:HB3	2.16	0.46
2:I:382:LEU:HD22	2:I:386:PHE:CE2	2.51	0.46
2:J:27:VAL:CG2	2:J:31:ILE:HD11	2.45	0.46
2:J:142:GLN:HE21	2:J:143:ASN:N	2.13	0.46
2:L:104:SER:HB3	2:L:108:GLY:CA	2.46	0.46
2:O:22:THR:CG2	2:O:73:LEU:HD12	2.46	0.46
1:A:245:LEU:O	1:A:246:HIS:HB2	2.16	0.46
1:A:428:GLN:OE1	1:A:456:PHE:CB	2.38	0.46
1:A:509:ALA:O	1:A:513:LEU:CG	2.55	0.46
1:A:821:SER:OG	1:A:822:THR:N	2.46	0.46
1:B:94:THR:O	1:B:94:THR:HG22	2.16	0.46
1:B:489:LEU:C	1:B:489:LEU:HD23	2.41	0.46
1:B:613:ASN:O	1:B:617:ARG:HG2	2.16	0.46
1:B:706:ALA:C	1:B:708:ARG:N	2.72	0.46
1:B:776:ALA:O	1:B:777:LYS:C	2.58	0.46
2:E:74:ASP:O	2:E:75:ALA:C	2.58	0.46
2:F:239:ASN:ND2	2:F:246:THR:HG22	2.29	0.46
2:H:106:ARG:O	2:H:107:ASN:CB	2.62	0.46
2:H:239:ASN:ND2	2:H:246:THR:HG22	2.30	0.46
2:K:346:VAL:CG2	2:K:385:VAL:HG13	2.44	0.46
1:A:549:LEU:HA	1:A:549:LEU:HD12	1.65	0.45
1:B:170:TYR:CZ	1:B:682:PHE:HB2	2.52	0.45
1:B:637:LYS:HA	1:B:641:ILE:HD11	1.97	0.45
1:B:675:GLU:O	1:B:677:ARG:N	2.49	0.45
2:D:6:SER:C	2:D:8:SER:N	2.73	0.45
2:G:5:TYR:HE2	2:G:131:ASN:HA	1.80	0.45
2:H:62:ASP:H	2:H:63:PHE:HD1	1.63	0.45
2:J:27:VAL:O	2:J:28:SER:C	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:382:LEU:HD22	2:J:386:PHE:CE2	2.52	0.45
2:K:382:LEU:HD22	2:K:386:PHE:CE2	2.51	0.45
2:O:34:PHE:O	2:O:35:ASN:C	2.59	0.45
1:A:552:TYR:O	1:A:553:ASN:C	2.59	0.45
1:A:622:VAL:O	1:A:623:ALA:C	2.59	0.45
1:A:756:PRO:C	1:A:757:VAL:CG2	2.89	0.45
1:B:282:VAL:HG13	1:B:283:ASN:N	2.31	0.45
1:B:379:PHE:O	1:B:380:LYS:C	2.59	0.45
1:B:508:GLU:OE2	2:J:70:LEU:CD2	2.65	0.45
1:B:583:SER:OG	1:B:584:LEU:N	2.48	0.45
1:B:772:ILE:HG22	1:B:809:PHE:CE2	2.51	0.45
2:D:31:ILE:O	2:D:32:GLN:C	2.59	0.45
2:F:17:LYS:HE2	2:H:130:ASP:OD2	2.16	0.45
2:F:24:TYR:C	2:F:26:ASN:H	2.24	0.45
2:F:60:ASN:C	2:F:61:PHE:CD1	2.95	0.45
2:G:109:ILE:HD12	2:G:109:ILE:O	2.17	0.45
2:H:21:GLY:O	2:H:22:THR:O	2.34	0.45
2:I:36:GLN:HB2	2:J:23:LEU:HD11	1.97	0.45
2:I:136:ILE:HG23	2:I:137:GLU:N	2.31	0.45
2:L:73:LEU:HD22	2:L:77:TYR:HD2	1.77	0.45
2:L:115:SER:O	2:L:119:LEU:HG	2.15	0.45
2:M:382:LEU:HD22	2:M:386:PHE:CE2	2.52	0.45
1:A:147:TYR:HE2	1:A:717:MET:HE2	1.79	0.45
1:A:353:LEU:HD22	1:A:531:ARG:HB3	1.98	0.45
1:A:526:LYS:HG3	1:A:527:ARG:N	2.31	0.45
1:A:609:ASN:O	1:A:610:PHE:C	2.59	0.45
1:A:688:ASN:O	1:A:691:GLN:N	2.49	0.45
1:A:706:ALA:O	1:A:708:ARG:N	2.45	0.45
1:B:87:GLN:C	1:B:89:GLU:H	2.25	0.45
1:B:498:ARG:CZ	2:J:25:SER:HB3	2.47	0.45
1:B:542:GLN:N	1:B:542:GLN:OE1	2.49	0.45
1:B:594:ILE:HD12	1:B:594:ILE:O	2.17	0.45
1:B:633:LEU:O	1:B:635:GLN:N	2.48	0.45
2:C:59:TRP:N	2:C:59:TRP:CD1	2.83	0.45
2:C:124:PHE:O	2:C:127:ILE:HG13	2.16	0.45
2:D:34:PHE:O	2:D:35:ASN:C	2.59	0.45
2:E:190:VAL:HG21	2:E:210:HIS:HB2	1.99	0.45
2:F:74:ASP:O	2:F:75:ALA:C	2.59	0.45
2:H:382:LEU:HD22	2:H:386:PHE:CE2	2.51	0.45
2:J:78:VAL:O	2:J:81:ALA:N	2.40	0.45
2:J:133:SER:O	2:J:134:GLU:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:24:TYR:O	2:K:27:VAL:HG22	2.16	0.45
2:L:22:THR:CG2	2:L:73:LEU:HD12	2.24	0.45
2:L:239:ASN:ND2	2:L:246:THR:HG22	2.29	0.45
2:M:53:ASN:HD22	2:M:354:ALA:HB3	1.81	0.45
2:N:24:TYR:CE1	2:N:31:ILE:HG13	2.51	0.45
2:N:34:PHE:O	2:N:35:ASN:C	2.59	0.45
1:A:518:PHE:CB	1:A:519:PRO:CD	2.94	0.45
1:A:688:ASN:O	1:A:690:ASP:N	2.50	0.45
1:A:760:VAL:HG12	1:A:761:GLY:N	2.30	0.45
1:B:119:GLN:CG	1:B:181:LEU:HD11	2.46	0.45
1:B:159:ASP:O	1:B:162:VAL:HB	2.16	0.45
2:D:133:SER:O	2:D:134:GLU:C	2.59	0.45
2:E:89:VAL:C	2:E:91:PHE:N	2.73	0.45
2:H:34:PHE:O	2:H:35:ASN:C	2.60	0.45
2:J:6:SER:C	2:J:8:SER:N	2.73	0.45
2:M:66:LEU:O	2:M:67:GLY:C	2.58	0.45
2:M:144:ARG:O	2:M:145:ARG:HB2	2.17	0.45
1:A:249:ASP:O	1:A:250:TYR:C	2.60	0.45
1:A:857:PHE:N	1:A:857:PHE:CD1	2.83	0.45
1:B:224:PHE:HE1	2:O:70:LEU:C	2.24	0.45
1:B:434:THR:O	1:B:435:ILE:CG1	2.65	0.45
1:B:543:LEU:O	1:B:544:VAL:C	2.58	0.45
1:B:854:LEU:HD22	1:B:855:LEU:H	1.82	0.45
2:C:382:LEU:HD22	2:C:386:PHE:CE2	2.51	0.45
2:D:190:VAL:HG21	2:D:210:HIS:HB2	1.99	0.45
2:D:382:LEU:HD22	2:D:386:PHE:CE2	2.52	0.45
2:E:65:LEU:C	2:E:66:LEU:HG	2.42	0.45
2:G:4:LEU:O	2:G:5:TYR:C	2.59	0.45
2:I:225:LEU:HD13	2:I:277:PHE:HD2	1.82	0.45
2:M:130:ASP:HA	2:N:17:LYS:HG2	1.98	0.45
2:N:110:ALA:HB1	2:N:111:PRO:HD2	1.99	0.45
1:A:154:THR:O	1:A:155:LEU:C	2.59	0.45
1:A:367:LEU:CD2	3:W:932:ARG:HB2	2.46	0.45
1:A:482:GLN:OE1	1:A:493:LEU:CD2	2.64	0.45
1:A:712:LEU:CG	1:A:819:PRO:HB2	2.40	0.45
1:A:804:SER:HB2	1:A:810:TYR:CA	2.47	0.45
1:A:822:THR:O	1:A:823:THR:CB	2.64	0.45
1:B:622:VAL:O	1:B:623:ALA:C	2.59	0.45
1:B:646:LEU:HD23	1:B:646:LEU:N	2.32	0.45
2:C:128:ASN:O	2:D:22:THR:HB	2.17	0.45
2:C:190:VAL:HG21	2:C:210:HIS:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:24:TYR:O	2:D:26:ASN:N	2.50	0.45
2:D:78:VAL:O	2:D:81:ALA:HB3	2.17	0.45
2:E:312:GLN:HB3	2:E:313:PRO:HA	1.99	0.45
2:H:107:ASN:ND2	2:H:109:ILE:HG23	2.32	0.45
2:H:190:VAL:HG21	2:H:210:HIS:HB2	1.99	0.45
2:I:16:ASP:HB3	2:K:131:ASN:C	2.42	0.45
2:I:31:ILE:O	2:I:32:GLN:C	2.59	0.45
2:L:190:VAL:HG21	2:L:210:HIS:HB2	1.99	0.45
2:M:155:PRO:HA	2:M:337:ASP:HB2	1.99	0.45
2:N:124:PHE:C	2:N:126:ARG:H	2.24	0.45
1:A:155:LEU:HA	1:A:156:PRO:HD3	1.55	0.45
1:A:319:ASP:OD2	1:A:571:LEU:N	2.49	0.45
1:A:546:LEU:HD13	1:A:584:LEU:HD23	1.97	0.45
1:B:373:GLN:O	1:B:374:ALA:C	2.59	0.45
1:B:477:ASN:C	1:B:479:GLN:N	2.75	0.45
1:B:554:TYR:O	1:B:558:MET:HB2	2.17	0.45
1:B:577:GLN:O	1:B:579:THR:N	2.50	0.45
1:B:601:PHE:CD1	1:B:601:PHE:N	2.80	0.45
1:B:742:GLY:O	1:B:744:TYR:HE2	1.98	0.45
2:D:54:LEU:HD12	2:D:55:PRO:CD	2.46	0.45
2:E:11:LEU:O	2:E:15:ARG:N	2.41	0.45
2:E:382:LEU:HD22	2:E:386:PHE:CE2	2.51	0.45
2:F:190:VAL:HG21	2:F:210:HIS:HB2	1.99	0.45
2:G:150:PHE:HB2	2:G:152:PHE:CZ	2.51	0.45
2:H:6:SER:C	2:H:8:SER:N	2.74	0.45
2:H:105:GLN:O	2:H:107:ASN:N	2.50	0.45
2:H:312:GLN:HB3	2:H:313:PRO:HA	1.99	0.45
2:L:74:ASP:O	2:L:75:ALA:C	2.59	0.45
2:L:382:LEU:HD22	2:L:386:PHE:CE2	2.52	0.45
2:M:31:ILE:O	2:M:32:GLN:C	2.60	0.45
2:M:110:ALA:HB1	2:M:111:PRO:HD2	1.99	0.45
2:N:23:LEU:HD22	2:N:25:SER:OG	2.17	0.45
1:A:252:PHE:CD2	1:A:684:LEU:CD2	3.00	0.45
1:A:421:ARG:C	1:A:423:SER:H	2.25	0.45
1:A:452:PRO:O	1:A:453:GLN:OE1	2.35	0.45
1:A:454:THR:O	1:A:457:GLN:HB3	2.17	0.45
1:A:503:ILE:O	1:A:505:GLN:N	2.50	0.45
1:A:506:LEU:CD2	1:A:544:VAL:CA	2.94	0.45
1:A:649:LEU:C	1:A:650:HIS:O	2.60	0.45
1:B:400:ASN:O	1:B:404:LEU:CD1	2.65	0.45
2:D:225:LEU:HD13	2:D:277:PHE:HD2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:154:LYS:N	2:E:327:GLU:O	2.42	0.45
2:F:312:GLN:HB3	2:F:313:PRO:HA	1.99	0.45
2:G:34:PHE:O	2:G:35:ASN:C	2.60	0.45
2:G:382:LEU:HD22	2:G:386:PHE:CE2	2.51	0.45
2:H:48:THR:O	2:H:56:ILE:HA	2.17	0.45
2:H:108:GLY:C	2:H:110:ALA:N	2.75	0.45
2:I:42:ASN:OD1	2:I:61:PHE:HB3	2.16	0.45
2:I:145:ARG:O	2:I:146:GLN:CG	2.65	0.45
2:J:225:LEU:HD13	2:J:277:PHE:HD2	1.82	0.45
2:M:4:LEU:O	2:M:5:TYR:C	2.58	0.45
2:M:225:LEU:HD13	2:M:277:PHE:HD2	1.82	0.45
2:O:217:VAL:HG22	2:O:286:ASP:HB3	1.99	0.45
1:A:186:MET:HG3	1:A:200:VAL:HG13	1.98	0.45
1:A:341:SER:O	1:A:342:THR:C	2.60	0.45
1:A:583:SER:OG	1:A:584:LEU:N	2.50	0.45
1:A:783:PHE:N	1:A:783:PHE:CD1	2.72	0.45
1:B:119:GLN:NE2	1:B:181:LEU:HD11	2.32	0.45
1:B:277:ARG:HB3	1:B:277:ARG:HH11	1.80	0.45
1:B:496:ASN:HB3	1:B:499:ASN:H	1.82	0.45
1:B:553:ASN:O	1:B:554:TYR:C	2.60	0.45
1:B:573:THR:CG2	1:B:574:GLU:N	2.45	0.45
1:B:771:VAL:HG21	1:B:809:PHE:O	2.17	0.45
1:B:786:ILE:HG22	1:B:792:VAL:HG12	1.98	0.45
2:C:127:ILE:HG22	2:C:127:ILE:O	2.15	0.45
2:C:136:ILE:HG23	2:C:137:GLU:N	2.32	0.45
2:D:45:GLU:C	2:D:46:PHE:CD1	2.94	0.45
2:E:225:LEU:HD13	2:E:277:PHE:HD2	1.82	0.45
2:F:225:LEU:HD13	2:F:277:PHE:HD2	1.82	0.45
2:F:382:LEU:HD22	2:F:386:PHE:CE2	2.52	0.45
2:I:217:VAL:HG22	2:I:286:ASP:HB3	1.99	0.45
2:J:70:LEU:HD22	2:J:72:ASN:O	2.16	0.45
2:K:6:SER:C	2:K:8:SER:N	2.74	0.45
2:L:4:LEU:O	2:L:5:TYR:C	2.59	0.45
2:L:133:SER:O	2:L:134:GLU:C	2.60	0.45
2:M:312:GLN:HB3	2:M:313:PRO:HA	1.99	0.45
2:O:131:ASN:N	2:O:131:ASN:HD22	2.14	0.45
2:O:190:VAL:HG21	2:O:210:HIS:HB2	1.99	0.45
2:O:225:LEU:HD13	2:O:277:PHE:HD2	1.82	0.45
1:A:269:ILE:HG21	1:A:298:TYR:CE2	2.51	0.45
1:A:380:LYS:O	1:A:381:THR:C	2.60	0.45
1:A:428:GLN:HG2	1:A:429:LEU:H	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:MET:HE3	1:A:463:ILE:HB	1.99	0.45
1:A:866:ILE:HG22	1:A:866:ILE:O	2.17	0.45
1:B:387:LEU:C	1:B:389:GLN:N	2.74	0.45
1:B:467:GLN:HE21	1:B:511:MET:HG2	1.82	0.45
1:B:772:ILE:CG2	1:B:809:PHE:HE2	2.29	0.45
1:B:846:LEU:HD12	1:B:847:THR:N	2.32	0.45
2:C:34:PHE:O	2:C:35:ASN:C	2.60	0.45
2:C:217:VAL:HG22	2:C:286:ASP:HB3	1.99	0.45
2:G:31:ILE:O	2:G:32:GLN:C	2.59	0.45
2:G:190:VAL:HG21	2:G:210:HIS:HB2	1.99	0.45
2:H:1:MET:C	2:H:3:VAL:N	2.74	0.45
2:J:217:VAL:HG22	2:J:286:ASP:HB3	1.99	0.45
2:J:312:GLN:HB3	2:J:313:PRO:HA	1.99	0.45
2:K:190:VAL:HG21	2:K:210:HIS:HB2	1.99	0.45
2:M:42:ASN:HA	2:M:61:PHE:CB	2.46	0.45
2:N:382:LEU:HD22	2:N:386:PHE:CE2	2.52	0.45
1:A:118:LYS:CG	1:A:119:GLN:H	2.29	0.44
1:A:420:ILE:HD11	1:A:423:SER:HB2	1.99	0.44
1:A:587:LEU:O	1:A:587:LEU:HD22	2.17	0.44
1:A:680:ASP:HA	1:A:683:ASN:HD22	1.81	0.44
1:B:428:GLN:CB	1:B:456:PHE:CD1	2.90	0.44
1:B:763:LEU:HD22	1:B:764:PRO:HD3	1.99	0.44
2:D:8:SER:O	2:D:9:LYS:C	2.60	0.44
2:D:51:ILE:O	2:D:52:GLY:C	2.58	0.44
2:D:136:ILE:HG23	2:D:137:GLU:N	2.32	0.44
2:D:217:VAL:HG22	2:D:286:ASP:HB3	1.99	0.44
2:E:44:ASN:HB3	2:E:46:PHE:HE1	1.81	0.44
2:G:78:VAL:O	2:G:81:ALA:HB3	2.18	0.44
2:G:312:GLN:HB3	2:G:313:PRO:HA	1.99	0.44
2:I:190:VAL:HG21	2:I:210:HIS:HB2	1.99	0.44
2:J:153:HIS:NE2	2:K:153:HIS:CD2	2.84	0.44
2:K:225:LEU:HD13	2:K:277:PHE:HD2	1.82	0.44
2:L:225:LEU:HD13	2:L:277:PHE:HD2	1.82	0.44
2:L:312:GLN:HB3	2:L:313:PRO:HA	1.99	0.44
2:M:1:MET:O	2:M:2:ASP:C	2.58	0.44
1:A:270:ILE:HD11	1:A:292:LEU:CD1	2.23	0.44
1:A:286:LEU:O	1:A:287:ASN:CB	2.65	0.44
1:A:348:LYS:O	1:A:351:GLN:HB2	2.17	0.44
1:B:148:TRP:HE1	1:B:833:PHE:HD1	1.64	0.44
1:B:226:ALA:O	1:B:228:MET:N	2.50	0.44
1:B:248:ILE:O	1:B:251:ALA:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:374:ALA:O	1:B:580:SER:HB2	2.17	0.44
1:B:420:ILE:O	1:B:420:ILE:HG23	2.18	0.44
1:B:463:ILE:HD12	1:B:472:LEU:CD1	2.47	0.44
1:B:498:ARG:HG3	1:B:505:GLN:CD	2.42	0.44
1:B:632:ASN:C	1:B:634:TYR:H	2.23	0.44
1:B:666:ARG:O	1:B:667:ASP:C	2.60	0.44
1:B:688:ASN:O	1:B:689:MET:C	2.59	0.44
1:B:852:SER:O	1:B:853:ASP:HB3	2.16	0.44
2:C:6:SER:C	2:C:8:SER:N	2.74	0.44
2:C:22:THR:HG23	2:C:73:LEU:CD1	2.46	0.44
2:C:54:LEU:HD12	2:C:55:PRO:CD	2.44	0.44
2:D:62:ASP:C	2:D:63:PHE:CD1	2.95	0.44
2:E:8:SER:O	2:E:9:LYS:C	2.61	0.44
2:F:31:ILE:O	2:F:32:GLN:C	2.60	0.44
2:F:78:VAL:O	2:F:81:ALA:N	2.43	0.44
2:G:133:SER:O	2:G:134:GLU:C	2.61	0.44
2:I:140:ASN:O	2:I:143:ASN:N	2.50	0.44
2:J:4:LEU:O	2:J:5:TYR:C	2.58	0.44
2:L:397:LYS:HZ1	2:N:150:PHE:HA	1.82	0.44
2:M:239:ASN:ND2	2:M:246:THR:HG22	2.30	0.44
2:N:6:SER:C	2:N:8:SER:N	2.75	0.44
2:N:225:LEU:HD13	2:N:277:PHE:HD2	1.82	0.44
2:O:31:ILE:O	2:O:32:GLN:C	2.59	0.44
2:O:382:LEU:HD22	2:O:386:PHE:CE2	2.51	0.44
1:A:218:GLU:O	1:A:219:GLY:C	2.60	0.44
1:A:229:ARG:O	1:A:242:PRO:HG3	2.18	0.44
1:A:556:THR:O	1:A:558:MET:N	2.51	0.44
1:A:660:ASP:OD1	1:A:661:GLN:N	2.50	0.44
1:A:674:VAL:HB	1:A:679:LEU:HB2	1.99	0.44
1:A:714:ARG:O	1:A:715:ASP:C	2.59	0.44
1:B:183:LEU:HD12	1:B:844:SER:CB	2.47	0.44
1:B:368:THR:HG22	1:B:371:ASN:ND2	2.26	0.44
1:B:382:LEU:HD12	1:B:382:LEU:HA	1.62	0.44
1:B:558:MET:O	1:B:559:ALA:C	2.60	0.44
1:B:757:VAL:HG12	1:B:758:ALA:N	2.32	0.44
1:B:870:ALA:C	1:B:872:ASP:H	2.21	0.44
2:C:27:VAL:O	2:C:30:LEU:HB3	2.17	0.44
2:C:69:THR:OG1	2:C:70:LEU:N	2.49	0.44
2:F:6:SER:C	2:F:8:SER:N	2.73	0.44
2:F:153:HIS:CD2	2:H:153:HIS:NE2	2.86	0.44
2:G:99:GLU:CD	2:G:112:GLN:H	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:151:THR:C	2:J:152:PHE:CD1	2.95	0.44
2:K:78:VAL:O	2:K:81:ALA:N	2.40	0.44
2:K:111:PRO:O	2:K:112:GLN:HG2	2.17	0.44
2:K:239:ASN:ND2	2:K:246:THR:HG22	2.29	0.44
2:L:136:ILE:HG23	2:L:137:GLU:N	2.32	0.44
2:M:149:GLY:C	2:M:150:PHE:CD1	2.96	0.44
1:A:589:GLY:C	1:A:591:ALA:N	2.66	0.44
1:A:597:PRO:HB3	1:A:860:ALA:HB1	1.99	0.44
1:A:758:ALA:C	1:A:759:LEU:HG	2.36	0.44
1:A:804:SER:CB	1:A:810:TYR:HA	2.48	0.44
1:B:250:TYR:HB2	1:B:840:HIS:CD2	2.53	0.44
1:B:416:ASN:CG	1:B:417:ASP:N	2.75	0.44
1:B:630:ARG:O	1:B:631:LEU:CG	2.62	0.44
1:B:751:LEU:O	1:B:754:ASN:HA	2.16	0.44
1:B:790:ARG:CG	1:B:791:LYS:N	2.71	0.44
2:C:63:PHE:CD2	2:C:84:THR:HG23	2.52	0.44
2:C:145:ARG:CB	2:C:145:ARG:HH11	2.30	0.44
2:C:152:PHE:O	2:C:328:SER:HA	2.17	0.44
2:D:125:LYS:C	2:D:127:ILE:H	2.25	0.44
2:E:66:LEU:HB3	2:E:77:TYR:OH	2.16	0.44
2:E:78:VAL:O	2:E:81:ALA:HB3	2.17	0.44
2:F:48:THR:HG22	2:F:115:SER:OG	2.18	0.44
2:J:225:LEU:HD13	2:J:277:PHE:CD2	2.53	0.44
2:K:27:VAL:CG2	2:K:31:ILE:HD11	2.48	0.44
2:L:34:PHE:O	2:L:37:MET:HB3	2.17	0.44
2:M:34:PHE:O	2:M:35:ASN:C	2.60	0.44
2:N:190:VAL:HG21	2:N:210:HIS:HB2	1.99	0.44
1:A:130:GLN:NE2	1:A:146:TRP:CZ2	2.85	0.44
1:A:305:GLN:CD	1:A:305:GLN:N	2.75	0.44
1:A:513:LEU:CA	1:A:516:GLN:NE2	2.65	0.44
1:B:277:ARG:CB	1:B:277:ARG:HH11	2.30	0.44
1:B:315:GLU:O	1:B:316:SER:C	2.59	0.44
1:B:446:HIS:O	1:B:447:TYR:CB	2.49	0.44
1:B:494:ASN:CG	1:B:495:ASP:N	2.75	0.44
1:B:498:ARG:HH11	1:B:502:VAL:HG11	1.83	0.44
1:B:707:TYR:N	1:B:707:TYR:CD1	2.85	0.44
1:B:773:SER:O	1:B:774:LEU:C	2.59	0.44
2:C:74:ASP:O	2:C:75:ALA:C	2.60	0.44
2:C:133:SER:O	2:C:134:GLU:C	2.60	0.44
2:D:75:ALA:HB3	2:L:76:ASN:HA	2.00	0.44
2:F:82:ARG:CZ	2:H:144:ARG:HD2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:133:SER:O	2:F:134:GLU:C	2.60	0.44
2:G:1:MET:O	2:G:2:ASP:C	2.60	0.44
2:G:239:ASN:ND2	2:G:246:THR:HG22	2.29	0.44
2:I:101:VAL:HG11	2:I:355:ILE:HG13	1.99	0.44
2:J:31:ILE:O	2:J:32:GLN:C	2.60	0.44
2:K:136:ILE:HG23	2:K:137:GLU:N	2.32	0.44
2:K:149:GLY:C	2:K:150:PHE:CD1	2.95	0.44
2:M:136:ILE:HG23	2:M:137:GLU:N	2.33	0.44
2:M:150:PHE:O	2:M:330:VAL:HG13	2.17	0.44
2:N:38:ILE:HG22	2:N:42:ASN:ND2	2.29	0.44
2:N:78:VAL:O	2:N:81:ALA:HB3	2.17	0.44
2:O:6:SER:C	2:O:8:SER:N	2.73	0.44
1:A:426:ALA:O	1:A:427:CYS:C	2.61	0.44
1:A:488:VAL:O	1:A:490:ASN:N	2.51	0.44
1:A:508:GLU:C	1:A:512:GLN:NE2	2.73	0.44
1:A:516:GLN:OE1	1:A:517:GLN:N	2.50	0.44
1:A:701:GLN:CG	1:A:826:TYR:CD2	3.00	0.44
1:A:727:LEU:O	1:A:727:LEU:CD1	2.65	0.44
1:A:771:VAL:HG13	1:A:772:ILE:N	2.22	0.44
1:A:807:ASN:C	1:A:809:PHE:H	2.25	0.44
1:B:230:GLN:CD	1:B:230:GLN:H	2.25	0.44
1:B:393:SER:HA	1:B:423:SER:CB	2.47	0.44
1:B:426:ALA:O	1:B:427:CYS:C	2.61	0.44
1:B:449:ASN:ND2	1:B:455:PRO:HG3	2.33	0.44
1:B:452:PRO:C	1:B:453:GLN:CD	2.86	0.44
1:B:680:ASP:HA	1:B:683:ASN:HD22	1.82	0.44
1:B:727:LEU:HD23	1:B:826:TYR:CE1	2.53	0.44
2:E:5:TYR:O	2:E:6:SER:C	2.60	0.44
2:E:133:SER:O	2:E:134:GLU:C	2.60	0.44
2:E:225:LEU:HD13	2:E:277:PHE:CD2	2.53	0.44
2:F:11:LEU:O	2:F:15:ARG:N	2.40	0.44
2:F:153:HIS:O	2:F:154:LYS:C	2.61	0.44
2:F:249:PHE:CE2	2:F:251:PRO:HG3	2.53	0.44
2:G:33:GLN:HB2	2:H:26:ASN:OD1	2.16	0.44
2:G:89:VAL:C	2:G:91:PHE:N	2.73	0.44
2:G:104:SER:O	2:G:108:GLY:CA	2.66	0.44
2:H:31:ILE:O	2:H:32:GLN:C	2.60	0.44
2:H:67:GLY:O	2:H:69:THR:N	2.51	0.44
2:I:24:TYR:N	2:I:71:LEU:O	2.51	0.44
2:I:133:SER:O	2:I:134:GLU:C	2.60	0.44
2:J:34:PHE:O	2:J:35:ASN:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:133:SER:O	2:K:134:GLU:C	2.60	0.44
2:L:1:MET:O	2:L:2:ASP:C	2.59	0.44
2:M:225:LEU:HD13	2:M:277:PHE:CD2	2.53	0.44
2:N:63:PHE:CD1	2:N:63:PHE:N	2.85	0.44
2:O:136:ILE:HG23	2:O:137:GLU:N	2.32	0.44
1:A:312:ASP:O	1:A:313:ASN:CB	2.63	0.44
1:A:795:LEU:HD12	1:A:795:LEU:HA	1.74	0.44
1:B:102:GLU:O	1:B:103:SER:C	2.61	0.44
1:B:324:SER:O	1:B:325:ASN:C	2.61	0.44
1:B:428:GLN:HA	1:B:431:ILE:CD1	2.42	0.44
1:B:519:PRO:O	1:B:520:THR:CB	2.66	0.44
1:B:738:LEU:HD12	1:B:738:LEU:HA	1.82	0.44
1:B:786:ILE:C	1:B:788:LYS:N	2.76	0.44
1:B:855:LEU:O	1:B:856:ALA:C	2.60	0.44
2:D:73:LEU:HD23	2:D:73:LEU:N	2.33	0.44
2:D:249:PHE:CE2	2:D:251:PRO:HG3	2.53	0.44
2:G:6:SER:C	2:G:8:SER:N	2.72	0.44
2:H:142:GLN:NE2	2:H:143:ASN:N	2.65	0.44
2:H:217:VAL:HG22	2:H:286:ASP:HB3	2.00	0.44
2:H:249:PHE:CE2	2:H:251:PRO:HG3	2.53	0.44
2:I:46:PHE:HE2	2:I:119:LEU:HD21	1.83	0.44
2:I:225:LEU:HD13	2:I:277:PHE:CD2	2.53	0.44
2:J:78:VAL:O	2:J:81:ALA:HB3	2.17	0.44
2:K:14:ALA:O	2:K:16:ASP:N	2.51	0.44
2:K:110:ALA:HB1	2:K:111:PRO:HD2	2.00	0.44
2:K:312:GLN:HB3	2:K:313:PRO:HA	1.99	0.44
2:M:249:PHE:CE2	2:M:251:PRO:HG3	2.53	0.44
2:N:133:SER:O	2:N:134:GLU:C	2.61	0.44
2:N:217:VAL:HG22	2:N:286:ASP:HB3	2.00	0.44
2:O:153:HIS:CD2	2:O:154:LYS:N	2.86	0.44
2:O:169:SER:HA	2:O:176:LEU:HD23	2.00	0.44
2:O:225:LEU:HD13	2:O:277:PHE:CD2	2.53	0.44
1:A:216:GLU:C	1:A:218:GLU:H	2.25	0.44
1:A:625:ILE:H	1:A:625:ILE:HG13	1.62	0.44
1:B:108:LEU:N	1:B:108:LEU:CD2	2.79	0.44
1:B:155:LEU:HA	1:B:156:PRO:HD3	1.81	0.44
1:B:282:VAL:HG13	1:B:283:ASN:H	1.83	0.44
1:B:305:GLN:OE1	1:B:305:GLN:HA	2.18	0.44
1:B:406:SER:O	1:B:407:GLY:C	2.60	0.44
1:B:482:GLN:C	1:B:483:VAL:HG23	2.43	0.44
1:B:487:GLY:O	1:B:488:VAL:CB	2.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:508:GLU:O	1:B:512:GLN:NE2	2.48	0.44
2:C:249:PHE:CE2	2:C:251:PRO:HG3	2.53	0.44
2:D:66:LEU:HA	2:D:66:LEU:HD23	1.72	0.44
2:D:149:GLY:C	2:D:150:PHE:CD1	2.95	0.44
2:E:217:VAL:HG22	2:E:286:ASP:HB3	2.00	0.44
2:F:169:SER:HA	2:F:176:LEU:HD23	2.00	0.44
2:G:169:SER:HA	2:G:176:LEU:HD23	2.00	0.44
2:I:153:HIS:O	2:I:154:LYS:C	2.59	0.44
2:J:103:GLU:OE1	2:J:358:GLY:HA3	2.18	0.44
2:K:135:TYR:CZ	2:K:342:MET:HE3	2.53	0.44
2:K:227:PRO:HD3	2:K:277:PHE:CG	2.53	0.44
2:L:225:LEU:HD13	2:L:277:PHE:CD2	2.53	0.44
2:M:217:VAL:HG22	2:M:286:ASP:HB3	1.99	0.44
2:N:8:SER:O	2:N:9:LYS:C	2.61	0.44
2:O:312:GLN:HB3	2:O:313:PRO:HA	1.99	0.44
1:A:160:TYR:HE1	1:A:633:LEU:HA	1.83	0.44
1:A:181:LEU:H	1:A:260:GLN:HE21	1.65	0.44
1:A:226:ALA:C	1:A:228:MET:N	2.76	0.44
1:A:245:LEU:O	1:A:246:HIS:CB	2.66	0.44
1:A:456:PHE:O	1:A:457:GLN:C	2.61	0.44
1:A:521:MET:HE3	1:A:521:MET:CA	2.38	0.44
1:A:604:TYR:O	1:A:605:ASN:C	2.59	0.44
1:A:618:ILE:HD13	1:A:645:PHE:HZ	1.83	0.44
1:A:799:LEU:HD22	1:A:800:TYR:H	1.82	0.44
1:A:872:ASP:CG	1:A:874:MET:HB2	2.43	0.44
1:B:101:LYS:HB2	1:B:102:GLU:H	1.68	0.44
1:B:111:ILE:HG22	1:B:113:PRO:CD	2.48	0.44
1:B:122:LEU:HD12	1:B:124:ARG:HH22	1.82	0.44
1:B:207:ILE:O	1:B:210:ALA:HB3	2.18	0.44
1:B:218:GLU:C	1:B:220:ALA:N	2.76	0.44
1:B:353:LEU:O	1:B:353:LEU:HD23	2.18	0.44
1:B:473:HIS:HB3	2:I:126:ARG:NH1	2.26	0.44
1:B:496:ASN:HD22	1:B:498:ARG:HB2	1.83	0.44
1:B:543:LEU:O	1:B:546:LEU:HB2	2.18	0.44
1:B:675:GLU:O	1:B:678:ARG:N	2.51	0.44
1:B:790:ARG:CG	1:B:791:LYS:H	2.18	0.44
2:C:67:GLY:C	2:C:69:THR:N	2.72	0.44
2:C:397:LYS:HZ1	2:E:150:PHE:HA	1.82	0.44
2:D:5:TYR:CE2	2:D:131:ASN:HA	2.52	0.44
2:D:169:SER:HA	2:D:176:LEU:HD23	2.00	0.44
2:E:45:GLU:C	2:E:46:PHE:CD1	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:249:PHE:CE2	2:E:251:PRO:HG3	2.53	0.44
2:G:100:MET:HG3	2:G:388:VAL:HG11	1.99	0.44
2:G:150:PHE:N	2:G:150:PHE:CD1	2.86	0.44
2:H:78:VAL:O	2:H:81:ALA:HB3	2.17	0.44
2:I:63:PHE:CD1	2:I:63:PHE:N	2.86	0.44
2:J:8:SER:O	2:J:9:LYS:C	2.60	0.44
2:K:49:GLY:HA2	2:K:54:LEU:HD23	1.99	0.44
2:L:34:PHE:O	2:L:35:ASN:C	2.60	0.44
2:L:63:PHE:CD2	2:L:84:THR:HG23	2.53	0.44
2:M:190:VAL:HG21	2:M:210:HIS:HB2	1.99	0.44
2:N:169:SER:HA	2:N:176:LEU:HD23	2.00	0.44
2:O:65:LEU:C	2:O:66:LEU:HG	2.43	0.44
2:O:78:VAL:O	2:O:81:ALA:HB3	2.18	0.44
2:O:106:ARG:HG2	2:O:107:ASN:H	1.83	0.44
1:A:119:GLN:NE2	1:A:178:PRO:HG2	2.33	0.43
1:A:428:GLN:HE22	1:A:455:PRO:HB2	1.74	0.43
1:B:293:PRO:O	1:B:295:THR:N	2.50	0.43
1:B:506:LEU:CD2	1:B:544:VAL:HA	2.39	0.43
1:B:510:LEU:O	1:B:513:LEU:N	2.51	0.43
1:B:529:ILE:O	1:B:533:ILE:HG13	2.18	0.43
1:B:638:MET:HE2	1:B:666:ARG:NH1	2.32	0.43
2:C:225:LEU:HD13	2:C:277:PHE:HD2	1.82	0.43
2:D:5:TYR:O	2:D:6:SER:C	2.61	0.43
2:D:312:GLN:HB3	2:D:313:PRO:HA	1.99	0.43
2:G:8:SER:O	2:G:9:LYS:C	2.60	0.43
2:G:225:LEU:HD13	2:G:277:PHE:CD2	2.53	0.43
2:H:4:LEU:O	2:H:5:TYR:C	2.59	0.43
2:H:225:LEU:HD13	2:H:277:PHE:CD2	2.53	0.43
2:H:225:LEU:HD13	2:H:277:PHE:HD2	1.82	0.43
2:J:125:LYS:O	2:J:127:ILE:N	2.42	0.43
2:J:150:PHE:HA	2:K:397:LYS:HZ1	1.83	0.43
2:L:217:VAL:HG22	2:L:286:ASP:HB3	2.00	0.43
2:N:2:ASP:HB2	2:N:128:ASN:HD21	1.83	0.43
2:N:31:ILE:O	2:N:32:GLN:C	2.61	0.43
2:N:62:ASP:H	2:N:63:PHE:HD1	1.66	0.43
2:N:155:PRO:O	2:N:186:SER:HB3	2.17	0.43
2:O:227:PRO:HD3	2:O:277:PHE:CG	2.53	0.43
1:A:141:GLU:O	1:A:142:LEU:CB	2.65	0.43
1:A:187:ALA:O	1:A:188:VAL:CG2	2.66	0.43
1:A:333:VAL:HB	1:A:380:LYS:HG2	2.00	0.43
1:A:722:ASN:ND2	1:A:823:THR:O	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:138:GLY:O	1:B:804:SER:HB3	2.18	0.43
1:B:190:ASN:O	1:B:192:ASN:O	2.35	0.43
1:B:201:ASP:CG	1:B:202:SER:N	2.74	0.43
1:B:374:ALA:CB	1:B:580:SER:HB3	2.44	0.43
1:B:491:GLN:CG	1:B:564:ASN:HB3	2.48	0.43
1:B:498:ARG:CD	2:I:32:GLN:NE2	2.82	0.43
1:B:503:ILE:HG12	1:B:547:THR:HB	2.00	0.43
1:B:504:ASN:C	1:B:506:LEU:N	2.73	0.43
2:C:153:HIS:NE2	2:D:153:HIS:NE2	2.66	0.43
2:C:227:PRO:HD3	2:C:277:PHE:CG	2.53	0.43
2:C:239:ASN:ND2	2:C:246:THR:HG22	2.29	0.43
2:C:312:GLN:HB3	2:C:313:PRO:HA	1.99	0.43
2:G:61:PHE:N	2:G:61:PHE:CD1	2.86	0.43
2:I:36:GLN:CB	2:J:23:LEU:HD11	2.48	0.43
2:K:217:VAL:HG22	2:K:286:ASP:HB3	2.00	0.43
2:L:14:ALA:O	2:L:18:ILE:HD12	2.18	0.43
2:L:35:ASN:O	2:L:37:MET:N	2.51	0.43
2:M:22:THR:OG1	2:M:26:ASN:ND2	2.45	0.43
2:M:169:SER:HA	2:M:176:LEU:HD23	2.00	0.43
2:O:249:PHE:CE2	2:O:251:PRO:HG3	2.53	0.43
1:A:143:ARG:HG3	1:A:144:ASN:N	2.34	0.43
1:A:181:LEU:N	1:A:260:GLN:HE21	2.16	0.43
1:A:252:PHE:O	1:A:253:ASN:C	2.61	0.43
1:A:396:PHE:HD2	1:A:578:LEU:HD11	1.84	0.43
1:A:501:HIS:CA	1:A:503:ILE:HG13	2.48	0.43
1:A:520:THR:O	1:A:521:MET:HE3	2.18	0.43
1:A:591:ALA:O	1:A:877:MET:SD	2.76	0.43
1:A:751:LEU:HD21	1:A:783:PHE:O	2.18	0.43
1:A:769:SER:CB	1:A:807:ASN:OD1	2.60	0.43
1:A:772:ILE:O	1:A:774:LEU:N	2.51	0.43
1:B:306:ASP:C	1:B:308:LEU:N	2.67	0.43
1:B:309:ASN:HA	1:B:311:HIS:CE1	2.54	0.43
1:B:415:PRO:C	1:B:417:ASP:N	2.77	0.43
1:B:549:LEU:O	1:B:550:LEU:C	2.59	0.43
1:B:791:LYS:HB3	1:B:792:VAL:H	1.59	0.43
2:D:63:PHE:CD1	2:D:63:PHE:N	2.86	0.43
2:E:78:VAL:O	2:E:81:ALA:N	2.41	0.43
2:F:217:VAL:HG22	2:F:286:ASP:HB3	1.99	0.43
2:G:53:ASN:ND2	2:G:354:ALA:HB3	2.33	0.43
2:G:225:LEU:HD13	2:G:277:PHE:HD2	1.82	0.43
2:H:133:SER:O	2:H:134:GLU:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:227:PRO:HD3	2:H:277:PHE:CG	2.53	0.43
2:I:169:SER:HA	2:I:176:LEU:HD23	2.00	0.43
2:K:5:TYR:HE2	2:K:131:ASN:HA	1.79	0.43
2:K:31:ILE:O	2:K:32:GLN:C	2.60	0.43
2:M:128:ASN:HB3	2:N:19:VAL:CG2	2.48	0.43
2:M:135:TYR:OH	2:M:342:MET:HE3	2.18	0.43
2:N:136:ILE:HG23	2:N:137:GLU:N	2.33	0.43
2:N:227:PRO:HD3	2:N:277:PHE:CG	2.53	0.43
1:A:383:ILE:O	1:A:386:MET:N	2.52	0.43
1:A:750:MET:CE	1:A:757:VAL:HG21	2.48	0.43
1:A:781:THR:HG22	1:A:782:VAL:N	2.34	0.43
1:B:510:LEU:HD22	1:B:540:LEU:CD1	2.30	0.43
1:B:510:LEU:HA	1:B:513:LEU:HD12	1.99	0.43
1:B:595:PRO:HB2	1:B:600:LEU:HD11	2.00	0.43
1:B:604:TYR:O	1:B:605:ASN:C	2.61	0.43
2:E:142:GLN:HE21	2:E:143:ASN:N	2.16	0.43
2:E:227:PRO:HD3	2:E:277:PHE:CG	2.53	0.43
2:F:227:PRO:HD3	2:F:277:PHE:CG	2.53	0.43
2:G:249:PHE:CE2	2:G:251:PRO:HG3	2.53	0.43
2:H:169:SER:HA	2:H:176:LEU:HD23	2.00	0.43
2:I:146:GLN:O	2:I:148:THR:HG23	2.19	0.43
2:I:227:PRO:HD3	2:I:277:PHE:CG	2.53	0.43
2:I:312:GLN:HB3	2:I:313:PRO:HA	1.99	0.43
2:K:225:LEU:HD13	2:K:277:PHE:CD2	2.53	0.43
2:L:42:ASN:CA	2:L:61:PHE:HB2	2.30	0.43
2:M:24:TYR:N	2:M:71:LEU:O	2.49	0.43
2:N:19:VAL:O	2:N:20:GLU:C	2.60	0.43
2:N:101:VAL:HG11	2:N:355:ILE:HG13	2.01	0.43
2:N:225:LEU:HD13	2:N:277:PHE:CD2	2.53	0.43
2:O:133:SER:O	2:O:134:GLU:C	2.61	0.43
1:A:149:LYS:NZ	1:A:697:ASP:CG	2.77	0.43
1:A:243:SER:O	1:A:839:MET:HG2	2.19	0.43
1:A:408:MET:HG2	1:A:471:TRP:CH2	2.53	0.43
1:A:415:PRO:O	1:A:417:ASP:N	2.43	0.43
1:A:546:LEU:HD23	1:A:546:LEU:HA	1.86	0.43
1:A:548:ARG:HH11	1:A:877:MET:H	1.67	0.43
1:A:714:ARG:HG2	1:A:720:TYR:CD2	2.54	0.43
1:A:799:LEU:HA	1:A:799:LEU:HD23	1.68	0.43
1:B:309:ASN:HA	1:B:311:HIS:NE2	2.33	0.43
1:B:451:ASP:H	1:B:452:PRO:CD	2.20	0.43
1:B:540:LEU:HD23	1:B:541:GLY:CA	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:703:VAL:CG1	1:B:704:ILE:N	2.81	0.43
1:B:772:ILE:O	1:B:775:ILE:N	2.51	0.43
2:C:8:SER:O	2:C:9:LYS:C	2.61	0.43
2:C:31:ILE:O	2:C:32:GLN:C	2.60	0.43
2:C:78:VAL:O	2:C:81:ALA:HB3	2.17	0.43
2:E:24:TYR:HE1	2:E:31:ILE:HG13	1.83	0.43
2:E:125:LYS:O	2:E:127:ILE:N	2.51	0.43
2:E:136:ILE:HG23	2:E:137:GLU:N	2.34	0.43
2:F:225:LEU:HD13	2:F:277:PHE:CD2	2.53	0.43
2:G:38:ILE:H	2:G:38:ILE:HG13	1.59	0.43
2:G:217:VAL:HG22	2:G:286:ASP:HB3	1.99	0.43
2:H:74:ASP:O	2:H:75:ALA:C	2.60	0.43
2:I:34:PHE:O	2:I:37:MET:HB3	2.18	0.43
2:J:5:TYR:O	2:J:6:SER:C	2.61	0.43
2:J:124:PHE:C	2:J:126:ARG:N	2.76	0.43
2:J:125:LYS:C	2:J:127:ILE:H	2.26	0.43
2:J:169:SER:HA	2:J:176:LEU:HD23	2.00	0.43
2:K:8:SER:O	2:K:9:LYS:C	2.60	0.43
2:L:169:SER:HA	2:L:176:LEU:HD23	2.00	0.43
2:L:249:PHE:CE2	2:L:251:PRO:HG3	2.53	0.43
2:M:63:PHE:HD2	2:M:84:THR:HG23	1.81	0.43
2:M:123:LYS:HG3	2:M:124:PHE:CD1	2.53	0.43
2:M:155:PRO:HA	2:M:337:ASP:CB	2.49	0.43
2:N:24:TYR:HE1	2:N:31:ILE:HG13	1.83	0.43
2:N:63:PHE:CD2	2:N:84:THR:HG23	2.54	0.43
2:N:145:ARG:HA	2:N:145:ARG:HE	1.83	0.43
2:N:312:GLN:HB3	2:N:313:PRO:HA	1.99	0.43
2:O:72:ASN:O	2:O:73:LEU:C	2.61	0.43
2:O:105:GLN:O	2:O:106:ARG:C	2.61	0.43
1:A:501:HIS:HA	1:A:503:ILE:HG13	2.01	0.43
1:A:521:MET:CB	1:A:522:PRO:HD3	2.26	0.43
1:A:675:GLU:HB3	1:A:678:ARG:HG2	2.01	0.43
1:B:104:ILE:O	1:B:105:LEU:C	2.62	0.43
1:B:224:PHE:CD1	2:O:71:LEU:HD13	2.54	0.43
1:B:231:ARG:HD2	1:B:231:ARG:HA	1.77	0.43
1:B:383:ILE:O	1:B:386:MET:N	2.51	0.43
1:B:669:LEU:C	1:B:671:LEU:H	2.25	0.43
1:B:772:ILE:CG2	1:B:773:SER:H	2.29	0.43
2:D:153:HIS:O	2:D:154:LYS:C	2.60	0.43
2:E:6:SER:C	2:E:8:SER:N	2.73	0.43
2:E:31:ILE:O	2:E:32:GLN:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:152:PHE:O	2:E:328:SER:HA	2.19	0.43
2:F:163:SER:HB3	2:F:181:TRP:CZ2	2.54	0.43
2:L:8:SER:O	2:L:9:LYS:C	2.61	0.43
2:L:31:ILE:O	2:L:32:GLN:C	2.61	0.43
2:M:133:SER:O	2:M:134:GLU:C	2.60	0.43
2:O:62:ASP:H	2:O:63:PHE:HD1	1.66	0.43
1:A:387:LEU:HD23	1:A:554:TYR:CE1	2.54	0.43
1:A:428:GLN:O	1:A:432:VAL:HG23	2.19	0.43
1:A:693:GLU:O	1:A:695:ALA:O	2.37	0.43
1:B:447:TYR:C	1:B:448:ARG:CG	2.91	0.43
1:B:508:GLU:OE1	2:J:71:LEU:HB3	2.18	0.43
1:B:620:ASP:O	1:B:624:ILE:HG13	2.19	0.43
1:B:666:ARG:HG2	1:B:667:ASP:N	2.32	0.43
1:B:841:MET:HE2	2:O:69:THR:OG1	2.19	0.43
2:C:78:VAL:O	2:C:81:ALA:N	2.40	0.43
2:D:11:LEU:O	2:D:15:ARG:N	2.40	0.43
2:E:169:SER:HA	2:E:176:LEU:HD23	2.00	0.43
2:F:34:PHE:O	2:F:35:ASN:C	2.60	0.43
2:G:145:ARG:HE	2:I:142:GLN:NE2	2.17	0.43
2:H:35:ASN:O	2:H:37:MET:N	2.52	0.43
2:J:14:ALA:O	2:J:16:ASP:N	2.50	0.43
2:J:136:ILE:HG23	2:J:137:GLU:N	2.33	0.43
2:L:78:VAL:O	2:L:81:ALA:HB3	2.18	0.43
2:N:154:LYS:N	2:N:155:PRO:CD	2.82	0.43
2:O:144:ARG:C	2:O:146:GLN:H	2.26	0.43
1:A:370:ILE:O	1:A:374:ALA:HB2	2.19	0.43
1:A:571:LEU:HD22	1:A:571:LEU:HA	1.74	0.43
1:A:709:ASP:O	1:A:710:MET:HB3	2.18	0.43
1:B:252:PHE:C	1:B:254:GLU:N	2.76	0.43
1:B:387:LEU:O	1:B:388:SER:C	2.62	0.43
1:B:658:PRO:HB2	1:B:661:GLN:CG	2.39	0.43
1:B:776:ALA:O	1:B:778:LEU:N	2.52	0.43
1:B:871:PHE:CD1	1:B:872:ASP:N	2.87	0.43
2:C:53:ASN:HD22	2:C:354:ALA:HB3	1.83	0.43
2:C:126:ARG:C	2:C:127:ILE:CG1	2.92	0.43
2:E:34:PHE:O	2:E:35:ASN:C	2.60	0.43
2:I:11:LEU:O	2:I:15:ARG:N	2.38	0.43
2:J:190:VAL:HG21	2:J:210:HIS:HB2	1.99	0.43
2:N:249:PHE:CE2	2:N:251:PRO:HG3	2.53	0.43
2:O:5:TYR:O	2:O:6:SER:C	2.60	0.43
1:A:393:SER:HB2	1:A:573:THR:CG2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:PHE:HB3	1:A:578:LEU:HG	2.00	0.43
1:A:420:ILE:HD12	1:A:422:GLU:CG	2.49	0.43
1:A:481:ARG:HH12	1:A:497:ILE:CD1	2.32	0.43
1:A:510:LEU:HD13	1:A:540:LEU:HB2	2.01	0.43
1:A:815:TYR:H	1:A:815:TYR:HD1	1.62	0.43
1:B:218:GLU:OE1	1:B:836:ARG:NH2	2.51	0.43
1:B:409:TRP:CZ3	1:B:413:VAL:HG23	2.54	0.43
1:B:475:VAL:C	1:B:477:ASN:H	2.27	0.43
1:B:625:ILE:H	1:B:625:ILE:HG13	1.60	0.43
1:B:870:ALA:O	1:B:872:ASP:N	2.52	0.43
2:C:14:ALA:O	2:C:16:ASP:N	2.52	0.43
2:C:35:ASN:O	2:C:37:MET:N	2.52	0.43
2:E:70:LEU:HB3	2:E:72:ASN:O	2.19	0.43
2:F:8:SER:O	2:F:9:LYS:C	2.61	0.43
2:H:8:SER:O	2:H:9:LYS:C	2.62	0.43
2:I:5:TYR:O	2:I:6:SER:C	2.60	0.43
2:I:8:SER:O	2:I:9:LYS:C	2.62	0.43
2:I:16:ASP:HB3	2:K:131:ASN:O	2.18	0.43
2:I:27:VAL:O	2:I:30:LEU:HB3	2.19	0.43
2:J:66:LEU:HA	2:J:66:LEU:HD23	1.81	0.43
2:K:163:SER:HB3	2:K:181:TRP:CZ2	2.54	0.43
2:M:23:LEU:O	2:M:24:TYR:C	2.62	0.43
2:N:24:TYR:C	2:N:26:ASN:H	2.27	0.43
2:N:50:GLY:O	2:N:51:ILE:CG2	2.61	0.43
1:A:319:ASP:OD2	1:A:572:THR:N	2.52	0.43
1:A:330:ARG:C	1:A:332:VAL:N	2.75	0.43
1:A:339:LEU:HD13	1:A:588:ILE:HG12	2.00	0.43
1:A:396:PHE:HB3	1:A:578:LEU:CG	2.47	0.43
1:A:496:ASN:O	1:A:498:ARG:N	2.51	0.43
1:A:553:ASN:O	1:A:554:TYR:C	2.62	0.43
1:A:598:GLN:H	1:A:598:GLN:HG3	1.61	0.43
1:A:656:ARG:HB3	1:B:347:GLN:NE2	2.34	0.43
1:B:89:GLU:O	1:B:91:LEU:N	2.52	0.43
1:B:97:THR:O	1:B:98:PHE:C	2.61	0.43
1:B:108:LEU:C	1:B:110:ASP:H	2.26	0.43
1:B:126:PHE:CB	1:B:149:LYS:O	2.67	0.43
1:B:134:TYR:CD1	1:B:134:TYR:N	2.86	0.43
1:B:281:ASP:O	1:B:282:VAL:C	2.61	0.43
1:B:434:THR:C	1:B:435:ILE:CG1	2.92	0.43
1:B:477:ASN:ND2	2:I:39:ILE:CG2	2.81	0.43
1:B:544:VAL:O	1:B:545:ASP:C	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:563:MET:C	1:B:564:ASN:O	2.60	0.43
2:D:225:LEU:HD13	2:D:277:PHE:CD2	2.53	0.43
2:E:49:GLY:HA2	2:E:54:LEU:HD23	2.01	0.43
2:G:74:ASP:O	2:G:75:ALA:C	2.61	0.43
2:J:34:PHE:O	2:J:37:MET:HB3	2.18	0.43
2:J:35:ASN:O	2:J:37:MET:N	2.52	0.43
2:K:27:VAL:O	2:K:30:LEU:N	2.52	0.43
2:K:74:ASP:O	2:K:75:ALA:C	2.61	0.43
2:M:34:PHE:O	2:M:37:MET:HB3	2.19	0.43
2:M:56:ILE:O	2:M:56:ILE:HG22	2.19	0.43
2:O:163:SER:HB3	2:O:181:TRP:CZ2	2.54	0.43
1:A:355:LEU:HD23	1:A:355:LEU:HA	1.79	0.42
1:A:499:ASN:O	1:A:500:GLY:C	2.61	0.42
1:A:540:LEU:C	1:A:540:LEU:CD2	2.91	0.42
1:B:99:GLU:HB3	1:B:100:PRO:CD	2.35	0.42
1:B:251:ALA:HA	2:N:69:THR:CG2	2.42	0.42
1:B:305:GLN:HG3	1:B:489:LEU:CD2	2.49	0.42
1:B:548:ARG:CD	1:B:877:MET:H	2.31	0.42
1:B:657:VAL:O	1:B:658:PRO:C	2.62	0.42
1:B:795:LEU:O	1:B:797:PRO:HD3	2.18	0.42
2:C:34:PHE:O	2:C:37:MET:HB3	2.19	0.42
2:C:38:ILE:H	2:C:38:ILE:HG13	1.58	0.42
2:D:150:PHE:HB2	2:D:152:PHE:CZ	2.53	0.42
2:D:227:PRO:HD3	2:D:277:PHE:CG	2.53	0.42
2:E:14:ALA:C	2:E:18:ILE:HD12	2.44	0.42
2:E:154:LYS:HG2	2:E:186:SER:OG	2.19	0.42
2:F:127:ILE:O	2:F:128:ASN:C	2.62	0.42
2:F:148:THR:HB	2:F:149:GLY:H	1.64	0.42
2:I:163:SER:HB3	2:I:181:TRP:CZ2	2.54	0.42
2:I:249:PHE:CE2	2:I:251:PRO:HG3	2.53	0.42
2:J:227:PRO:HD3	2:J:277:PHE:CG	2.53	0.42
2:J:249:PHE:CE2	2:J:251:PRO:HG3	2.53	0.42
2:L:38:ILE:H	2:L:38:ILE:HG13	1.55	0.42
2:M:8:SER:O	2:M:9:LYS:C	2.62	0.42
2:N:35:ASN:O	2:N:37:MET:N	2.52	0.42
2:O:23:LEU:CD2	2:O:24:TYR:N	2.82	0.42
1:A:273:TYR:O	1:A:273:TYR:HD2	2.01	0.42
1:A:613:ASN:O	1:A:617:ARG:HG2	2.19	0.42
1:B:308:LEU:HB3	1:B:310:LEU:CD2	2.49	0.42
1:B:346:ILE:HA	1:B:349:MET:HB2	2.01	0.42
1:B:393:SER:H	1:B:573:THR:CG2	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:491:GLN:NE2	1:B:566:GLN:CG	2.79	0.42
1:B:498:ARG:CD	2:I:32:GLN:HE21	2.32	0.42
2:C:163:SER:HB3	2:C:181:TRP:CZ2	2.54	0.42
2:C:169:SER:HA	2:C:176:LEU:HD23	2.00	0.42
2:C:225:LEU:HD13	2:C:277:PHE:CD2	2.53	0.42
2:D:14:ALA:O	2:D:16:ASP:N	2.52	0.42
2:E:150:PHE:HB2	2:E:152:PHE:HE1	1.81	0.42
2:G:5:TYR:O	2:G:6:SER:C	2.62	0.42
2:G:227:PRO:HD3	2:G:277:PHE:CG	2.54	0.42
2:I:51:ILE:O	2:I:54:LEU:HB3	2.19	0.42
2:I:61:PHE:O	2:I:62:ASP:HB3	2.19	0.42
2:J:54:LEU:HD12	2:J:55:PRO:HD2	2.00	0.42
2:K:145:ARG:C	2:K:146:GLN:HG2	2.44	0.42
2:K:169:SER:HA	2:K:176:LEU:HD23	2.00	0.42
2:K:249:PHE:CE2	2:K:251:PRO:HG3	2.53	0.42
2:L:227:PRO:HD3	2:L:277:PHE:CG	2.53	0.42
2:M:227:PRO:HD3	2:M:277:PHE:CG	2.53	0.42
2:O:113:SER:O	2:O:117:ARG:HG3	2.18	0.42
1:A:265:LEU:HB3	1:A:296:ALA:HB1	2.00	0.42
1:A:370:ILE:O	1:A:374:ALA:CB	2.68	0.42
1:A:391:THR:O	1:A:573:THR:HA	2.19	0.42
1:A:510:LEU:HA	1:A:513:LEU:HD12	2.01	0.42
1:A:548:ARG:NH1	1:A:877:MET:CA	2.78	0.42
1:A:827:LYS:C	1:A:828:GLN:O	2.62	0.42
1:A:846:LEU:O	1:A:847:THR:C	2.62	0.42
1:B:177:MET:HE3	1:B:677:ARG:NE	2.34	0.42
1:B:609:ASN:O	1:B:610:PHE:C	2.62	0.42
1:B:636:LYS:O	1:B:637:LYS:CB	2.66	0.42
2:C:26:ASN:OD1	2:C:26:ASN:N	2.52	0.42
2:C:111:PRO:HB3	2:C:116:LEU:HD23	2.01	0.42
2:D:27:VAL:CG2	2:D:31:ILE:HD11	2.49	0.42
2:D:35:ASN:O	2:D:37:MET:N	2.53	0.42
2:E:19:VAL:O	2:E:20:GLU:C	2.62	0.42
2:E:63:PHE:CD1	2:E:63:PHE:N	2.87	0.42
2:G:1:MET:C	2:G:3:VAL:N	2.75	0.42
2:H:38:ILE:H	2:H:38:ILE:HG13	1.57	0.42
2:I:17:LYS:HG2	2:K:130:ASP:HA	2.01	0.42
2:I:36:GLN:NE2	2:I:126:ARG:HD3	2.34	0.42
2:L:106:ARG:H	2:L:106:ARG:CD	2.20	0.42
2:L:140:ASN:O	2:L:143:ASN:N	2.50	0.42
2:M:5:TYR:O	2:M:6:SER:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:116:LEU:O	2:N:119:LEU:N	2.48	0.42
1:A:383:ILE:HD11	1:A:550:LEU:CD2	2.49	0.42
1:A:402:MET:C	1:A:404:LEU:N	2.77	0.42
1:A:548:ARG:HH11	1:A:877:MET:N	2.17	0.42
1:A:660:ASP:CA	1:B:539:ARG:NH1	2.83	0.42
1:A:666:ARG:HA	1:A:669:LEU:HD12	2.00	0.42
1:A:714:ARG:CG	1:A:720:TYR:HD2	2.32	0.42
1:A:812:VAL:C	1:A:814:ASN:N	2.73	0.42
1:B:192:ASN:O	1:B:193:SER:HB3	2.19	0.42
1:B:239:VAL:CG2	1:B:844:SER:O	2.61	0.42
1:B:300:ARG:HA	1:B:301:PRO:HD3	1.76	0.42
1:B:478:ASN:O	1:B:478:ASN:CG	2.61	0.42
1:B:482:GLN:CA	1:B:493:LEU:HD22	2.49	0.42
1:B:621:ALA:O	1:B:622:VAL:C	2.60	0.42
1:B:735:LEU:O	1:B:736:GLU:C	2.63	0.42
1:B:789:LEU:O	1:B:790:ARG:O	2.37	0.42
1:B:853:ASP:O	1:B:854:LEU:CB	2.67	0.42
1:B:879:GLU:O	1:B:880:LEU:OXT	2.37	0.42
2:C:5:TYR:O	2:C:6:SER:C	2.61	0.42
2:C:46:PHE:CE2	2:C:119:LEU:HD21	2.54	0.42
2:C:227:PRO:O	2:C:228:ASP:HB2	2.20	0.42
2:E:227:PRO:O	2:E:228:ASP:HB2	2.19	0.42
2:F:123:LYS:HG3	2:F:124:PHE:CD1	2.53	0.42
2:F:136:ILE:HG23	2:F:137:GLU:N	2.34	0.42
2:F:168:ARG:HD2	2:F:175:ASN:O	2.20	0.42
2:I:151:THR:C	2:I:152:PHE:CD1	2.97	0.42
2:J:131:ASN:N	2:J:131:ASN:ND2	2.67	0.42
2:J:163:SER:HB3	2:J:181:TRP:CZ2	2.54	0.42
2:K:5:TYR:O	2:K:6:SER:C	2.62	0.42
2:K:139:TRP:HE1	2:K:143:ASN:HD22	1.66	0.42
2:L:24:TYR:O	2:L:26:ASN:N	2.52	0.42
2:L:62:ASP:H	2:L:63:PHE:HD1	1.66	0.42
2:L:163:SER:HB3	2:L:181:TRP:CZ2	2.54	0.42
2:N:163:SER:HB3	2:N:181:TRP:CZ2	2.54	0.42
2:N:168:ARG:HD2	2:N:175:ASN:O	2.20	0.42
1:A:319:ASP:OD2	1:A:570:THR:HG22	2.19	0.42
1:A:400:ASN:O	1:A:403:SER:HB2	2.20	0.42
1:A:570:THR:CG2	1:A:571:LEU:N	2.74	0.42
1:B:113:PRO:CG	1:B:609:ASN:HB3	2.49	0.42
1:B:146:TRP:O	1:B:833:PHE:HB3	2.20	0.42
1:B:470:ASN:O	1:B:471:TRP:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:496:ASN:C	1:B:498:ARG:N	2.73	0.42
1:B:603:TYR:O	1:B:604:TYR:C	2.62	0.42
2:C:128:ASN:O	2:C:129:PHE:HB2	2.20	0.42
2:E:24:TYR:CE1	2:E:31:ILE:HG13	2.54	0.42
2:F:153:HIS:NE2	2:G:153:HIS:NE2	2.67	0.42
2:G:136:ILE:HG23	2:G:137:GLU:N	2.33	0.42
2:G:163:SER:HB3	2:G:181:TRP:CZ2	2.54	0.42
2:I:168:ARG:HD2	2:I:175:ASN:O	2.20	0.42
2:K:23:LEU:H	2:K:26:ASN:ND2	2.17	0.42
2:L:66:LEU:HB3	2:L:67:GLY:H	1.66	0.42
2:L:227:PRO:O	2:L:228:ASP:HB2	2.20	0.42
2:M:14:ALA:O	2:M:16:ASP:N	2.52	0.42
2:M:78:VAL:O	2:M:81:ALA:HB3	2.19	0.42
2:M:145:ARG:CB	2:M:145:ARG:HH11	2.32	0.42
2:N:21:GLY:O	2:N:22:THR:O	2.36	0.42
2:N:34:PHE:O	2:N:37:MET:HB3	2.20	0.42
2:O:8:SER:O	2:O:9:LYS:C	2.62	0.42
2:O:99:GLU:CD	2:O:112:GLN:H	2.28	0.42
2:O:227:PRO:O	2:O:228:ASP:HB2	2.20	0.42
1:A:200:VAL:CG2	1:A:241:TYR:HD2	2.32	0.42
1:A:271:PHE:HA	1:A:274:ILE:CD1	2.47	0.42
1:A:351:GLN:O	1:A:353:LEU:N	2.53	0.42
1:A:443:GLN:HE22	1:A:522:PRO:HG3	1.84	0.42
1:A:546:LEU:HD21	1:A:588:ILE:HD12	1.99	0.42
1:A:593:VAL:HG12	1:A:594:ILE:N	2.35	0.42
1:A:594:ILE:HG23	1:A:595:PRO:HD2	2.01	0.42
1:A:876:ILE:O	1:A:877:MET:CB	2.68	0.42
1:B:199:VAL:HG13	1:B:242:PRO:O	2.20	0.42
1:B:555:GLU:OE2	1:B:871:PHE:CE2	2.69	0.42
2:C:9:LYS:HE3	2:C:13:ASP:OD1	2.19	0.42
2:E:59:TRP:CD1	2:E:59:TRP:N	2.87	0.42
2:E:163:SER:HB3	2:E:181:TRP:CZ2	2.54	0.42
2:E:340:GLU:HB3	2:E:342:MET:HE2	2.02	0.42
2:G:168:ARG:HD2	2:G:175:ASN:O	2.20	0.42
2:H:83:ASN:CG	2:I:122:LEU:HB2	2.38	0.42
2:I:78:VAL:O	2:I:81:ALA:HB3	2.20	0.42
2:J:227:PRO:O	2:J:228:ASP:HB2	2.20	0.42
2:N:101:VAL:HG12	2:N:350:ARG:HG2	2.01	0.42
1:A:125:ILE:HD12	1:A:125:ILE:H	1.77	0.42
1:A:554:TYR:OH	1:A:558:MET:HE1	2.20	0.42
1:A:571:LEU:CD2	1:B:531:ARG:CZ	2.97	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:709:ASP:OD2	1:A:820:THR:HG21	2.20	0.42
1:A:775:ILE:HG13	1:A:775:ILE:H	1.35	0.42
1:A:810:TYR:O	1:A:811:LEU:C	2.63	0.42
1:A:839:MET:CG	1:A:840:HIS:N	2.83	0.42
1:A:853:ASP:O	1:A:854:LEU:HB2	2.18	0.42
1:A:855:LEU:C	1:A:857:PHE:N	2.77	0.42
1:B:177:MET:HE2	1:B:677:ARG:HG2	2.02	0.42
1:B:243:SER:HB3	1:B:842:LEU:HD12	2.01	0.42
1:B:390:ARG:HG3	1:B:391:THR:N	2.34	0.42
1:B:409:TRP:CZ3	1:B:413:VAL:CG2	3.02	0.42
1:B:496:ASN:HD22	1:B:498:ARG:CB	2.32	0.42
2:E:168:ARG:HD2	2:E:175:ASN:O	2.20	0.42
2:F:227:PRO:O	2:F:228:ASP:HB2	2.20	0.42
2:G:9:LYS:HE3	2:G:13:ASP:OD1	2.19	0.42
2:H:136:ILE:HG23	2:H:137:GLU:N	2.34	0.42
2:H:142:GLN:NE2	2:H:142:GLN:C	2.77	0.42
2:K:78:VAL:O	2:K:81:ALA:HB3	2.19	0.42
2:L:45:GLU:C	2:L:46:PHE:CD1	2.98	0.42
2:L:168:ARG:HD2	2:L:175:ASN:O	2.20	0.42
2:L:340:GLU:HB3	2:L:342:MET:HE2	2.02	0.42
2:N:5:TYR:O	2:N:6:SER:C	2.61	0.42
2:N:227:PRO:O	2:N:228:ASP:HB2	2.19	0.42
2:N:340:GLU:HB3	2:N:342:MET:HE2	2.02	0.42
1:A:517:GLN:O	1:A:517:GLN:HG3	2.20	0.42
1:A:707:TYR:N	1:A:707:TYR:CD1	2.88	0.42
1:B:218:GLU:C	1:B:220:ALA:H	2.27	0.42
1:B:482:GLN:O	1:B:483:VAL:CG2	2.68	0.42
1:B:546:LEU:HD23	1:B:546:LEU:HA	1.81	0.42
2:C:155:PRO:HA	2:C:337:ASP:HB2	2.02	0.42
2:E:9:LYS:HE3	2:E:13:ASP:OD1	2.20	0.42
2:F:4:LEU:O	2:F:5:TYR:C	2.60	0.42
2:F:5:TYR:O	2:F:6:SER:C	2.61	0.42
2:F:102:ARG:C	2:F:103:GLU:HG3	2.44	0.42
2:G:253:ILE:HG13	2:H:234:PHE:CE1	2.55	0.42
2:H:5:TYR:O	2:H:6:SER:C	2.63	0.42
2:K:34:PHE:O	2:K:35:ASN:C	2.61	0.42
2:L:42:ASN:HB3	2:L:62:ASP:N	2.35	0.42
2:L:61:PHE:CD1	2:L:61:PHE:N	2.88	0.42
2:L:116:LEU:C	2:L:118:LYS:N	2.77	0.42
2:M:153:HIS:O	2:M:154:LYS:C	2.62	0.42
2:M:163:SER:HB3	2:M:181:TRP:CZ2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:355:ILE:HA	2:M:356:PRO:HD3	1.96	0.42
2:O:23:LEU:HG	2:O:24:TYR:H	1.85	0.42
2:O:124:PHE:O	2:O:127:ILE:HG13	2.19	0.42
1:A:141:GLU:O	1:A:142:LEU:HD12	2.20	0.42
1:A:201:ASP:O	1:A:202:SER:C	2.62	0.42
1:A:216:GLU:N	1:A:216:GLU:OE1	2.50	0.42
1:A:219:GLY:C	1:A:221:VAL:N	2.77	0.42
1:A:421:ARG:C	1:A:423:SER:N	2.78	0.42
1:A:487:GLY:O	1:A:488:VAL:CB	2.68	0.42
1:A:549:LEU:O	1:A:550:LEU:C	2.63	0.42
1:A:726:ASN:O	1:A:727:LEU:C	2.62	0.42
1:B:253:ASN:O	1:B:256:PHE:HB2	2.20	0.42
1:B:310:LEU:H	1:B:310:LEU:HG	1.44	0.42
1:B:454:THR:CG2	1:B:476:ASN:ND2	2.61	0.42
1:B:570:THR:HG22	1:B:571:LEU:N	2.34	0.42
1:B:597:PRO:O	1:B:598:GLN:C	2.62	0.42
1:B:646:LEU:HG	1:B:646:LEU:H	1.51	0.42
2:D:163:SER:HB3	2:D:181:TRP:CZ2	2.54	0.42
2:E:24:TYR:C	2:E:26:ASN:H	2.27	0.42
2:E:61:PHE:CD1	2:E:61:PHE:N	2.87	0.42
2:E:129:PHE:CE1	2:E:130:ASP:HB3	2.54	0.42
2:I:104:SER:HB3	2:I:108:GLY:HA2	2.02	0.42
2:I:340:GLU:HB3	2:I:342:MET:HE2	2.02	0.42
2:I:397:LYS:NZ	2:K:150:PHE:HA	2.34	0.42
2:J:73:LEU:HD22	2:J:77:TYR:CD2	2.54	0.42
2:J:253:ILE:HG13	2:K:234:PHE:CE1	2.55	0.42
2:K:9:LYS:HE3	2:K:13:ASP:OD1	2.20	0.42
2:K:227:PRO:O	2:K:228:ASP:HB2	2.20	0.42
2:M:7:LEU:H	2:M:7:LEU:HG	1.53	0.42
2:N:14:ALA:O	2:N:16:ASP:N	2.53	0.42
1:A:195:ASP:CG	1:A:196:ALA:N	2.73	0.42
1:A:201:ASP:O	1:A:204:THR:N	2.52	0.42
1:A:266:ASN:O	1:A:267:ASN:C	2.63	0.42
1:A:492:VAL:CG1	1:A:493:LEU:N	2.82	0.42
1:A:548:ARG:HB2	1:A:877:MET:HE2	2.01	0.42
1:A:695:ALA:O	1:A:696:SER:HB3	2.20	0.42
1:A:810:TYR:O	1:A:813:ALA:N	2.53	0.42
1:B:148:TRP:NE1	1:B:833:PHE:HD1	2.18	0.42
1:B:287:ASN:HD22	1:B:287:ASN:HA	1.60	0.42
1:B:416:ASN:C	1:B:418:MET:N	2.77	0.42
1:B:544:VAL:HG12	1:B:548:ARG:HE	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:746:GLN:HE22	2:D:64:GLY:HA2	1.85	0.42
1:B:756:PRO:C	1:B:757:VAL:CG2	2.93	0.42
2:C:168:ARG:HD2	2:C:175:ASN:O	2.20	0.42
2:E:14:ALA:O	2:E:16:ASP:N	2.52	0.42
2:G:23:LEU:HD23	2:G:25:SER:H	1.85	0.42
2:H:152:PHE:O	2:H:328:SER:HA	2.19	0.42
2:H:163:SER:HB3	2:H:181:TRP:CZ2	2.54	0.42
2:I:35:ASN:O	2:I:37:MET:N	2.52	0.42
2:K:35:ASN:O	2:K:37:MET:N	2.53	0.42
2:K:51:ILE:HG23	2:K:51:ILE:O	2.20	0.42
2:K:61:PHE:CD1	2:K:61:PHE:N	2.88	0.42
2:M:227:PRO:O	2:M:228:ASP:HB2	2.20	0.42
2:N:59:TRP:CD1	2:N:59:TRP:N	2.88	0.42
2:O:1:MET:HG3	2:O:2:ASP:N	2.34	0.42
2:O:239:ASN:ND2	2:O:246:THR:HG22	2.29	0.42
1:A:129:ARG:HG2	1:A:130:GLN:H	1.84	0.41
1:A:162:VAL:O	1:A:165:TYR:HB3	2.20	0.41
1:A:174:LEU:HA	1:A:177:MET:HB2	2.01	0.41
1:A:365:GLN:C	1:A:366:PHE:CD1	2.98	0.41
1:A:842:LEU:HD23	1:A:842:LEU:HA	1.76	0.41
1:A:853:ASP:OD1	1:A:854:LEU:N	2.53	0.41
1:B:224:PHE:CE1	2:O:71:LEU:N	2.87	0.41
1:B:501:HIS:O	1:B:503:ILE:N	2.53	0.41
1:B:526:LYS:O	1:B:530:GLN:HG2	2.20	0.41
1:B:549:LEU:HD22	1:B:877:MET:HE1	2.03	0.41
1:B:611:HIS:O	1:B:612:SER:C	2.63	0.41
1:B:799:LEU:HD22	1:B:799:LEU:C	2.38	0.41
2:C:235:PRO:HA	2:C:249:PHE:O	2.20	0.41
2:E:106:ARG:HB3	2:E:107:ASN:H	1.54	0.41
2:E:239:ASN:ND2	2:E:246:THR:HG22	2.30	0.41
2:F:119:LEU:C	2:F:121:GLY:N	2.78	0.41
2:H:227:PRO:O	2:H:228:ASP:HB2	2.20	0.41
2:I:27:VAL:O	2:I:31:ILE:HG12	2.19	0.41
2:I:122:LEU:C	2:I:124:PHE:N	2.78	0.41
2:L:5:TYR:O	2:L:6:SER:C	2.63	0.41
2:L:124:PHE:O	2:L:126:ARG:N	2.53	0.41
2:L:235:PRO:HA	2:L:249:PHE:O	2.20	0.41
2:M:127:ILE:O	2:M:128:ASN:C	2.62	0.41
2:N:76:ASN:HA	2:O:75:ALA:HB3	2.01	0.41
2:O:125:LYS:O	2:O:127:ILE:N	2.51	0.41
1:A:124:ARG:HD2	1:A:203:GLU:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:PRO:CG	1:A:278:ILE:HD11	2.50	0.41
1:A:314:PHE:HZ	1:A:664:ARG:HG2	1.84	0.41
1:A:379:PHE:O	1:A:380:LYS:C	2.62	0.41
1:A:404:LEU:HD22	1:A:435:ILE:HD11	2.02	0.41
1:A:493:LEU:HD11	1:A:566:GLN:O	2.20	0.41
1:A:611:HIS:O	1:A:612:SER:C	2.63	0.41
1:A:656:ARG:O	1:A:657:VAL:HG23	2.20	0.41
1:A:803:ASN:O	1:A:803:ASN:CG	2.63	0.41
1:B:406:SER:O	1:B:409:TRP:N	2.51	0.41
1:B:466:PHE:CE1	2:H:80:THR:HG22	2.55	0.41
2:C:142:GLN:OE1	2:N:145:ARG:NH1	2.48	0.41
2:C:234:PHE:CE1	2:E:253:ILE:HG13	2.55	0.41
2:C:340:GLU:HB3	2:C:342:MET:HE2	2.02	0.41
2:D:70:LEU:CD1	2:D:71:LEU:N	2.82	0.41
2:D:116:LEU:O	2:D:119:LEU:N	2.50	0.41
2:F:27:VAL:O	2:F:31:ILE:HG12	2.20	0.41
2:F:234:PHE:CE1	2:H:253:ILE:HG13	2.55	0.41
2:H:168:ARG:HD2	2:H:175:ASN:O	2.20	0.41
2:K:168:ARG:HD2	2:K:175:ASN:O	2.20	0.41
2:L:2:ASP:O	2:L:3:VAL:C	2.63	0.41
2:M:155:PRO:O	2:M:186:SER:HB3	2.20	0.41
2:M:340:GLU:HB3	2:M:342:MET:HE2	2.02	0.41
2:N:127:ILE:O	2:N:128:ASN:C	2.63	0.41
2:O:38:ILE:HG22	2:O:42:ASN:ND2	2.33	0.41
1:A:170:TYR:CZ	1:A:682:PHE:HB2	2.55	0.41
1:A:195:ASP:O	1:A:196:ALA:C	2.63	0.41
1:A:236:ARG:HB2	1:A:238:VAL:CG2	2.47	0.41
1:A:293:PRO:C	1:A:295:THR:H	2.28	0.41
1:A:324:SER:O	1:A:325:ASN:C	2.63	0.41
1:A:382:LEU:O	1:A:385:ALA:HB3	2.20	0.41
1:A:647:LYS:HG2	1:A:654:VAL:HG21	1.99	0.41
1:B:456:PHE:O	1:B:457:GLN:O	2.38	0.41
1:B:548:ARG:O	1:B:549:LEU:C	2.63	0.41
1:B:646:LEU:O	1:B:649:LEU:HB2	2.20	0.41
1:B:721:VAL:CG1	1:B:722:ASN:H	2.30	0.41
2:C:119:LEU:C	2:C:121:GLY:N	2.78	0.41
2:D:168:ARG:HD2	2:D:175:ASN:O	2.20	0.41
2:E:35:ASN:O	2:E:37:MET:N	2.53	0.41
2:E:128:ASN:O	2:E:129:PHE:CB	2.68	0.41
2:G:144:ARG:O	2:G:145:ARG:CB	2.67	0.41
2:G:235:PRO:HA	2:G:249:PHE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:14:ALA:O	2:I:16:ASP:N	2.53	0.41
2:I:116:LEU:C	2:I:118:LYS:N	2.77	0.41
2:J:239:ASN:ND2	2:J:246:THR:HG22	2.29	0.41
2:K:34:PHE:O	2:K:37:MET:HB3	2.20	0.41
2:K:45:GLU:C	2:K:46:PHE:CD1	2.98	0.41
2:L:48:THR:O	2:L:56:ILE:HA	2.20	0.41
2:M:153:HIS:NE2	2:N:153:HIS:CD2	2.88	0.41
2:M:253:ILE:HG13	2:N:234:PHE:CE1	2.55	0.41
2:N:91:PHE:O	2:N:92:VAL:C	2.64	0.41
2:N:148:THR:OG1	2:N:332:GLU:HG2	2.20	0.41
2:N:239:ASN:ND2	2:N:246:THR:HG22	2.29	0.41
1:A:163:ARG:NE	1:A:631:LEU:O	2.54	0.41
1:B:275:PRO:HB2	1:B:278:ILE:HD13	2.03	0.41
1:B:322:THR:HG22	1:B:390:ARG:HD3	2.02	0.41
1:B:369:GLY:C	1:B:371:ASN:H	2.28	0.41
1:B:449:ASN:ND2	1:B:455:PRO:HB3	2.36	0.41
1:B:743:ASP:OD2	1:B:745:ALA:CA	2.68	0.41
2:C:153:HIS:CD2	2:E:153:HIS:CE1	3.08	0.41
2:C:253:ILE:HG13	2:D:234:PHE:CE1	2.55	0.41
2:D:34:PHE:O	2:D:37:MET:HB3	2.20	0.41
2:G:35:ASN:O	2:G:37:MET:N	2.54	0.41
2:J:116:LEU:C	2:J:118:LYS:N	2.78	0.41
2:M:35:ASN:O	2:M:37:MET:N	2.53	0.41
2:N:78:VAL:O	2:N:81:ALA:N	2.39	0.41
2:O:61:PHE:CD1	2:O:61:PHE:N	2.87	0.41
2:O:119:LEU:C	2:O:121:GLY:N	2.79	0.41
1:A:542:GLN:N	1:A:542:GLN:OE1	2.53	0.41
1:A:810:TYR:CD1	1:A:810:TYR:C	2.97	0.41
1:B:191:LYS:HD3	1:B:191:LYS:HA	1.90	0.41
1:B:735:LEU:CG	1:B:760:VAL:O	2.59	0.41
2:D:227:PRO:O	2:D:228:ASP:HB2	2.20	0.41
2:D:253:ILE:HG13	2:E:234:PHE:CE1	2.55	0.41
2:G:11:LEU:HA	2:G:14:ALA:HB3	2.02	0.41
2:G:34:PHE:O	2:G:37:MET:HB3	2.20	0.41
2:H:9:LYS:HE3	2:H:13:ASP:OD1	2.20	0.41
2:H:34:PHE:O	2:H:37:MET:HB3	2.20	0.41
2:I:34:PHE:O	2:I:35:ASN:C	2.62	0.41
2:K:111:PRO:C	2:K:112:GLN:HG2	2.46	0.41
2:L:9:LYS:HE3	2:L:13:ASP:OD1	2.21	0.41
2:O:53:ASN:HD22	2:O:354:ALA:HB3	1.86	0.41
2:O:129:PHE:CD1	2:O:129:PHE:C	2.99	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:PHE:C	1:A:254:GLU:N	2.78	0.41
1:A:830:PRO:O	1:A:831:GLN:C	2.64	0.41
1:B:117:LYS:HB2	1:B:179:ASP:CG	2.46	0.41
1:B:190:ASN:HB2	1:B:199:VAL:CG2	2.50	0.41
1:B:206:SER:O	1:B:207:ILE:C	2.63	0.41
1:B:270:ILE:HG23	1:B:854:LEU:HD21	2.03	0.41
1:B:493:LEU:CD1	1:B:567:HIS:HB2	2.50	0.41
1:B:712:LEU:HG	1:B:721:VAL:O	2.19	0.41
2:D:239:ASN:ND2	2:D:246:THR:HG22	2.29	0.41
2:H:142:GLN:HE21	2:H:142:GLN:C	2.27	0.41
2:I:234:PHE:CE1	2:K:253:ILE:HG13	2.55	0.41
2:I:235:PRO:HA	2:I:249:PHE:O	2.21	0.41
2:I:239:ASN:ND2	2:I:246:THR:HG22	2.30	0.41
2:I:253:ILE:HG13	2:J:234:PHE:CE1	2.55	0.41
2:J:51:ILE:O	2:J:52:GLY:C	2.64	0.41
2:J:59:TRP:CD1	2:J:59:TRP:N	2.86	0.41
2:L:135:TYR:OH	2:L:342:MET:HE3	2.20	0.41
2:N:116:LEU:C	2:N:118:LYS:N	2.78	0.41
2:O:14:ALA:O	2:O:16:ASP:N	2.52	0.41
1:A:178:PRO:CD	1:A:256:PHE:HE2	2.32	0.41
1:A:304:LEU:H	1:A:615:ASN:ND2	2.19	0.41
1:A:345:GLN:HG3	1:A:349:MET:CE	2.51	0.41
1:A:396:PHE:CD2	1:A:578:LEU:HD11	2.56	0.41
1:A:405:ILE:O	1:A:408:MET:HB2	2.21	0.41
1:A:679:LEU:O	1:A:681:ILE:N	2.54	0.41
1:B:136:ALA:O	1:B:137:ASN:HB3	2.21	0.41
1:B:166:PHE:CE2	1:B:689:MET:CA	2.99	0.41
1:B:178:PRO:CD	1:B:256:PHE:CE2	3.04	0.41
1:B:435:ILE:C	1:B:438:PRO:HD2	2.41	0.41
1:B:515:ARG:HG3	1:B:515:ARG:O	2.21	0.41
1:B:521:MET:N	1:B:521:MET:SD	2.94	0.41
2:C:61:PHE:CD1	2:C:61:PHE:N	2.89	0.41
2:D:124:PHE:N	2:D:124:PHE:CD1	2.89	0.41
2:F:253:ILE:HG13	2:G:234:PHE:CE1	2.55	0.41
2:G:227:PRO:O	2:G:228:ASP:HB2	2.20	0.41
2:I:2:ASP:O	2:I:3:VAL:C	2.64	0.41
2:J:11:LEU:HA	2:J:14:ALA:HB3	2.03	0.41
2:J:14:ALA:O	2:J:18:ILE:HD12	2.21	0.41
2:K:110:ALA:HB1	2:K:111:PRO:CD	2.50	0.41
2:L:21:GLY:O	2:L:22:THR:O	2.38	0.41
2:M:235:PRO:HA	2:M:249:PHE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:19:VAL:O	2:O:20:GLU:C	2.63	0.41
2:O:35:ASN:O	2:O:37:MET:N	2.53	0.41
2:O:91:PHE:O	2:O:92:VAL:C	2.64	0.41
1:A:120:THR:HB	1:A:121:LYS:H	1.66	0.41
1:A:310:LEU:HD11	1:A:614:TYR:OH	2.21	0.41
1:A:503:ILE:HG13	1:A:503:ILE:H	1.72	0.41
1:A:701:GLN:CB	1:A:826:TYR:HD2	2.33	0.41
1:B:184:LYS:C	1:B:186:MET:N	2.78	0.41
1:B:286:LEU:O	1:B:287:ASN:ND2	2.54	0.41
1:B:310:LEU:C	1:B:312:ASP:H	2.28	0.41
1:B:721:VAL:HG12	1:B:799:LEU:HD21	1.98	0.41
2:C:100:MET:HG3	2:C:388:VAL:HG11	2.01	0.41
2:C:145:ARG:NH1	2:C:145:ARG:CB	2.79	0.41
2:D:9:LYS:HE3	2:D:13:ASP:OD1	2.21	0.41
2:E:116:LEU:C	2:E:118:LYS:N	2.77	0.41
2:F:150:PHE:HA	2:G:397:LYS:HZ1	1.85	0.41
2:F:340:GLU:HB3	2:F:342:MET:HE2	2.02	0.41
2:G:14:ALA:O	2:G:16:ASP:N	2.54	0.41
2:H:235:PRO:HA	2:H:249:PHE:O	2.21	0.41
2:H:340:GLU:HB3	2:H:342:MET:HE2	2.02	0.41
2:I:153:HIS:CD2	2:K:153:HIS:CE1	3.08	0.41
2:J:136:ILE:HD12	2:J:139:TRP:HB3	2.03	0.41
2:K:2:ASP:O	2:K:3:VAL:C	2.64	0.41
2:L:23:LEU:HD22	2:L:72:ASN:OD1	2.21	0.41
2:L:35:ASN:OD1	2:L:65:LEU:HD22	2.21	0.41
2:L:150:PHE:O	2:L:330:VAL:HG13	2.20	0.41
2:L:253:ILE:HG13	2:M:234:PHE:CE1	2.55	0.41
2:M:124:PHE:CD1	2:M:124:PHE:N	2.89	0.41
2:M:168:ARG:HD2	2:M:175:ASN:O	2.20	0.41
2:N:7:LEU:H	2:N:7:LEU:HG	1.54	0.41
2:O:168:ARG:HD2	2:O:175:ASN:O	2.20	0.41
1:A:202:SER:O	1:A:205:ALA:HB3	2.21	0.41
1:A:283:ASN:HD21	1:A:869:VAL:H	1.69	0.41
1:A:287:ASN:O	1:A:858:VAL:HA	2.20	0.41
1:A:368:THR:HG23	1:A:579:THR:O	2.21	0.41
1:A:374:ALA:HB1	1:A:580:SER:HA	2.02	0.41
1:A:382:LEU:HD12	1:A:382:LEU:HA	1.60	0.41
1:A:440:PHE:C	1:A:442:MET:N	2.78	0.41
1:A:459:ALA:C	1:A:462:GLN:HB2	2.44	0.41
1:A:472:LEU:N	1:A:472:LEU:HD23	2.36	0.41
1:A:548:ARG:O	1:A:549:LEU:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:597:PRO:O	1:A:598:GLN:C	2.62	0.41
1:A:601:PHE:CD1	1:A:601:PHE:N	2.80	0.41
1:A:621:ALA:O	1:A:622:VAL:C	2.63	0.41
1:A:706:ALA:C	1:A:708:ARG:N	2.76	0.41
1:A:710:MET:HE3	1:A:710:MET:HB2	1.91	0.41
1:A:782:VAL:CG2	1:A:798:ILE:HD11	2.51	0.41
1:A:862:THR:HG22	1:A:863:VAL:N	2.36	0.41
1:B:159:ASP:OD2	1:B:761:GLY:CA	2.69	0.41
1:B:492:VAL:O	1:B:493:LEU:O	2.38	0.41
1:B:763:LEU:HA	1:B:763:LEU:HD23	1.80	0.41
1:B:771:VAL:O	1:B:775:ILE:HD13	2.21	0.41
1:B:791:LYS:O	1:B:792:VAL:CG1	2.66	0.41
2:C:33:GLN:O	2:C:36:GLN:HB3	2.21	0.41
2:C:126:ARG:C	2:C:127:ILE:HG13	2.46	0.41
2:D:2:ASP:O	2:D:3:VAL:C	2.63	0.41
2:D:6:SER:O	2:D:7:LEU:C	2.64	0.41
2:D:128:ASN:HD22	2:E:19:VAL:CG2	2.34	0.41
2:D:235:PRO:HA	2:D:249:PHE:O	2.21	0.41
2:E:23:LEU:HD22	2:E:25:SER:OG	2.21	0.41
2:F:9:LYS:HE3	2:F:13:ASP:OD1	2.21	0.41
2:G:340:GLU:HB3	2:G:342:MET:HE2	2.02	0.41
2:H:91:PHE:O	2:H:95:VAL:HG23	2.21	0.41
2:I:9:LYS:HE3	2:I:13:ASP:OD1	2.20	0.41
2:I:106:ARG:HG2	2:I:107:ASN:H	1.84	0.41
2:I:227:PRO:O	2:I:228:ASP:HB2	2.20	0.41
2:J:9:LYS:HE3	2:J:13:ASP:OD1	2.21	0.41
2:J:168:ARG:HD2	2:J:175:ASN:O	2.20	0.41
2:J:340:GLU:HB3	2:J:342:MET:HE2	2.02	0.41
2:K:340:GLU:HB3	2:K:342:MET:HE2	2.02	0.41
2:L:14:ALA:O	2:L:16:ASP:N	2.54	0.41
2:L:26:ASN:OD1	2:N:33:GLN:HB2	2.21	0.41
2:M:119:LEU:C	2:M:121:GLY:N	2.79	0.41
2:O:5:TYR:CE2	2:O:131:ASN:HA	2.55	0.41
2:O:23:LEU:CG	2:O:24:TYR:N	2.83	0.41
2:O:136:ILE:O	2:O:137:GLU:C	2.64	0.41
2:O:147:ARG:O	2:O:148:THR:CB	2.66	0.41
2:O:152:PHE:CD1	2:O:152:PHE:N	2.89	0.41
1:A:158:GLY:O	1:A:159:ASP:C	2.63	0.41
1:A:370:ILE:HD11	3:W:933:LEU:HA	2.01	0.41
1:A:587:LEU:C	1:A:588:ILE:CG1	2.94	0.41
1:A:726:ASN:HD22	1:A:726:ASN:HA	1.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:763:LEU:HA	1:A:764:PRO:HD3	1.68	0.41
1:A:771:VAL:HG12	1:A:809:PHE:CB	2.51	0.41
1:A:786:ILE:O	1:A:787:VAL:C	2.64	0.41
1:B:207:ILE:HG13	1:B:207:ILE:H	1.62	0.41
1:B:229:ARG:HD2	1:B:230:GLN:NE2	2.31	0.41
1:B:411:LEU:HD23	1:B:411:LEU:HA	1.83	0.41
1:B:415:PRO:HB3	1:B:480:PHE:HB2	2.01	0.41
1:B:451:ASP:N	1:B:452:PRO:CD	2.82	0.41
1:B:672:LEU:O	1:B:673:PRO:O	2.38	0.41
2:C:5:TYR:HE2	2:C:130:ASP:O	2.04	0.41
2:C:204:ASN:HB3	2:C:296:ARG:HB3	2.03	0.41
2:D:204:ASN:HB3	2:D:296:ARG:HB3	2.03	0.41
2:E:142:GLN:HE21	2:E:142:GLN:C	2.29	0.41
2:H:14:ALA:O	2:H:16:ASP:N	2.54	0.41
2:H:123:LYS:HG3	2:H:124:PHE:CD1	2.56	0.41
2:I:6:SER:O	2:I:7:LEU:C	2.64	0.41
2:J:27:VAL:O	2:J:31:ILE:HG12	2.20	0.41
2:J:142:GLN:NE2	2:J:142:GLN:C	2.79	0.41
2:K:235:PRO:HA	2:K:249:PHE:O	2.21	0.41
2:L:42:ASN:CB	2:L:62:ASP:HA	2.51	0.41
2:M:116:LEU:C	2:M:118:LYS:N	2.78	0.41
2:N:235:PRO:HA	2:N:249:PHE:O	2.21	0.41
1:A:594:ILE:HA	1:A:595:PRO:HD3	1.86	0.40
1:A:697:ASP:C	1:A:699:ILE:H	2.28	0.40
1:A:774:LEU:HD12	1:A:774:LEU:C	2.46	0.40
1:B:401:TYR:CD1	1:B:401:TYR:N	2.74	0.40
1:B:517:GLN:C	1:B:518:PHE:CD1	2.99	0.40
1:B:743:ASP:OD1	1:B:744:TYR:N	2.53	0.40
1:B:747:ILE:H	1:B:747:ILE:HG22	1.51	0.40
1:B:854:LEU:HD22	1:B:855:LEU:N	2.36	0.40
1:B:869:VAL:HG13	1:B:873:ASN:CA	2.51	0.40
2:D:38:ILE:H	2:D:38:ILE:HG13	1.57	0.40
2:D:122:LEU:C	2:D:124:PHE:H	2.29	0.40
2:D:144:ARG:O	2:D:145:ARG:CB	2.65	0.40
2:D:340:GLU:HB3	2:D:342:MET:HE2	2.02	0.40
2:E:2:ASP:O	2:E:3:VAL:C	2.64	0.40
2:E:235:PRO:HA	2:E:249:PHE:O	2.21	0.40
2:I:11:LEU:HA	2:I:14:ALA:HB3	2.02	0.40
2:I:116:LEU:O	2:I:119:LEU:N	2.50	0.40
2:I:144:ARG:HD2	2:J:82:ARG:CZ	2.51	0.40
2:J:110:ALA:CB	2:J:111:PRO:CD	2.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:126:ARG:NH1	2:K:72:ASN:ND2	2.69	0.40
2:J:355:ILE:HA	2:J:356:PRO:HD3	1.96	0.40
2:K:38:ILE:H	2:K:38:ILE:HG13	1.58	0.40
2:L:131:ASN:N	2:L:131:ASN:HD22	2.19	0.40
2:L:234:PHE:CE1	2:N:253:ILE:HG13	2.55	0.40
2:O:153:HIS:C	2:O:153:HIS:CD2	2.99	0.40
1:A:200:VAL:O	1:A:201:ASP:HB3	2.21	0.40
1:A:264:PRO:O	1:A:265:LEU:HB2	2.22	0.40
1:A:283:ASN:ND2	1:A:869:VAL:H	2.18	0.40
1:A:343:GLU:O	1:A:344:ALA:C	2.64	0.40
1:A:460:GLU:C	1:A:462:GLN:N	2.79	0.40
1:A:594:ILE:HG23	1:A:595:PRO:N	2.36	0.40
1:A:785:GLN:HB2	1:A:786:ILE:H	1.60	0.40
1:A:793:ASP:OD1	1:A:793:ASP:N	2.54	0.40
1:B:150:LEU:CD1	1:B:696:SER:HA	2.50	0.40
1:B:402:MET:C	1:B:404:LEU:N	2.77	0.40
1:B:706:ALA:C	1:B:707:TYR:HD1	2.29	0.40
1:B:839:MET:HE2	1:B:840:HIS:O	2.21	0.40
1:B:847:THR:O	1:B:847:THR:HG22	2.20	0.40
2:D:214:LEU:HD23	2:D:214:LEU:N	2.36	0.40
2:E:91:PHE:O	2:E:95:VAL:HG23	2.22	0.40
2:F:65:LEU:HB3	2:F:66:LEU:H	1.69	0.40
2:G:104:SER:O	2:G:108:GLY:HA2	2.21	0.40
2:H:65:LEU:O	2:H:66:LEU:HD23	2.22	0.40
2:H:152:PHE:HB3	2:H:337:ASP:CB	2.51	0.40
2:I:204:ASN:HB3	2:I:296:ARG:HB3	2.03	0.40
2:L:1:MET:C	2:L:3:VAL:N	2.74	0.40
2:L:153:HIS:CE1	2:M:153:HIS:CD2	3.09	0.40
2:N:124:PHE:C	2:N:126:ARG:N	2.78	0.40
2:O:21:GLY:O	2:O:22:THR:C	2.64	0.40
2:O:144:ARG:C	2:O:146:GLN:N	2.79	0.40
1:A:338:GLU:O	1:A:339:LEU:HG	2.22	0.40
1:A:362:SER:HA	1:A:365:GLN:HE21	1.87	0.40
1:A:451:ASP:O	1:A:452:PRO:O	2.39	0.40
1:A:506:LEU:HD21	1:A:544:VAL:N	2.36	0.40
1:A:542:GLN:HA	1:A:545:ASP:OD2	2.20	0.40
1:A:707:TYR:H	1:A:707:TYR:HD1	1.69	0.40
1:A:715:ASP:O	1:A:718:TYR:O	2.39	0.40
1:B:497:ILE:HG23	2:I:68:THR:CG2	2.52	0.40
1:B:743:ASP:OD2	1:B:745:ALA:N	2.54	0.40
2:C:214:LEU:HD23	2:C:214:LEU:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:136:ILE:HD12	2:E:139:TRP:HB3	2.04	0.40
2:F:14:ALA:O	2:F:16:ASP:N	2.54	0.40
2:F:155:PRO:O	2:F:186:SER:HB3	2.21	0.40
2:F:204:ASN:HB3	2:F:296:ARG:HB3	2.03	0.40
2:H:21:GLY:O	2:H:22:THR:C	2.65	0.40
2:H:23:LEU:H	2:H:26:ASN:HD21	1.67	0.40
2:H:70:LEU:O	2:H:71:LEU:C	2.64	0.40
2:I:127:ILE:O	2:I:128:ASN:C	2.64	0.40
2:I:145:ARG:NH1	2:I:145:ARG:CB	2.65	0.40
2:J:2:ASP:O	2:J:3:VAL:C	2.64	0.40
2:J:124:PHE:O	2:J:126:ARG:N	2.54	0.40
2:J:142:GLN:HE21	2:J:142:GLN:C	2.28	0.40
2:K:48:THR:O	2:K:56:ILE:HA	2.20	0.40
2:K:88:PHE:O	2:K:91:PHE:HB3	2.22	0.40
2:K:136:ILE:O	2:K:137:GLU:C	2.65	0.40
2:M:11:LEU:HA	2:M:14:ALA:HB3	2.04	0.40
2:M:131:ASN:N	2:M:131:ASN:ND2	2.70	0.40
2:M:204:ASN:HB3	2:M:296:ARG:HB3	2.04	0.40
2:O:9:LYS:HE3	2:O:13:ASP:OD1	2.21	0.40
2:O:204:ASN:HB3	2:O:296:ARG:HB3	2.03	0.40
1:A:163:ARG:NH2	1:A:736:GLU:OE1	2.52	0.40
1:A:293:PRO:C	1:A:295:THR:N	2.78	0.40
1:A:304:LEU:N	1:A:615:ASN:ND2	2.67	0.40
1:A:536:LEU:N	1:A:536:LEU:HD22	2.36	0.40
1:A:563:MET:HA	1:A:563:MET:HE3	1.92	0.40
1:A:653:ASP:O	1:A:654:VAL:C	2.64	0.40
1:A:657:VAL:HA	1:A:658:PRO:HD3	1.64	0.40
1:A:854:LEU:HD22	1:A:855:LEU:H	1.86	0.40
1:B:190:ASN:HB3	1:B:197:GLY:O	2.21	0.40
1:B:239:VAL:HG21	1:B:845:ASN:O	2.21	0.40
1:B:244:ILE:HG23	1:B:244:ILE:O	2.22	0.40
1:B:275:PRO:C	1:B:277:ARG:N	2.79	0.40
1:B:332:VAL:O	1:B:333:VAL:C	2.63	0.40
1:B:400:ASN:OD1	1:B:400:ASN:C	2.64	0.40
1:B:639:LYS:O	1:B:641:ILE:N	2.55	0.40
1:B:804:SER:O	1:B:805:ASP:HB2	2.22	0.40
2:C:125:LYS:C	2:C:127:ILE:H	2.30	0.40
2:D:11:LEU:HA	2:D:14:ALA:HB3	2.03	0.40
2:D:91:PHE:O	2:D:92:VAL:C	2.65	0.40
2:D:116:LEU:C	2:D:118:LYS:N	2.78	0.40
2:D:124:PHE:O	2:D:126:ARG:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:6:SER:O	2:E:7:LEU:C	2.64	0.40
2:F:11:LEU:HB2	2:F:395:LEU:HD21	2.04	0.40
2:K:11:LEU:HA	2:K:14:ALA:HB3	2.03	0.40
2:L:59:TRP:CD1	2:L:59:TRP:N	2.88	0.40
2:M:27:VAL:O	2:M:28:SER:C	2.63	0.40
2:N:91:PHE:O	2:N:95:VAL:HG23	2.21	0.40
2:O:34:PHE:O	2:O:37:MET:HB3	2.21	0.40
2:O:100:MET:HG3	2:O:388:VAL:CG1	2.51	0.40
2:O:144:ARG:O	2:O:145:ARG:CG	2.69	0.40
2:O:340:GLU:HB3	2:O:342:MET:HE2	2.02	0.40
1:A:131:LEU:HA	1:A:132:PRO:HD3	1.90	0.40
1:A:149:LYS:HZ2	1:A:697:ASP:CG	2.29	0.40
1:A:303:LEU:HA	1:A:615:ASN:HD21	1.82	0.40
1:A:359:THR:O	1:A:359:THR:HG22	2.22	0.40
1:A:510:LEU:HA	1:A:513:LEU:CD1	2.51	0.40
1:A:536:LEU:N	1:A:536:LEU:CD2	2.85	0.40
1:A:663:TYR:C	1:A:665:LEU:N	2.79	0.40
1:A:815:TYR:CD1	1:A:815:TYR:N	2.85	0.40
1:B:112:LYS:O	1:B:113:PRO:C	2.64	0.40
1:B:425:VAL:O	1:B:426:ALA:C	2.65	0.40
1:B:556:THR:HG22	1:B:557:LEU:N	2.36	0.40
1:B:746:GLN:O	1:B:750:MET:HG3	2.21	0.40
2:C:2:ASP:O	2:C:3:VAL:C	2.65	0.40
2:C:14:ALA:O	2:C:18:ILE:HD12	2.21	0.40
2:D:128:ASN:O	2:D:129:PHE:HB3	2.21	0.40
2:D:378:ARG:O	2:D:382:LEU:HB2	2.22	0.40
2:E:100:MET:HG3	2:E:388:VAL:HG11	2.04	0.40
2:F:235:PRO:HA	2:F:249:PHE:O	2.21	0.40
2:G:131:ASN:N	2:G:131:ASN:HD22	2.20	0.40
2:K:116:LEU:O	2:K:119:LEU:N	2.50	0.40
2:K:204:ASN:HB3	2:K:296:ARG:HB3	2.04	0.40
2:L:355:ILE:HA	2:L:356:PRO:HD3	1.96	0.40
2:O:101:VAL:HG23	2:O:102:ARG:N	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	779/880 (88%)	431 (55%)	199 (26%)	149 (19%)	0	2
1	B	808/880 (92%)	458 (57%)	204 (25%)	146 (18%)	0	2
2	C	395/397 (100%)	318 (80%)	54 (14%)	23 (6%)	1	13
2	D	395/397 (100%)	315 (80%)	50 (13%)	30 (8%)	1	9
2	E	395/397 (100%)	323 (82%)	49 (12%)	23 (6%)	1	13
2	F	395/397 (100%)	324 (82%)	47 (12%)	24 (6%)	1	12
2	G	395/397 (100%)	323 (82%)	49 (12%)	23 (6%)	1	13
2	H	395/397 (100%)	323 (82%)	50 (13%)	22 (6%)	1	14
2	I	395/397 (100%)	320 (81%)	51 (13%)	24 (6%)	1	12
2	J	395/397 (100%)	320 (81%)	53 (13%)	22 (6%)	1	14
2	K	395/397 (100%)	318 (80%)	52 (13%)	25 (6%)	1	12
2	L	395/397 (100%)	322 (82%)	47 (12%)	26 (7%)	1	11
2	M	395/397 (100%)	322 (82%)	52 (13%)	21 (5%)	1	14
2	N	395/397 (100%)	317 (80%)	50 (13%)	28 (7%)	1	10
2	O	395/397 (100%)	317 (80%)	47 (12%)	31 (8%)	1	9
3	W	933/1089 (86%)	807 (86%)	93 (10%)	33 (4%)	3	20
All	All	7655/8010 (96%)	5858 (76%)	1147 (15%)	650 (8%)	0	8

All (650) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	LYS
1	A	130	GLN
1	A	193	SER
1	A	198	LYS
1	A	220	ALA
1	A	234	ALA

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Mol	Chain	Res	Type
1	A	246	HIS
1	A	252	PHE
1	A	260	GLN
1	A	275	PRO
1	A	283	ASN
1	A	287	ASN
1	A	306	ASP
1	A	315	GLU
1	A	338	GLU
1	A	340	VAL
1	A	356	GLU
1	A	358	LEU
1	A	370	ILE
1	A	413	VAL
1	A	443	GLN
1	A	446	HIS
1	A	451	ASP
1	A	452	PRO
1	A	453	GLN
1	A	484	VAL
1	A	485	ILE
1	A	488	VAL
1	A	489	LEU
1	A	501	HIS
1	A	523	VAL
1	A	558	MET
1	A	564	ASN
1	A	570	THR
1	A	573	THR
1	A	585	CYS
1	A	650	HIS
1	A	651	ILE
1	A	660	ASP
1	A	661	GLN
1	A	689	MET
1	A	701	GLN
1	A	715	ASP
1	A	743	ASP
1	A	745	ALA
1	A	770	SER
1	A	771	VAL
1	A	772	ILE

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Mol	Chain	Res	Type
1	A	781	THR
1	A	782	VAL
1	A	785	GLN
1	A	786	ILE
1	A	808	ASP
1	A	811	LEU
1	A	814	ASN
1	A	828	GLN
1	A	854	LEU
1	A	855	LEU
1	A	856	ALA
1	A	857	PHE
1	B	191	LYS
1	B	194	ARG
1	B	195	ASP
1	B	196	ALA
1	B	200	VAL
1	B	215	GLU
1	B	218	GLU
1	B	226	ALA
1	B	227	GLU
1	B	252	PHE
1	B	306	ASP
1	B	355	LEU
1	B	361	GLN
1	B	369	GLY
1	B	400	ASN
1	B	417	ASP
1	B	446	HIS
1	B	447	TYR
1	B	451	ASP
1	B	457	GLN
1	B	458	ILE
1	B	479	GLN
1	B	481	ARG
1	B	503	ILE
1	B	504	ASN
1	B	574	GLU
1	B	585	CYS
1	B	634	TYR
1	B	640	ALA
1	B	651	ILE

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Mol	Chain	Res	Type
1	B	655	ALA
1	B	673	PRO
1	B	699	ILE
1	B	702	GLY
1	B	724	ALA
1	B	764	PRO
1	B	765	PHE
1	B	777	LYS
1	B	782	VAL
1	B	785	GLN
1	B	786	ILE
1	B	790	ARG
1	B	792	VAL
1	B	805	ASP
1	B	806	SER
1	B	855	LEU
1	B	856	ALA
1	B	875	ARG
2	C	22	THR
2	C	70	LEU
2	C	134	GLU
2	D	25	SER
2	D	70	LEU
2	D	126	ARG
2	D	128	ASN
2	D	134	GLU
2	D	148	THR
2	E	22	THR
2	E	25	SER
2	E	106	ARG
2	E	134	GLU
2	F	22	THR
2	F	62	ASP
2	F	70	LEU
2	F	105	GLN
2	F	134	GLU
2	F	145	ARG
2	F	148	THR
2	G	20	GLU
2	G	22	THR
2	G	134	GLU
2	G	148	THR

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Mol	Chain	Res	Type
2	H	22	THR
2	H	107	ASN
2	H	134	GLU
2	I	25	SER
2	I	62	ASP
2	I	134	GLU
2	I	148	THR
2	J	20	GLU
2	J	70	LEU
2	J	106	ARG
2	J	134	GLU
2	K	22	THR
2	K	70	LEU
2	K	126	ARG
2	K	128	ASN
2	K	134	GLU
2	K	148	THR
2	L	22	THR
2	L	62	ASP
2	L	126	ARG
2	L	134	GLU
2	L	145	ARG
2	L	148	THR
2	M	22	THR
2	M	25	SER
2	M	128	ASN
2	M	134	GLU
2	N	22	THR
2	N	25	SER
2	N	70	LEU
2	N	128	ASN
2	N	134	GLU
2	N	148	THR
2	O	65	LEU
2	O	68	THR
2	O	70	LEU
2	O	134	GLU
2	O	145	ARG
2	O	148	THR
3	W	54	SER
3	W	397	MET
3	W	401	SER

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Mol	Chain	Res	Type
3	W	864	PRO
3	W	1082	ASN
3	W	1083	ALA
3	W	1084	ASN
1	A	143	ARG
1	A	202	SER
1	A	215	GLU
1	A	219	GLY
1	A	226	ALA
1	A	227	GLU
1	A	253	ASN
1	A	264	PRO
1	A	307	ARG
1	A	336	LEU
1	A	352	ASP
1	A	369	GLY
1	A	415	PRO
1	A	438	PRO
1	A	441	GLY
1	A	458	ILE
1	A	465	ASN
1	A	503	ILE
1	A	559	ALA
1	A	571	LEU
1	A	590	ASN
1	A	608	VAL
1	A	630	ARG
1	A	654	VAL
1	A	680	ASP
1	A	739	MET
1	A	804	SER
1	A	815	TYR
1	A	823	THR
1	A	847	THR
1	A	866	ILE
1	B	73	LEU
1	B	141	GLU
1	B	142	LEU
1	B	212	PHE
1	B	230	GLN
1	B	253	ASN
1	B	261	LEU

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Mol	Chain	Res	Type
1	B	264	PRO
1	B	265	LEU
1	B	278	ILE
1	B	282	VAL
1	B	283	ASN
1	B	307	ARG
1	B	313	ASN
1	B	338	GLU
1	B	388	SER
1	B	436	ILE
1	B	438	PRO
1	B	443	GLN
1	B	452	PRO
1	B	465	ASN
1	B	478	ASN
1	B	487	GLY
1	B	488	VAL
1	B	489	LEU
1	B	493	LEU
1	B	496	ASN
1	B	500	GLY
1	B	520	THR
1	B	524	ASP
1	B	608	VAL
1	B	631	LEU
1	B	637	LYS
1	B	638	MET
1	B	654	VAL
1	B	674	VAL
1	B	676	VAL
1	B	787	VAL
1	B	854	LEU
2	C	7	LEU
2	C	20	GLU
2	C	25	SER
2	C	62	ASP
2	C	106	ARG
2	C	130	ASP
2	C	148	THR
2	D	7	LEU
2	D	20	GLU
2	D	42	ASN

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Mol	Chain	Res	Type
2	D	65	LEU
2	D	67	GLY
2	D	69	THR
2	D	72	ASN
2	D	90	ASP
2	D	106	ARG
2	D	147	ARG
2	E	7	LEU
2	E	62	ASP
2	E	90	ASP
2	E	126	ARG
2	E	128	ASN
2	E	130	ASP
2	E	148	THR
2	F	7	LEU
2	F	25	SER
2	F	128	ASN
2	G	7	LEU
2	G	25	SER
2	G	125	LYS
2	G	126	ARG
2	H	7	LEU
2	H	25	SER
2	H	42	ASN
2	H	51	ILE
2	H	62	ASP
2	H	68	THR
2	H	109	ILE
2	H	128	ASN
2	I	7	LEU
2	I	90	ASP
2	I	125	LYS
2	I	147	ARG
2	J	7	LEU
2	J	51	ILE
2	J	62	ASP
2	J	90	ASP
2	J	126	ARG
2	J	128	ASN
2	J	130	ASP
2	K	7	LEU
2	K	20	GLU

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Mol	Chain	Res	Type
2	K	62	ASP
2	K	106	ARG
2	K	125	LYS
2	L	7	LEU
2	L	25	SER
2	L	69	THR
2	L	72	ASN
2	L	106	ARG
2	L	128	ASN
2	L	147	ARG
2	M	7	LEU
2	M	42	ASN
2	M	90	ASP
2	N	7	LEU
2	N	42	ASN
2	N	62	ASP
2	N	65	LEU
2	N	90	ASP
2	N	145	ARG
2	O	7	LEU
2	O	22	THR
2	O	25	SER
2	O	62	ASP
2	O	90	ASP
2	O	105	GLN
3	W	102	LEU
3	W	201	TYR
3	W	521	VAL
3	W	825	ASN
3	W	862	GLN
3	W	865	VAL
3	W	1002	GLY
1	A	137	ASN
1	A	142	LEU
1	A	218	GLU
1	A	254	GLU
1	A	265	LEU
1	A	276	GLU
1	A	496	ASN
1	A	497	ILE
1	A	521	MET
1	A	525	TYR

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Mol	Chain	Res	Type
1	A	579	THR
1	A	597	PRO
1	A	648	ARG
1	A	658	PRO
1	A	676	VAL
1	A	687	MET
1	A	696	SER
1	A	773	SER
1	A	816	ASP
1	A	849	THR
1	B	237	ASN
1	B	254	GLU
1	B	273	TYR
1	B	359	THR
1	B	387	LEU
1	B	421	ARG
1	B	549	LEU
1	B	579	THR
1	B	581	VAL
1	B	590	ASN
1	B	635	GLN
1	B	656	ARG
1	B	670	ARG
1	B	675	GLU
1	B	794	THR
1	B	849	THR
2	C	13	ASP
2	C	42	ASN
2	C	69	THR
2	C	90	ASP
2	C	126	ARG
2	D	13	ASP
2	D	32	GLN
2	D	62	ASP
2	D	68	THR
2	D	125	LYS
2	E	13	ASP
2	E	32	GLN
2	E	70	LEU
2	F	13	ASP
2	F	32	GLN
2	F	90	ASP

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Mol	Chain	Res	Type
2	F	126	ARG
2	F	130	ASP
2	G	13	ASP
2	G	32	GLN
2	G	42	ASN
2	G	90	ASP
2	G	128	ASN
2	H	13	ASP
2	H	32	GLN
2	H	90	ASP
2	I	13	ASP
2	I	32	GLN
2	I	126	ARG
2	I	128	ASN
2	I	146	GLN
2	J	13	ASP
2	J	42	ASN
2	K	13	ASP
2	K	25	SER
2	K	32	GLN
2	K	90	ASP
2	K	111	PRO
2	L	13	ASP
2	L	20	GLU
2	L	41	MET
2	L	90	ASP
2	L	125	LYS
2	M	13	ASP
2	M	106	ARG
2	N	13	ASP
2	N	67	GLY
2	N	106	ARG
2	N	125	LYS
2	N	155	PRO
2	O	20	GLU
2	O	24	TYR
2	O	32	GLN
2	O	42	ASN
2	O	73	LEU
2	O	106	ARG
2	O	126	ARG
2	O	155	PRO

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Mol	Chain	Res	Type
3	W	81	LYS
3	W	582	LYS
3	W	870	SER
1	A	131	LEU
1	A	144	ASN
1	A	155	LEU
1	A	187	ALA
1	A	195	ASP
1	A	206	SER
1	A	212	PHE
1	A	299	ILE
1	A	333	VAL
1	A	372	SER
1	A	387	LEU
1	A	457	GLN
1	A	518	PHE
1	A	524	ASP
1	A	549	LEU
1	A	552	TYR
1	A	557	LEU
1	A	581	VAL
1	A	700	ALA
1	A	730	PHE
1	A	853	ASP
1	A	877	MET
1	B	85	GLU
1	B	101	LYS
1	B	185	ASP
1	B	193	SER
1	B	206	SER
1	B	294	SER
1	B	302	ASN
1	B	372	SER
1	B	442	MET
1	B	466	PHE
1	B	483	VAL
1	B	552	TYR
1	B	564	ASN
1	B	597	PRO
1	B	639	LYS
1	B	680	ASP
1	B	731	GLN

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Mol	Chain	Res	Type
2	C	32	GLN
2	C	38	ILE
2	C	89	VAL
2	D	38	ILE
2	D	41	MET
2	D	89	VAL
2	D	123	LYS
2	D	145	ARG
2	E	38	ILE
2	F	20	GLU
2	F	38	ILE
2	F	42	ASN
2	G	38	ILE
2	G	130	ASP
2	G	145	ARG
2	H	36	GLN
2	H	38	ILE
2	H	89	VAL
2	H	106	ARG
2	I	36	GLN
2	I	38	ILE
2	I	42	ASN
2	I	89	VAL
2	I	145	ARG
2	J	32	GLN
2	J	36	GLN
2	J	38	ILE
2	J	89	VAL
2	K	9	LYS
2	K	36	GLN
2	K	38	ILE
2	K	89	VAL
2	L	32	GLN
2	L	36	GLN
2	L	38	ILE
2	M	20	GLU
2	M	32	GLN
2	M	38	ILE
2	M	55	PRO
2	M	89	VAL
2	M	126	ARG
2	N	20	GLU

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Mol	Chain	Res	Type
2	N	32	GLN
2	N	36	GLN
2	N	38	ILE
2	N	89	VAL
2	N	126	ARG
2	O	13	ASP
2	O	38	ILE
2	O	89	VAL
2	O	128	ASN
3	W	256	ASP
3	W	463	PHE
3	W	464	ILE
3	W	596	THR
3	W	760	ASN
3	W	790	SER
3	W	795	LYS
1	A	152	LYS
1	A	196	ALA
1	A	351	GLN
1	B	86	ILE
1	B	103	SER
1	B	207	ILE
1	B	277	ARG
1	B	399	THR
1	B	416	ASN
1	B	437	TYR
1	B	827	LYS
2	C	36	GLN
2	C	145	ARG
2	D	9	LYS
2	D	36	GLN
2	E	36	GLN
2	E	55	PRO
2	E	89	VAL
2	F	9	LYS
2	F	36	GLN
2	F	89	VAL
2	G	36	GLN
2	G	89	VAL
2	G	123	LYS
2	G	155	PRO
2	H	9	LYS

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Mol	Chain	Res	Type
2	H	130	ASP
2	I	9	LYS
2	I	41	MET
2	J	125	LYS
2	K	42	ASN
2	K	130	ASP
2	L	9	LYS
2	L	65	LEU
2	L	89	VAL
2	M	36	GLN
2	M	41	MET
2	M	145	ARG
2	N	9	LYS
2	N	69	THR
2	O	9	LYS
2	O	36	GLN
2	O	41	MET
3	W	192	GLU
3	W	586	TYR
1	A	207	ILE
1	A	422	GLU
1	A	622	VAL
1	A	733	ILE
1	A	819	PRO
1	B	521	MET
1	B	557	LEU
1	B	622	VAL
1	B	677	ARG
1	B	781	THR
1	B	857	PHE
2	C	3	VAL
2	E	9	LYS
2	E	20	GLU
2	E	42	ASN
2	F	55	PRO
2	G	3	VAL
2	G	9	LYS
2	I	123	LYS
2	J	3	VAL
2	J	9	LYS
2	J	69	THR
2	K	3	VAL

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Mol	Chain	Res	Type
2	K	147	ARG
2	L	3	VAL
2	N	3	VAL
2	O	3	VAL
3	W	1078	SER
1	A	247	PRO
1	A	334	PRO
1	B	519	PRO
1	B	723	ILE
1	B	865	PRO
2	D	3	VAL
2	E	3	VAL
2	F	3	VAL
2	H	3	VAL
2	I	3	VAL
2	M	3	VAL
3	W	200	PRO
3	W	246	SER
3	W	301	VAL
3	W	901	PRO
1	A	502	VAL
1	A	606	VAL
1	B	415	PRO
2	E	78	VAL
2	I	78	VAL
2	I	101	VAL
2	L	78	VAL
2	N	78	VAL
3	W	798	ILE
1	A	405	ILE
1	A	699	ILE
1	B	128	PRO
1	B	370	ILE
1	B	405	ILE
1	B	413	VAL
2	C	78	VAL
2	F	78	VAL
2	H	78	VAL
2	J	78	VAL
2	K	78	VAL
2	M	78	VAL
2	M	101	VAL

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Mol	Chain	Res	Type
2	N	101	VAL
2	O	51	ILE
2	O	78	VAL
2	O	101	VAL
3	W	446	PRO
1	A	500	GLY
1	B	435	ILE
1	B	606	VAL
2	C	67	GLY
2	D	78	VAL
2	G	78	VAL
1	A	787	VAL
1	B	246	HIS
1	B	544	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	715/809 (88%)	604 (84%)	111 (16%)	2	12
1	B	744/809 (92%)	633 (85%)	111 (15%)	3	13
2	C	350/350 (100%)	326 (93%)	24 (7%)	14	36
2	D	350/350 (100%)	324 (93%)	26 (7%)	13	34
2	E	350/350 (100%)	327 (93%)	23 (7%)	15	37
2	F	350/350 (100%)	329 (94%)	21 (6%)	17	39
2	G	350/350 (100%)	329 (94%)	21 (6%)	17	39
2	H	350/350 (100%)	331 (95%)	19 (5%)	20	42
2	I	350/350 (100%)	330 (94%)	20 (6%)	18	40
2	J	350/350 (100%)	329 (94%)	21 (6%)	17	39
2	K	350/350 (100%)	330 (94%)	20 (6%)	18	40
2	L	350/350 (100%)	324 (93%)	26 (7%)	13	34
2	M	350/350 (100%)	325 (93%)	25 (7%)	13	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	N	350/350 (100%)	328 (94%)	22 (6%)	16	38
2	O	350/350 (100%)	329 (94%)	21 (6%)	17	39
3	W	885/990 (89%)	820 (93%)	65 (7%)	13	34
All	All	6894/7158 (96%)	6318 (92%)	576 (8%)	10	30

All (576) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	PRO
1	A	122	LEU
1	A	125	ILE
1	A	126	PHE
1	A	142	LEU
1	A	147	TYR
1	A	154	THR
1	A	157	ASP
1	A	169	LEU
1	A	193	SER
1	A	203	GLU
1	A	204	THR
1	A	215	GLU
1	A	216	GLU
1	A	227	GLU
1	A	230	GLN
1	A	239	VAL
1	A	247	PRO
1	A	259	HIS
1	A	262	VAL
1	A	273	TYR
1	A	275	PRO
1	A	276	GLU
1	A	278	ILE
1	A	280	ASN
1	A	285	ILE
1	A	286	LEU
1	A	288	MET
1	A	295	THR
1	A	298	TYR
1	A	303	LEU
1	A	305	GLN
1	A	310	LEU

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Mol	Chain	Res	Type
1	A	311	HIS
1	A	316	SER
1	A	318	TRP
1	A	342	THR
1	A	347	GLN
1	A	348	LYS
1	A	354	GLN
1	A	366	PHE
1	A	371	ASN
1	A	382	LEU
1	A	389	GLN
1	A	391	THR
1	A	392	MET
1	A	395	ASP
1	A	401	TYR
1	A	408	MET
1	A	410	LEU
1	A	414	VAL
1	A	424	LEU
1	A	428	GLN
1	A	436	ILE
1	A	443	GLN
1	A	471	TRP
1	A	473	HIS
1	A	476	ASN
1	A	495	ASP
1	A	505	GLN
1	A	506	LEU
1	A	515	ARG
1	A	516	GLN
1	A	520	THR
1	A	521	MET
1	A	534	LEU
1	A	540	LEU
1	A	542	GLN
1	A	543	LEU
1	A	563	MET
1	A	565	MET
1	A	571	LEU
1	A	587	LEU
1	A	594	ILE
1	A	601	PHE

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Mol	Chain	Res	Type
1	A	641	ILE
1	A	646	LEU
1	A	676	VAL
1	A	680	ASP
1	A	701	GLN
1	A	704	ILE
1	A	707	TYR
1	A	712	LEU
1	A	717	MET
1	A	718	TYR
1	A	720	TYR
1	A	721	VAL
1	A	723	ILE
1	A	726	ASN
1	A	730	PHE
1	A	737	GLU
1	A	743	ASP
1	A	744	TYR
1	A	747	ILE
1	A	753	ASN
1	A	759	LEU
1	A	771	VAL
1	A	775	ILE
1	A	782	VAL
1	A	793	ASP
1	A	798	ILE
1	A	799	LEU
1	A	802	ILE
1	A	816	ASP
1	A	829	VAL
1	A	837	ASN
1	A	839	MET
1	A	848	PHE
1	A	849	THR
1	A	861	ASP
1	A	864	GLU
1	B	74	GLU
1	B	126	PHE
1	B	134	TYR
1	B	135	ARG
1	B	153	ASP
1	B	157	ASP

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Mol	Chain	Res	Type
1	B	169	LEU
1	B	177	MET
1	B	180	TYR
1	B	182	LEU
1	B	190	ASN
1	B	194	ARG
1	B	201	ASP
1	B	203	GLU
1	B	204	THR
1	B	215	GLU
1	B	217	THR
1	B	239	VAL
1	B	276	GLU
1	B	286	LEU
1	B	287	ASN
1	B	298	TYR
1	B	310	LEU
1	B	311	HIS
1	B	312	ASP
1	B	314	PHE
1	B	316	SER
1	B	318	TRP
1	B	322	THR
1	B	332	VAL
1	B	336	LEU
1	B	342	THR
1	B	347	GLN
1	B	348	LYS
1	B	352	ASP
1	B	353	LEU
1	B	358	LEU
1	B	382	LEU
1	B	389	GLN
1	B	392	MET
1	B	396	PHE
1	B	397	VAL
1	B	401	TYR
1	B	408	MET
1	B	424	LEU
1	B	428	GLN
1	B	436	ILE
1	B	453	GLN

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Mol	Chain	Res	Type
1	B	471	TRP
1	B	473	HIS
1	B	476	ASN
1	B	492	VAL
1	B	495	ASP
1	B	497	ILE
1	B	498	ARG
1	B	505	GLN
1	B	506	LEU
1	B	516	GLN
1	B	518	PHE
1	B	521	MET
1	B	522	PRO
1	B	525	TYR
1	B	534	LEU
1	B	540	LEU
1	B	542	GLN
1	B	543	LEU
1	B	560	CYS
1	B	562	THR
1	B	568	VAL
1	B	590	ASN
1	B	601	PHE
1	B	638	MET
1	B	641	ILE
1	B	646	LEU
1	B	652	PHE
1	B	660	ASP
1	B	674	VAL
1	B	676	VAL
1	B	680	ASP
1	B	697	ASP
1	B	707	TYR
1	B	710	MET
1	B	725	ARG
1	B	727	LEU
1	B	728	ASP
1	B	730	PHE
1	B	737	GLU
1	B	744	TYR
1	B	747	ILE
1	B	759	LEU

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Mol	Chain	Res	Type
1	B	771	VAL
1	B	774	LEU
1	B	782	VAL
1	B	783	PHE
1	B	786	ILE
1	B	789	LEU
1	B	790	ARG
1	B	792	VAL
1	B	798	ILE
1	B	799	LEU
1	B	808	ASP
1	B	810	TYR
1	B	811	LEU
1	B	812	VAL
1	B	818	VAL
1	B	823	THR
1	B	832	GLN
1	B	857	PHE
1	B	872	ASP
1	B	873	ASN
1	B	876	ILE
2	C	2	ASP
2	C	13	ASP
2	C	22	THR
2	C	26	ASN
2	C	59	TRP
2	C	68	THR
2	C	103	GLU
2	C	106	ARG
2	C	109	ILE
2	C	128	ASN
2	C	129	PHE
2	C	142	GLN
2	C	147	ARG
2	C	150	PHE
2	C	152	PHE
2	C	170	GLN
2	C	214	LEU
2	C	225	LEU
2	C	255	ARG
2	C	274	GLN
2	C	370	LEU

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Mol	Chain	Res	Type
2	C	378	ARG
2	C	382	LEU
2	C	385	VAL
2	D	2	ASP
2	D	13	ASP
2	D	19	VAL
2	D	45	GLU
2	D	58	ASN
2	D	68	THR
2	D	70	LEU
2	D	73	LEU
2	D	103	GLU
2	D	106	ARG
2	D	109	ILE
2	D	117	ARG
2	D	129	PHE
2	D	142	GLN
2	D	143	ASN
2	D	150	PHE
2	D	152	PHE
2	D	170	GLN
2	D	214	LEU
2	D	225	LEU
2	D	255	ARG
2	D	274	GLN
2	D	370	LEU
2	D	378	ARG
2	D	382	LEU
2	D	385	VAL
2	E	1	MET
2	E	2	ASP
2	E	13	ASP
2	E	26	ASN
2	E	58	ASN
2	E	59	TRP
2	E	69	THR
2	E	103	GLU
2	E	109	ILE
2	E	129	PHE
2	E	142	GLN
2	E	148	THR
2	E	150	PHE

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Mol	Chain	Res	Type
2	E	152	PHE
2	E	170	GLN
2	E	214	LEU
2	E	225	LEU
2	E	255	ARG
2	E	274	GLN
2	E	370	LEU
2	E	378	ARG
2	E	382	LEU
2	E	385	VAL
2	F	2	ASP
2	F	13	ASP
2	F	25	SER
2	F	60	ASN
2	F	61	PHE
2	F	109	ILE
2	F	128	ASN
2	F	129	PHE
2	F	142	GLN
2	F	148	THR
2	F	150	PHE
2	F	152	PHE
2	F	170	GLN
2	F	214	LEU
2	F	225	LEU
2	F	255	ARG
2	F	274	GLN
2	F	370	LEU
2	F	378	ARG
2	F	382	LEU
2	F	385	VAL
2	G	2	ASP
2	G	13	ASP
2	G	26	ASN
2	G	63	PHE
2	G	103	GLU
2	G	106	ARG
2	G	109	ILE
2	G	129	PHE
2	G	142	GLN
2	G	143	ASN
2	G	145	ARG

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Mol	Chain	Res	Type
2	G	152	PHE
2	G	170	GLN
2	G	214	LEU
2	G	225	LEU
2	G	255	ARG
2	G	274	GLN
2	G	370	LEU
2	G	378	ARG
2	G	382	LEU
2	G	385	VAL
2	H	2	ASP
2	H	13	ASP
2	H	103	GLU
2	H	106	ARG
2	H	109	ILE
2	H	128	ASN
2	H	129	PHE
2	H	142	GLN
2	H	150	PHE
2	H	152	PHE
2	H	170	GLN
2	H	214	LEU
2	H	225	LEU
2	H	255	ARG
2	H	274	GLN
2	H	370	LEU
2	H	378	ARG
2	H	382	LEU
2	H	385	VAL
2	I	2	ASP
2	I	13	ASP
2	I	48	THR
2	I	61	PHE
2	I	103	GLU
2	I	106	ARG
2	I	109	ILE
2	I	129	PHE
2	I	142	GLN
2	I	150	PHE
2	I	152	PHE
2	I	170	GLN
2	I	214	LEU

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Mol	Chain	Res	Type
2	I	225	LEU
2	I	255	ARG
2	I	274	GLN
2	I	370	LEU
2	I	378	ARG
2	I	382	LEU
2	I	385	VAL
2	J	2	ASP
2	J	13	ASP
2	J	19	VAL
2	J	59	TRP
2	J	71	LEU
2	J	106	ARG
2	J	109	ILE
2	J	128	ASN
2	J	129	PHE
2	J	142	GLN
2	J	150	PHE
2	J	152	PHE
2	J	170	GLN
2	J	214	LEU
2	J	225	LEU
2	J	255	ARG
2	J	274	GLN
2	J	370	LEU
2	J	378	ARG
2	J	382	LEU
2	J	385	VAL
2	K	2	ASP
2	K	13	ASP
2	K	59	TRP
2	K	62	ASP
2	K	103	GLU
2	K	109	ILE
2	K	129	PHE
2	K	142	GLN
2	K	143	ASN
2	K	150	PHE
2	K	152	PHE
2	K	170	GLN
2	K	214	LEU
2	K	225	LEU

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Mol	Chain	Res	Type
2	K	255	ARG
2	K	274	GLN
2	K	370	LEU
2	K	378	ARG
2	K	382	LEU
2	K	385	VAL
2	L	1	MET
2	L	2	ASP
2	L	13	ASP
2	L	19	VAL
2	L	22	THR
2	L	25	SER
2	L	59	TRP
2	L	62	ASP
2	L	72	ASN
2	L	103	GLU
2	L	106	ARG
2	L	109	ILE
2	L	125	LYS
2	L	129	PHE
2	L	142	GLN
2	L	150	PHE
2	L	152	PHE
2	L	170	GLN
2	L	214	LEU
2	L	225	LEU
2	L	255	ARG
2	L	274	GLN
2	L	370	LEU
2	L	378	ARG
2	L	382	LEU
2	L	385	VAL
2	M	2	ASP
2	M	13	ASP
2	M	22	THR
2	M	23	LEU
2	M	59	TRP
2	M	71	LEU
2	M	103	GLU
2	M	106	ARG
2	M	107	ASN
2	M	109	ILE

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Mol	Chain	Res	Type
2	M	117	ARG
2	M	125	LYS
2	M	129	PHE
2	M	142	GLN
2	M	150	PHE
2	M	152	PHE
2	M	170	GLN
2	M	214	LEU
2	M	225	LEU
2	M	255	ARG
2	M	274	GLN
2	M	370	LEU
2	M	378	ARG
2	M	382	LEU
2	M	385	VAL
2	N	2	ASP
2	N	13	ASP
2	N	58	ASN
2	N	66	LEU
2	N	73	LEU
2	N	103	GLU
2	N	106	ARG
2	N	107	ASN
2	N	109	ILE
2	N	129	PHE
2	N	142	GLN
2	N	145	ARG
2	N	152	PHE
2	N	170	GLN
2	N	214	LEU
2	N	225	LEU
2	N	255	ARG
2	N	274	GLN
2	N	370	LEU
2	N	378	ARG
2	N	382	LEU
2	N	385	VAL
2	O	2	ASP
2	O	13	ASP
2	O	23	LEU
2	O	25	SER
2	O	51	ILE

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Mol	Chain	Res	Type
2	O	58	ASN
2	O	106	ARG
2	O	107	ASN
2	O	109	ILE
2	O	129	PHE
2	O	142	GLN
2	O	150	PHE
2	O	170	GLN
2	O	214	LEU
2	O	225	LEU
2	O	255	ARG
2	O	274	GLN
2	O	370	LEU
2	O	378	ARG
2	O	382	LEU
2	O	385	VAL
3	W	35	GLU
3	W	46	LEU
3	W	47	GLU
3	W	51	ASN
3	W	70	THR
3	W	79	TYR
3	W	99	GLU
3	W	121	THR
3	W	143	ASN
3	W	150	GLU
3	W	155	ASP
3	W	171	THR
3	W	178	ASN
3	W	186	ASN
3	W	195	VAL
3	W	215	MET
3	W	246	SER
3	W	252	VAL
3	W	283	GLN
3	W	290	GLN
3	W	305	LYS
3	W	311	LEU
3	W	320	PRO
3	W	324	LYS
3	W	339	MET
3	W	341	ASP

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Mol	Chain	Res	Type
3	W	375	LEU
3	W	394	LEU
3	W	404	GLU
3	W	408	LEU
3	W	426	ASP
3	W	430	ASN
3	W	439	PRO
3	W	447	ILE
3	W	451	ARG
3	W	499	GLN
3	W	517	LEU
3	W	518	TYR
3	W	608	ILE
3	W	619	HIS
3	W	623	THR
3	W	628	VAL
3	W	629	ASP
3	W	663	ASN
3	W	690	ARG
3	W	709	GLN
3	W	721	ARG
3	W	723	ARG
3	W	734	THR
3	W	750	LEU
3	W	758	THR
3	W	782	VAL
3	W	820	LEU
3	W	835	GLU
3	W	838	LYS
3	W	886	THR
3	W	892	LEU
3	W	906	ASN
3	W	939	VAL
3	W	967	ILE
3	W	1003	CYS
3	W	1050	SER
3	W	1068	LYS
3	W	1078	SER
3	W	1084	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (297) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	GLN
1	A	137	ASN
1	A	168	ASN
1	A	230	GLN
1	A	246	HIS
1	A	260	GLN
1	A	309	ASN
1	A	365	GLN
1	A	371	ASN
1	A	428	GLN
1	A	443	GLN
1	A	453	GLN
1	A	467	GLN
1	A	470	ASN
1	A	473	HIS
1	A	477	ASN
1	A	490	ASN
1	A	496	ASN
1	A	553	ASN
1	A	605	ASN
1	A	607	ASN
1	A	609	ASN
1	A	613	ASN
1	A	615	ASN
1	A	661	GLN
1	A	683	ASN
1	A	701	GLN
1	A	722	ASN
1	A	726	ASN
1	A	803	ASN
1	A	807	ASN
1	A	840	HIS
1	A	867	ASN
1	A	873	ASN
1	B	168	ASN
1	B	190	ASN
1	B	230	GLN
1	B	233	GLN
1	B	237	ASN
1	B	246	HIS
1	B	260	GLN
1	B	287	ASN
1	B	302	ASN

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Mol	Chain	Res	Type
1	B	305	GLN
1	B	309	ASN
1	B	311	HIS
1	B	325	ASN
1	B	347	GLN
1	B	361	GLN
1	B	371	ASN
1	B	428	GLN
1	B	446	HIS
1	B	449	ASN
1	B	462	GLN
1	B	470	ASN
1	B	473	HIS
1	B	476	ASN
1	B	477	ASN
1	B	491	GLN
1	B	499	ASN
1	B	505	GLN
1	B	517	GLN
1	B	553	ASN
1	B	564	ASN
1	B	590	ASN
1	B	602	HIS
1	B	605	ASN
1	B	609	ASN
1	B	611	HIS
1	B	615	ASN
1	B	629	ASN
1	B	635	GLN
1	B	731	GLN
1	B	746	GLN
1	B	749	ASN
1	B	807	ASN
1	B	814	ASN
1	B	831	GLN
1	B	840	HIS
1	B	878	ASN
2	C	26	ASN
2	C	35	ASN
2	C	53	ASN
2	C	72	ASN
2	C	107	ASN

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Mol	Chain	Res	Type
2	C	128	ASN
2	C	131	ASN
2	C	138	ASN
2	C	143	ASN
2	C	146	GLN
2	C	167	ASN
2	C	183	ASN
2	C	239	ASN
2	C	274	GLN
2	C	284	ASN
2	D	26	ASN
2	D	36	GLN
2	D	128	ASN
2	D	131	ASN
2	D	142	GLN
2	D	143	ASN
2	D	146	GLN
2	D	167	ASN
2	D	183	ASN
2	D	239	ASN
2	D	274	GLN
2	D	284	ASN
2	E	26	ASN
2	E	53	ASN
2	E	58	ASN
2	E	94	ASN
2	E	128	ASN
2	E	131	ASN
2	E	142	GLN
2	E	167	ASN
2	E	183	ASN
2	E	239	ASN
2	E	274	GLN
2	E	284	ASN
2	F	32	GLN
2	F	35	ASN
2	F	53	ASN
2	F	72	ASN
2	F	94	ASN
2	F	128	ASN
2	F	131	ASN
2	F	142	GLN

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Mol	Chain	Res	Type
2	F	167	ASN
2	F	183	ASN
2	F	239	ASN
2	F	274	GLN
2	F	284	ASN
2	G	26	ASN
2	G	35	ASN
2	G	53	ASN
2	G	128	ASN
2	G	131	ASN
2	G	138	ASN
2	G	142	GLN
2	G	167	ASN
2	G	183	ASN
2	G	239	ASN
2	G	274	GLN
2	G	284	ASN
2	H	26	ASN
2	H	35	ASN
2	H	53	ASN
2	H	72	ASN
2	H	83	ASN
2	H	94	ASN
2	H	105	GLN
2	H	107	ASN
2	H	128	ASN
2	H	131	ASN
2	H	142	GLN
2	H	167	ASN
2	H	183	ASN
2	H	239	ASN
2	H	274	GLN
2	H	284	ASN
2	I	32	GLN
2	I	33	GLN
2	I	35	ASN
2	I	47	GLN
2	I	53	ASN
2	I	76	ASN
2	I	94	ASN
2	I	128	ASN
2	I	131	ASN

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Mol	Chain	Res	Type
2	I	143	ASN
2	I	146	GLN
2	I	167	ASN
2	I	183	ASN
2	I	239	ASN
2	I	274	GLN
2	I	284	ASN
2	J	26	ASN
2	J	35	ASN
2	J	53	ASN
2	J	94	ASN
2	J	128	ASN
2	J	131	ASN
2	J	138	ASN
2	J	142	GLN
2	J	146	GLN
2	J	167	ASN
2	J	183	ASN
2	J	239	ASN
2	J	274	GLN
2	J	284	ASN
2	K	26	ASN
2	K	33	GLN
2	K	35	ASN
2	K	53	ASN
2	K	72	ASN
2	K	94	ASN
2	K	107	ASN
2	K	131	ASN
2	K	138	ASN
2	K	143	ASN
2	K	167	ASN
2	K	183	ASN
2	K	239	ASN
2	K	274	GLN
2	K	284	ASN
2	L	33	GLN
2	L	36	GLN
2	L	53	ASN
2	L	72	ASN
2	L	131	ASN
2	L	143	ASN

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Mol	Chain	Res	Type
2	L	146	GLN
2	L	167	ASN
2	L	183	ASN
2	L	239	ASN
2	L	274	GLN
2	L	284	ASN
2	M	36	GLN
2	M	53	ASN
2	M	105	GLN
2	M	128	ASN
2	M	131	ASN
2	M	142	GLN
2	M	143	ASN
2	M	167	ASN
2	M	183	ASN
2	M	239	ASN
2	M	274	GLN
2	M	284	ASN
2	N	26	ASN
2	N	32	GLN
2	N	35	ASN
2	N	53	ASN
2	N	58	ASN
2	N	76	ASN
2	N	94	ASN
2	N	128	ASN
2	N	131	ASN
2	N	142	GLN
2	N	143	ASN
2	N	146	GLN
2	N	167	ASN
2	N	183	ASN
2	N	239	ASN
2	N	274	GLN
2	N	284	ASN
2	O	26	ASN
2	O	33	GLN
2	O	35	ASN
2	O	53	ASN
2	O	131	ASN
2	O	140	ASN
2	O	142	GLN

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Mol	Chain	Res	Type
2	O	143	ASN
2	O	146	GLN
2	O	153	HIS
2	O	167	ASN
2	O	183	ASN
2	O	239	ASN
2	O	274	GLN
2	O	284	ASN
3	W	31	ASN
3	W	36	ASN
3	W	42	HIS
3	W	48	ASN
3	W	141	ASN
3	W	143	ASN
3	W	185	HIS
3	W	186	ASN
3	W	283	GLN
3	W	289	ASN
3	W	290	GLN
3	W	308	GLN
3	W	346	GLN
3	W	402	ASN
3	W	423	HIS
3	W	499	GLN
3	W	565	GLN
3	W	604	ASN
3	W	649	GLN
3	W	653	ASN
3	W	694	ASN
3	W	698	ASN
3	W	703	GLN
3	W	706	GLN
3	W	810	ASN
3	W	818	GLN
3	W	824	ASN
3	W	853	GLN
3	W	862	GLN
3	W	906	ASN
3	W	956	ASN
3	W	1005	GLN
3	W	1010	ASN
3	W	1043	ASN

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Mol	Chain	Res	Type
3	W	1048	ASN
3	W	1072	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	781/880 (88%)	0.06	40 (5%)	33 32	62, 136, 196, 209	0
1	B	810/880 (92%)	-0.09	24 (2%)	52 43	53, 131, 186, 209	0
2	C	397/397 (100%)	0.32	39 (9%)	13 18	81, 147, 203, 209	0
2	D	397/397 (100%)	0.36	42 (10%)	11 16	90, 154, 208, 209	0
2	E	397/397 (100%)	0.45	47 (11%)	9 14	72, 151, 201, 209	0
2	F	397/397 (100%)	0.36	34 (8%)	16 20	100, 182, 209, 209	0
2	G	397/397 (100%)	0.82	68 (17%)	4 10	82, 176, 209, 209	0
2	H	397/397 (100%)	0.46	37 (9%)	14 19	96, 174, 209, 209	0
2	I	397/397 (100%)	0.44	42 (10%)	11 16	83, 157, 208, 209	0
2	J	397/397 (100%)	0.65	54 (13%)	7 12	77, 155, 203, 209	0
2	K	397/397 (100%)	0.41	35 (8%)	15 20	79, 156, 208, 209	0
2	L	397/397 (100%)	0.50	56 (14%)	6 12	77, 150, 207, 209	0
2	M	397/397 (100%)	0.67	58 (14%)	6 12	81, 150, 208, 209	0
2	N	397/397 (100%)	0.20	26 (6%)	25 27	83, 150, 201, 209	0
2	O	397/397 (100%)	0.04	14 (3%)	47 40	75, 150, 200, 209	0
3	W	975/1089 (89%)	4.61	748 (76%)	0 1	0, 17, 40, 40	975 (100%)
All	All	7727/8010 (96%)	0.87	1364 (17%)	4 9	0, 147, 207, 209	975 (12%)

All (1364) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	W	1074	THR	23.9
3	W	174	ALA	22.2
3	W	450	GLY	21.6
3	W	683	ALA	20.6
3	W	334	PHE	20.5

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Mol	Chain	Res	Type	RSRZ
3	W	133	ALA	20.2
3	W	720	ASN	20.1
3	W	527	SER	19.6
3	W	26	ILE	19.2
3	W	724	GLY	18.5
3	W	112	ASN	18.2
3	W	924	ASP	17.5
3	W	619	HIS	17.3
3	W	492	GLU	17.2
3	W	30	SER	17.2
3	W	925	GLY	17.1
3	W	1075	SER	16.3
3	W	528	GLN	16.0
3	W	691	ALA	15.8
3	W	686	LYS	15.3
3	W	172	ILE	15.3
3	W	428	MET	14.3
2	H	60	ASN	14.3
3	W	291	MET	14.1
3	W	805	SER	14.1
3	W	17	ASN	13.5
3	W	964	SER	13.3
3	W	496	GLN	13.3
3	W	704	SER	13.3
3	W	1073	ILE	13.1
3	W	283	GLN	13.1
3	W	192	GLU	13.0
3	W	223	TYR	12.9
3	W	114	MET	12.8
3	W	286	ASP	12.8
3	W	78	SER	12.6
3	W	67	GLU	12.6
3	W	719	VAL	12.2
3	W	337	GLN	12.1
3	W	459	THR	12.1
3	W	139	SER	12.1
3	W	893	PRO	12.0
3	W	227	LYS	11.9
3	W	449	LEU	11.7
3	W	117	GLU	11.7
3	W	64	ASP	11.7
3	W	874	ILE	11.5

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Mol	Chain	Res	Type	RSRZ
3	W	202	TYR	11.5
3	W	592	GLY	11.4
3	W	37	ARG	11.3
3	W	161	LYS	11.1
3	W	246	SER	11.1
3	W	93	ALA	11.1
3	W	158	GLU	11.0
3	W	420	LYS	10.9
3	W	247	PRO	10.7
3	W	709	GLN	10.7
3	W	153	GLU	10.7
3	W	256	ASP	10.6
3	W	38	CYS	10.5
3	W	315	SER	10.5
2	L	49	GLY	10.5
3	W	86	GLU	10.5
3	W	1019	ARG	10.5
3	W	853	GLN	10.5
3	W	935	SER	10.4
3	W	168	ASP	10.4
3	W	654	ASP	10.4
3	W	390	GLU	10.4
3	W	137	SER	10.4
3	W	692	GLY	10.3
3	W	212	GLU	10.3
3	W	238	SER	10.3
3	W	178	ASN	10.2
3	W	795	LYS	10.2
3	W	876	ASP	10.2
3	W	82	TYR	10.1
3	W	74	ILE	10.0
3	W	625	ILE	10.0
3	W	926	SER	10.0
3	W	328	TRP	9.9
3	W	281	PRO	9.9
3	W	610	THR	9.9
3	W	818	GLN	9.8
3	W	401	SER	9.8
3	W	433	TYR	9.8
3	W	755	ARG	9.8
3	W	663	ASN	9.6
3	W	97	PRO	9.6

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Mol	Chain	Res	Type	RSRZ
3	W	411	GLY	9.6
3	W	1072	ASN	9.6
3	W	760	ASN	9.5
3	W	877	ILE	9.5
3	W	1084	ASN	9.4
3	W	716	ASN	9.4
3	W	173	VAL	9.4
3	W	430	ASN	9.4
2	G	110	ALA	9.4
3	W	316	ILE	9.4
1	B	99	GLU	9.3
3	W	405	SER	9.3
3	W	596	THR	9.3
3	W	605	LEU	9.2
2	H	233	SER	9.1
3	W	175	SER	9.1
3	W	312	VAL	9.1
3	W	141	ASN	9.0
2	L	289	ARG	9.0
3	W	80	ASP	9.0
3	W	718	ILE	8.9
3	W	73	SER	8.9
3	W	725	PHE	8.9
3	W	36	ASN	8.8
3	W	18	SER	8.8
3	W	664	ALA	8.8
3	W	16	TYR	8.8
3	W	201	TYR	8.7
3	W	200	PRO	8.7
3	W	600	ASN	8.7
3	W	895	GLN	8.7
3	W	319	PHE	8.7
2	I	262	GLU	8.7
3	W	76	SER	8.6
3	W	392	ALA	8.6
3	W	807	THR	8.6
3	W	753	SER	8.5
3	W	402	ASN	8.5
3	W	670	VAL	8.4
3	W	854	ILE	8.4
3	W	327	SER	8.3
3	W	226	ALA	8.3

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Mol	Chain	Res	Type	RSRZ
3	W	817	GLU	8.3
3	W	1081	THR	8.3
3	W	135	LEU	8.2
3	W	33	GLU	8.2
3	W	702	GLY	8.1
3	W	416	PHE	8.1
3	W	723	ARG	8.1
3	W	136	THR	8.1
3	W	590	ALA	8.1
3	W	630	GLY	8.1
3	W	194	ASP	8.1
3	W	470	PHE	8.1
3	W	910	ILE	8.0
3	W	79	TYR	8.0
3	W	165	ARG	8.0
3	W	464	ILE	8.0
3	W	768	SER	8.0
2	J	221	ALA	8.0
3	W	255	VAL	8.0
3	W	460	ARG	8.0
2	G	284	ASN	8.0
3	W	131	ASP	7.9
3	W	806	SER	7.9
3	W	591	SER	7.8
3	W	593	GLU	7.8
3	W	111	ASN	7.8
3	W	594	LYS	7.8
3	W	409	LYS	7.8
3	W	71	LEU	7.7
3	W	529	HIS	7.7
3	W	780	ASP	7.6
3	W	920	GLN	7.6
3	W	289	ASN	7.6
3	W	825	ASN	7.6
3	W	335	ARG	7.6
3	W	688	PHE	7.5
3	W	1076	LEU	7.5
3	W	185	HIS	7.5
3	W	25	PRO	7.5
3	W	588	ALA	7.5
3	W	313	ASP	7.5
3	W	366	LEU	7.4

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Mol	Chain	Res	Type	RSRZ
3	W	1050	SER	7.4
3	W	421	ASN	7.4
3	W	896	TYR	7.4
3	W	733	LEU	7.4
3	W	906	ASN	7.4
3	W	99	GLU	7.4
3	W	696	LEU	7.4
3	W	698	ASN	7.4
3	W	341	ASP	7.4
3	W	342	ALA	7.3
3	W	711	ALA	7.3
3	W	193	TYR	7.3
3	W	451	ARG	7.3
3	W	597	LYS	7.3
3	W	1060	LYS	7.3
3	W	27	TYR	7.3
3	W	89	LEU	7.3
3	W	730	GLU	7.3
3	W	132	PRO	7.3
2	M	324	LEU	7.3
3	W	729	ARG	7.3
3	W	574	GLN	7.3
3	W	525	ASP	7.2
3	W	363	TYR	7.2
3	W	163	TYR	7.2
3	W	913	CYS	7.2
3	W	602	ILE	7.2
2	M	224	THR	7.1
2	K	132	SER	7.1
3	W	693	ILE	7.1
3	W	766	PHE	7.1
3	W	701	ARG	7.0
3	W	846	SER	7.0
3	W	771	PHE	7.0
3	W	345	ASP	6.9
3	W	389	SER	6.8
3	W	23	GLN	6.8
2	J	340	GLU	6.8
3	W	530	ASN	6.8
3	W	737	MET	6.8
2	G	179	THR	6.8
2	D	132	SER	6.8

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Mol	Chain	Res	Type	RSRZ
3	W	448	PRO	6.8
3	W	871	LYS	6.8
3	W	703	GLN	6.8
2	L	120	SER	6.8
3	W	863	LYS	6.7
3	W	726	GLU	6.7
3	W	1007	PHE	6.7
3	W	184	ARG	6.7
3	W	50	LYS	6.7
3	W	721	ARG	6.7
3	W	699	GLU	6.6
3	W	314	ARG	6.6
2	M	216	ARG	6.6
3	W	581	ILE	6.6
3	W	232	LEU	6.6
3	W	653	ASN	6.6
3	W	1000	ASN	6.6
3	W	239	THR	6.6
3	W	68	ASN	6.6
3	W	115	THR	6.6
3	W	140	SER	6.6
3	W	919	TYR	6.5
3	W	823	LYS	6.5
3	W	658	THR	6.5
3	W	509	PHE	6.5
3	W	526	SER	6.5
3	W	236	ASN	6.5
3	W	301	VAL	6.5
3	W	248	MET	6.5
3	W	134	ILE	6.5
3	W	869	SER	6.5
2	E	192	GLY	6.5
3	W	364	THR	6.5
3	W	65	VAL	6.4
2	H	68	THR	6.4
2	E	224	THR	6.4
3	W	54	SER	6.4
3	W	414	THR	6.4
3	W	287	GLU	6.4
2	O	50	GLY	6.3
3	W	128	SER	6.3
3	W	824	ASN	6.3

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Mol	Chain	Res	Type	RSRZ
3	W	462	ILE	6.3
2	E	288	ILE	6.3
3	W	608	ILE	6.3
2	G	193	PHE	6.3
2	F	222	THR	6.3
3	W	589	VAL	6.3
3	W	931	SER	6.2
3	W	431	GLU	6.2
3	W	587	GLY	6.2
3	W	388	ASP	6.2
3	W	862	GLN	6.1
3	W	728	ASP	6.1
2	C	151	THR	6.1
3	W	170	PHE	6.1
3	W	761	SER	6.1
3	W	412	ARG	6.1
3	W	108	ASP	6.1
2	D	55	PRO	6.1
3	W	31	ASN	6.1
3	W	484	ALA	6.0
3	W	290	GLN	6.0
3	W	827	VAL	6.0
3	W	77	TYR	6.0
3	W	32	SER	6.0
3	W	790	SER	6.0
3	W	779	VAL	6.0
3	W	370	GLU	6.0
3	W	743	ALA	6.0
2	N	50	GLY	6.0
3	W	498	ASN	6.0
3	W	417	SER	6.0
3	W	474	HIS	5.9
3	W	903	LEU	5.9
1	B	630	ARG	5.9
2	H	336	ALA	5.9
3	W	426	ASP	5.9
3	W	524	TRP	5.9
3	W	164	LYS	5.9
3	W	293	ASP	5.9
3	W	138	LEU	5.9
3	W	1048	ASN	5.9
3	W	444	ASP	5.8

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Mol	Chain	Res	Type	RSRZ
3	W	1085	PHE	5.8
3	W	873	THR	5.8
3	W	905	ASP	5.8
2	H	72	ASN	5.8
3	W	940	TYR	5.8
3	W	1058	TYR	5.8
3	W	758	THR	5.8
3	W	143	ASN	5.7
2	G	261	VAL	5.7
3	W	22	VAL	5.7
3	W	667	LYS	5.7
3	W	157	ALA	5.7
3	W	106	GLU	5.7
2	I	184	ALA	5.7
2	F	291	SER	5.7
3	W	35	GLU	5.7
3	W	866	THR	5.7
3	W	814	ARG	5.7
3	W	228	GLU	5.7
3	W	29	SER	5.6
3	W	722	LEU	5.6
3	W	894	ILE	5.6
3	W	391	LEU	5.6
3	W	87	ARG	5.6
2	D	313	PRO	5.6
3	W	81	LYS	5.6
3	W	66	ILE	5.6
1	A	300	ARG	5.6
2	J	209	GLU	5.6
3	W	404	GLU	5.5
3	W	288	LEU	5.5
2	M	325	ARG	5.5
3	W	154	ASN	5.5
3	W	209	SER	5.5
3	W	902	THR	5.4
3	W	786	ARG	5.4
2	L	146	GLN	5.4
2	L	56	ILE	5.4
3	W	148	TRP	5.4
3	W	851	ARG	5.4
3	W	235	SER	5.4
3	W	601	SER	5.4

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Mol	Chain	Res	Type	RSRZ
3	W	1078	SER	5.4
3	W	150	GLU	5.4
3	W	224	LEU	5.4
2	M	246	THR	5.3
3	W	429	ALA	5.4
3	W	912	GLN	5.3
3	W	469	TYR	5.3
3	W	749	ARG	5.3
3	W	1055	PHE	5.3
3	W	440	PRO	5.3
3	W	837	ALA	5.3
3	W	169	LEU	5.3
3	W	695	LEU	5.3
3	W	889	ASP	5.3
2	J	318	ALA	5.3
3	W	661	ARG	5.2
3	W	146	MET	5.2
3	W	45	CYS	5.2
3	W	152	HIS	5.2
3	W	96	LYS	5.2
2	G	219	THR	5.2
3	W	843	ALA	5.2
2	G	155	PRO	5.2
3	W	142	LEU	5.2
3	W	499	GLN	5.2
3	W	110	GLU	5.2
2	J	2	ASP	5.2
3	W	419	LYS	5.2
3	W	424	VAL	5.2
3	W	585	GLN	5.2
3	W	304	PRO	5.1
3	W	606	ALA	5.1
3	W	990	GLU	5.1
2	G	203	ALA	5.1
3	W	495	SER	5.1
3	W	151	LYS	5.1
3	W	939	VAL	5.1
2	L	262	GLU	5.1
3	W	676	GLU	5.1
3	W	819	LEU	5.1
2	N	207	GLN	5.1
2	L	188	ILE	5.1

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Mol	Chain	Res	Type	RSRZ
3	W	318	LYS	5.0
3	W	49	SER	5.0
2	G	47	GLN	5.0
2	L	207	GLN	5.0
2	N	120	SER	5.0
3	W	183	PRO	5.0
2	C	336	ALA	5.0
3	W	458	ARG	5.0
2	G	133	SER	5.0
3	W	881	ILE	5.0
3	W	603	ALA	5.0
3	W	100	ALA	5.0
3	W	1004	TYR	5.0
3	W	767	ASP	5.0
3	W	967	ILE	5.0
3	W	1006	LEU	5.0
3	W	461	ILE	4.9
3	W	107	LEU	4.9
2	G	309	PRO	4.9
3	W	821	PHE	4.9
3	W	486	HIS	4.9
3	W	984	ASP	4.9
2	C	147	ARG	4.9
3	W	69	ALA	4.9
3	W	710	ALA	4.9
3	W	95	GLY	4.9
3	W	918	THR	4.9
3	W	463	PHE	4.9
3	W	872	ILE	4.9
3	W	909	TYR	4.9
2	E	159	PRO	4.9
3	W	987	ARG	4.9
2	N	133	SER	4.9
2	E	21	GLY	4.9
2	J	192	GLY	4.9
3	W	575	ILE	4.9
3	W	773	ILE	4.9
3	W	797	GLY	4.9
3	W	1049	GLY	4.9
3	W	166	ARG	4.9
3	W	303	ILE	4.9
3	W	684	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
2	M	133	SER	4.9
2	J	148	THR	4.9
3	W	199	LYS	4.9
3	W	34	LEU	4.8
3	W	578	GLY	4.8
3	W	941	LYS	4.8
2	M	340	GLU	4.8
2	H	193	PHE	4.8
2	J	151	THR	4.8
2	G	314	PHE	4.8
3	W	63	ASN	4.8
3	W	804	ALA	4.8
3	W	399	SER	4.7
3	W	1066	LEU	4.7
3	W	1013	ASP	4.7
3	W	1056	CYS	4.7
3	W	225	ILE	4.7
3	W	650	ASP	4.7
3	W	240	LEU	4.7
2	D	289	ARG	4.7
3	W	713	LEU	4.7
2	I	193	PHE	4.7
3	W	928	SER	4.7
1	A	611	HIS	4.7
2	O	67	GLY	4.6
3	W	697	ASN	4.6
3	W	665	LYS	4.6
2	D	186	SER	4.6
3	W	13	SER	4.6
3	W	249	SER	4.6
2	G	213	GLN	4.6
3	W	880	ASP	4.6
3	W	996	LEU	4.6
2	M	193	PHE	4.6
3	W	777	THR	4.6
3	W	965	LEU	4.6
2	C	318	ALA	4.5
2	L	47	GLN	4.5
3	W	898	LYS	4.5
2	I	260	GLU	4.5
3	W	338	LYS	4.5
2	H	133	SER	4.5

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Mol	Chain	Res	Type	RSRZ
3	W	822	SER	4.5
2	M	291	SER	4.5
3	W	707	TRP	4.5
2	D	188	ILE	4.5
3	W	257	ILE	4.5
3	W	573	VAL	4.5
3	W	1082	ASN	4.5
2	L	20	GLU	4.5
2	J	58	ASN	4.4
3	W	809	LYS	4.4
3	W	901	PRO	4.4
3	W	1012	PRO	4.4
2	G	184	ALA	4.4
3	W	803	ALA	4.4
3	W	297	LYS	4.4
3	W	662	MET	4.4
3	W	180	TYR	4.4
3	W	523	GLN	4.4
3	W	155	ASP	4.4
2	J	332	GLU	4.4
3	W	294	ASN	4.4
3	W	310	TRP	4.4
3	W	320	PRO	4.4
3	W	584	ILE	4.4
3	W	690	ARG	4.4
3	W	195	VAL	4.4
2	L	255	ARG	4.4
3	W	120	PRO	4.4
3	W	700	LYS	4.4
2	J	282	ALA	4.3
2	J	281	ILE	4.3
3	W	346	GLN	4.3
3	W	213	MET	4.3
2	D	262	GLU	4.3
2	F	72	ASN	4.3
3	W	561	TYR	4.3
3	W	649	GLN	4.3
2	L	21	GLY	4.3
3	W	52	GLY	4.3
3	W	343	ALA	4.3
3	W	829	ARG	4.3
3	W	336	LYS	4.3

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Mol	Chain	Res	Type	RSRZ
2	I	103	GLU	4.3
2	I	336	ALA	4.3
3	W	39	ILE	4.3
2	C	46	PHE	4.3
3	W	455	PRO	4.3
2	K	326	ILE	4.3
3	W	922	GLU	4.3
2	N	336	ALA	4.3
2	G	20	GLU	4.2
3	W	668	ALA	4.2
2	G	146	GLN	4.2
2	G	259	VAL	4.2
3	W	562	LYS	4.2
2	L	332	GLU	4.2
3	W	717	TYR	4.2
3	W	754	GLU	4.2
3	W	1080	TYR	4.2
2	E	319	THR	4.2
3	W	6	LEU	4.2
2	M	60	ASN	4.2
3	W	4	TYR	4.2
2	M	225	LEU	4.2
3	W	607	LEU	4.2
3	W	302	ASP	4.2
3	W	810	ASN	4.1
2	F	20	GLU	4.1
2	F	159	PRO	4.1
3	W	234	TYR	4.1
3	W	330	PHE	4.1
2	N	149	GLY	4.1
3	W	490	TYR	4.1
3	W	747	SER	4.1
3	W	494	TYR	4.1
3	W	830	GLY	4.1
3	W	237	ARG	4.1
3	W	85	VAL	4.1
3	W	468	GLU	4.1
3	W	751	PHE	4.1
2	H	188	ILE	4.1
2	M	278	GLY	4.1
2	O	121	GLY	4.1
2	K	131	ASN	4.1

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Mol	Chain	Res	Type	RSRZ
3	W	856	ALA	4.1
3	W	9	SER	4.1
3	W	933	LEU	4.1
3	W	324	LYS	4.1
2	K	19	VAL	4.1
2	M	288	ILE	4.1
3	W	1077	ARG	4.0
2	L	324	LEU	4.0
3	W	427	ASP	4.0
2	H	323	THR	4.0
3	W	42	HIS	4.0
2	L	111	PRO	4.0
2	G	218	LEU	4.0
2	L	186	SER	4.0
2	C	380	ASP	4.0
3	W	694	ASN	4.0
3	W	1062	GLU	4.0
3	W	482	ILE	4.0
3	W	828	SER	4.0
3	W	171	THR	4.0
3	W	811	TYR	4.0
3	W	868	LYS	4.0
2	O	128	ASN	4.0
3	W	579	ASN	4.0
2	H	318	ALA	4.0
2	I	288	ILE	3.9
2	K	86	ASP	3.9
3	W	167	LEU	3.9
3	W	254	LEU	3.9
3	W	465	LEU	3.9
3	W	855	SER	3.9
2	J	260	GLU	3.9
3	W	317	GLU	3.9
2	I	194	ASP	3.9
3	W	88	LYS	3.9
1	A	102	GLU	3.9
2	D	324	LEU	3.9
3	W	555	LEU	3.9
3	W	497	SER	3.9
3	W	988	ILE	3.9
3	W	406	ARG	3.9
3	W	407	GLN	3.9

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Mol	Chain	Res	Type	RSRZ
3	W	794	GLN	3.9
3	W	867	PHE	3.9
2	F	267	GLY	3.9
3	W	418	THR	3.9
1	B	653	ASP	3.9
3	W	504	GLY	3.9
3	W	840	ASN	3.9
2	G	216	ARG	3.9
2	K	328	SER	3.9
3	W	453	ASP	3.8
2	F	223	ILE	3.8
2	G	156	ASN	3.8
2	G	381	ASN	3.8
2	G	163	SER	3.8
2	F	23	LEU	3.8
3	W	145	VAL	3.8
3	W	687	ILE	3.8
2	F	210	HIS	3.8
3	W	888	SER	3.8
2	M	149	GLY	3.8
2	N	209	GLU	3.8
2	L	72	ASN	3.8
3	W	473	GLN	3.8
2	K	208	PHE	3.8
3	W	124	GLU	3.8
3	W	769	GLU	3.8
2	M	178	GLY	3.7
2	G	285	PHE	3.7
3	W	870	SER	3.7
3	W	520	ASP	3.7
2	C	150	PHE	3.7
3	W	611	VAL	3.7
3	W	727	THR	3.7
2	F	209	GLU	3.7
3	W	493	PHE	3.7
3	W	331	HIS	3.7
2	J	294	LEU	3.7
3	W	732	ILE	3.7
3	W	1054	LEU	3.7
2	G	148	THR	3.7
2	F	208	PHE	3.7
2	H	89	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
3	W	746	GLY	3.7
3	W	995	ASN	3.7
2	M	179	THR	3.7
3	W	123	GLU	3.7
2	J	128	ASN	3.7
2	M	261	VAL	3.7
3	W	705	THR	3.7
3	W	478	GLU	3.7
3	W	1069	LYS	3.7
3	W	472	ALA	3.7
3	W	105	ASN	3.6
2	H	50	GLY	3.6
3	W	752	PRO	3.6
2	D	329	ALA	3.6
2	E	191	ALA	3.6
3	W	622	ALA	3.6
1	A	487	GLY	3.6
2	J	280	ILE	3.6
3	W	762	THR	3.6
3	W	371	VAL	3.6
3	W	847	LEU	3.6
3	W	652	SER	3.6
2	F	292	PHE	3.6
3	W	206	TRP	3.6
2	K	278	GLY	3.6
3	W	245	SER	3.6
3	W	396	SER	3.6
3	W	656	ARG	3.6
3	W	1067	TRP	3.6
3	W	958	ILE	3.6
3	W	1079	PRO	3.6
2	L	115	SER	3.6
3	W	187	ALA	3.6
3	W	742	VAL	3.6
2	E	324	LEU	3.6
2	K	149	GLY	3.6
2	C	315	GLU	3.6
3	W	176	THR	3.6
1	A	106	LYS	3.6
2	E	326	ILE	3.5
3	W	1018	ILE	3.5
2	E	216	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
2	G	159	PRO	3.5
2	J	329	ALA	3.5
3	W	467	TYR	3.5
3	W	1083	ALA	3.5
1	A	651	ILE	3.5
3	W	398	SER	3.5
2	J	20	GLU	3.5
2	L	45	GLU	3.5
3	W	321	LEU	3.5
3	W	852	ALA	3.5
2	I	188	ILE	3.5
2	L	326	ILE	3.5
1	A	675	GLU	3.5
3	W	734	THR	3.5
3	W	1017	LEU	3.5
2	K	89	VAL	3.5
3	W	179	LYS	3.5
2	I	315	GLU	3.5
2	N	47	GLN	3.5
3	W	689	PHE	3.5
2	M	251	PRO	3.5
3	W	198	ASP	3.5
2	I	50	GLY	3.5
3	W	875	ASN	3.5
3	W	899	PHE	3.5
1	A	828	GLN	3.5
2	F	47	GLN	3.5
2	I	246	THR	3.5
2	M	206	GLN	3.5
3	W	565	GLN	3.5
3	W	113	LYS	3.5
2	J	273	TYR	3.5
3	W	637	LEU	3.5
2	K	102	ARG	3.5
3	W	329	SER	3.5
2	E	251	PRO	3.5
2	M	86	ASP	3.4
2	I	206	GLN	3.4
3	W	635	ALA	3.4
3	W	583	LYS	3.4
3	W	849	LYS	3.4
3	W	358	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
2	H	241	ALA	3.4
2	J	233	SER	3.4
3	W	189	TYR	3.4
2	J	52	GLY	3.4
2	M	190	VAL	3.4
3	W	714	TYR	3.4
3	W	119	PHE	3.4
2	C	108	GLY	3.4
2	H	149	GLY	3.4
3	W	400	ALA	3.4
2	J	55	PRO	3.4
2	H	25	SER	3.4
2	M	132	SER	3.4
3	W	483	TYR	3.4
2	C	60	ASN	3.4
2	C	2	ASP	3.4
2	J	146	GLN	3.4
2	J	102	ARG	3.4
2	L	215	ARG	3.4
3	W	217	VAL	3.4
3	W	452	ARG	3.4
3	W	907	VAL	3.4
2	M	272	THR	3.4
1	A	303	LEU	3.4
2	E	316	HIS	3.4
3	W	826	ILE	3.4
2	J	71	LEU	3.4
2	E	255	ARG	3.3
3	W	59	PHE	3.3
3	W	636	VAL	3.3
1	B	719	GLY	3.3
2	D	375	SER	3.3
2	L	113	SER	3.3
3	W	793	SER	3.3
2	I	53	ASN	3.3
2	I	60	ASN	3.3
3	W	323	ALA	3.3
2	M	187	GLU	3.3
3	W	10	GLU	3.3
3	W	62	TYR	3.3
2	G	178	GLY	3.3
3	W	250	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
3	W	576	PRO	3.3
2	C	340	GLU	3.3
2	E	262	GLU	3.3
3	W	770	ASP	3.3
2	G	99	GLU	3.3
2	G	93	ASP	3.3
2	C	282	ALA	3.3
2	I	186	SER	3.3
3	W	892	LEU	3.3
3	W	1042	ILE	3.3
2	J	315	GLU	3.3
2	N	108	GLY	3.3
2	I	319	THR	3.3
3	W	883	PRO	3.3
2	G	315	GLU	3.3
2	N	49	GLY	3.3
2	K	126	ARG	3.3
2	M	155	PRO	3.3
2	E	279	THR	3.3
2	M	326	ILE	3.3
2	I	331	CYS	3.2
2	M	331	CYS	3.2
3	W	609	LYS	3.2
2	G	312	GLN	3.2
3	W	98	LEU	3.2
3	W	92	TYR	3.2
3	W	3	LYS	3.2
1	B	753	ASN	3.2
2	D	103	GLU	3.2
2	M	260	GLU	3.2
3	W	61	GLU	3.2
3	W	1009	PHE	3.2
3	W	660	ALA	3.2
2	C	319	THR	3.2
2	E	115	SER	3.2
2	J	46	PHE	3.2
2	M	262	GLU	3.2
3	W	657	GLU	3.2
3	W	951	ILE	3.2
3	W	242	LYS	3.2
3	W	28	TYR	3.2
2	C	133	SER	3.2

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Mol	Chain	Res	Type	RSRZ
2	E	325	ARG	3.2
3	W	454	VAL	3.2
2	E	20	GLU	3.2
3	W	15	ILE	3.2
3	W	598	ALA	3.2
3	W	91	LYS	3.2
2	L	55	PRO	3.2
2	J	54	LEU	3.2
2	L	50	GLY	3.2
3	W	333	GLY	3.2
3	W	884	PHE	3.2
2	G	126	ARG	3.2
2	E	332	GLU	3.2
2	H	319	THR	3.2
3	W	241	ALA	3.2
3	W	929	ALA	3.2
2	C	202	PRO	3.2
2	D	49	GLY	3.2
3	W	1002	GLY	3.2
2	L	187	GLU	3.1
2	D	208	PHE	3.1
3	W	1068	LYS	3.1
2	G	114	ASP	3.1
2	D	272	THR	3.1
3	W	757	LEU	3.1
2	J	149	GLY	3.1
1	A	375	ALA	3.1
3	W	282	ASP	3.1
2	N	151	THR	3.1
3	W	791	LEU	3.1
3	W	841	SER	3.1
2	L	208	PHE	3.1
3	W	864	PRO	3.1
2	C	321	GLY	3.1
2	G	196	SER	3.1
2	E	50	GLY	3.1
3	W	485	LYS	3.1
3	W	517	LEU	3.1
2	F	332	GLU	3.1
2	J	313	PRO	3.1
3	W	425	MET	3.1
2	G	324	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
2	C	230	GLU	3.1
2	G	45	GLU	3.1
2	F	49	GLY	3.1
2	L	288	ILE	3.1
3	W	911	ILE	3.1
2	M	186	SER	3.1
2	L	53	ASN	3.1
2	M	138	ASN	3.1
2	I	364	GLY	3.0
2	M	146	GLN	3.0
3	W	859	THR	3.0
3	W	599	ALA	3.0
2	K	53	ASN	3.0
2	D	99	GLU	3.0
3	W	40	GLU	3.0
3	W	848	GLU	3.0
3	W	669	LEU	3.0
3	W	103	THR	3.0
3	W	296	ARG	3.0
3	W	776	GLY	3.0
3	W	986	TYR	3.0
2	L	323	THR	3.0
3	W	1071	TRP	3.0
1	A	304	LEU	3.0
2	L	256	PRO	3.0
2	L	151	THR	3.0
2	M	319	THR	3.0
3	W	233	SER	3.0
3	W	816	SER	3.0
3	W	789	MET	3.0
3	W	11	TYR	3.0
3	W	586	TYR	3.0
2	K	134	GLU	3.0
2	E	272	THR	3.0
3	W	938	SER	3.0
3	W	915	GLY	3.0
3	W	956	ASN	3.0
2	C	292	PHE	3.0
3	W	410	PHE	3.0
3	W	785	GLN	3.0
2	J	59	TRP	3.0
3	W	190	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
3	W	471	ILE	3.0
1	A	120	THR	3.0
2	K	161	SER	3.0
2	N	233	SER	3.0
2	I	159	PRO	3.0
2	C	200	ASN	3.0
2	E	189	GLN	3.0
2	J	296	ARG	3.0
2	L	261	VAL	3.0
3	W	917	ARG	3.0
2	K	377	SER	2.9
2	G	202	PRO	2.9
3	W	326	TYR	2.9
2	G	46	PHE	2.9
2	J	193	PHE	2.9
2	M	191	ALA	2.9
2	J	47	GLN	2.9
3	W	519	THR	2.9
3	W	923	ASP	2.9
2	K	329	ALA	2.9
2	H	387	THR	2.9
2	K	68	THR	2.9
3	W	218	PHE	2.9
3	W	834	THR	2.9
2	L	114	ASP	2.9
2	N	130	ASP	2.9
2	M	189	GLN	2.9
3	W	681	TYR	2.9
2	E	163	SER	2.9
2	E	320	VAL	2.9
2	L	287	THR	2.9
2	G	194	ASP	2.9
2	K	47	GLN	2.9
3	W	147	PHE	2.9
2	L	290	LEU	2.9
2	J	255	ARG	2.9
3	W	981	TYR	2.9
3	W	1001	TYR	2.9
2	D	210	HIS	2.9
3	W	949	LYS	2.9
3	W	897	GLN	2.9
3	W	46	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
2	H	135	TYR	2.8
2	M	135	TYR	2.8
2	C	329	ALA	2.8
2	O	244	ALA	2.8
1	A	821	SER	2.8
2	C	169	SER	2.8
3	W	916	SER	2.8
3	W	14	PHE	2.8
2	D	317	HIS	2.8
2	E	193	PHE	2.8
1	B	659	ASP	2.8
3	W	879	ARG	2.8
2	G	180	MET	2.8
3	W	360	TYR	2.8
2	C	119	LEU	2.8
1	A	775	ILE	2.8
2	G	377	SER	2.8
2	I	279	THR	2.8
1	B	808	ASP	2.8
2	J	247	TRP	2.8
3	W	944	ILE	2.8
3	W	359	MET	2.8
2	H	376	PRO	2.8
2	D	58	ASN	2.8
3	W	208	ASN	2.8
3	W	447	ILE	2.8
2	E	108	GLY	2.8
2	E	340	GLU	2.8
2	F	134	GLU	2.8
2	G	205	THR	2.8
3	W	2	GLY	2.8
3	W	446	PRO	2.8
1	A	722	ASN	2.8
2	I	176	LEU	2.8
2	O	334	VAL	2.8
3	W	756	VAL	2.8
2	O	321	GLY	2.8
2	F	22	THR	2.8
2	L	22	THR	2.8
2	L	291	SER	2.8
2	D	318	ALA	2.8
2	M	310	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
3	W	556	GLN	2.8
3	W	801	GLU	2.8
2	E	254	LEU	2.8
3	W	857	LEU	2.8
2	H	86	ASP	2.8
3	W	534	PHE	2.8
1	A	488	VAL	2.7
2	C	128	ASN	2.7
2	D	53	ASN	2.7
3	W	850	ARG	2.7
3	W	932	ARG	2.7
3	W	479	LYS	2.7
3	W	961	TYR	2.7
1	B	406	SER	2.7
2	K	224	THR	2.7
3	W	126	THR	2.7
3	W	844	PRO	2.7
2	G	90	ASP	2.7
3	W	387	ARG	2.7
2	M	21	GLY	2.7
2	C	221	ALA	2.7
1	A	350	SER	2.7
2	F	161	SER	2.7
2	H	51	ILE	2.7
3	W	44	LYS	2.7
3	W	397	MET	2.7
3	W	900	MET	2.7
2	M	109	ILE	2.7
2	D	328	SER	2.7
3	W	558	LEU	2.7
2	I	191	ALA	2.7
3	W	759	THR	2.7
1	A	324	SER	2.7
2	C	291	SER	2.7
3	W	216	SER	2.7
2	J	70	LEU	2.7
3	W	344	LEU	2.7
2	I	229	ALA	2.7
1	A	477	ASN	2.7
2	K	138	ASN	2.7
2	G	376	PRO	2.7
1	A	408	MET	2.7

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Mol	Chain	Res	Type	RSRZ
3	W	878	LEU	2.7
2	I	183	ASN	2.7
2	G	207	GLN	2.7
3	W	1005	GLN	2.7
2	N	121	GLY	2.7
1	B	185	ASP	2.6
1	B	815	TYR	2.6
2	G	154	LYS	2.6
3	W	367	ILE	2.6
3	W	311	LEU	2.6
3	W	820	LEU	2.6
2	I	333	SER	2.6
2	J	291	SER	2.6
3	W	991	SER	2.6
3	W	177	ILE	2.6
3	W	211	ILE	2.6
2	H	117	ARG	2.6
3	W	118	LEU	2.6
3	W	904	PRO	2.6
2	O	258	ASN	2.6
2	E	379	GLU	2.6
2	F	46	PHE	2.6
2	G	123	LYS	2.6
3	W	284	THR	2.6
3	W	557	THR	2.6
3	W	210	SER	2.6
1	B	720	TYR	2.6
3	W	655	VAL	2.6
3	W	845	ILE	2.6
2	F	372	THR	2.6
2	M	210	HIS	2.6
2	D	189	GLN	2.6
2	J	140	ASN	2.6
3	W	129	LEU	2.6
3	W	144	ALA	2.6
3	W	466	PRO	2.6
3	W	369	ASP	2.6
2	J	326	ILE	2.6
1	A	307	ARG	2.6
2	K	289	ARG	2.6
3	W	1070	MET	2.6
3	W	125	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
2	M	205	THR	2.6
2	G	375	SER	2.5
1	A	430	ALA	2.5
3	W	298	ALA	2.5
3	W	948	TYR	2.5
2	G	263	PHE	2.5
2	J	263	PHE	2.5
2	L	161	SER	2.5
3	W	307	ILE	2.5
2	D	21	GLY	2.5
2	F	114	ASP	2.5
2	C	258	ASN	2.5
2	M	309	PRO	2.5
2	C	59	TRP	2.5
2	E	179	THR	2.5
3	W	712	ILE	2.5
1	B	740	ARG	2.5
2	D	133	SER	2.5
3	W	362	GLU	2.5
2	C	118	LYS	2.5
2	L	58	ASN	2.5
3	W	243	LEU	2.5
2	M	148	THR	2.5
3	W	580	VAL	2.5
3	W	865	VAL	2.5
2	C	375	SER	2.5
2	E	120	SER	2.5
3	W	571	SER	2.5
2	H	45	GLU	2.5
3	W	395	LEU	2.5
3	W	476	VAL	2.5
2	K	110	ALA	2.5
3	W	1034	HIS	2.5
2	H	186	SER	2.5
2	G	12	LYS	2.5
3	W	309	ASP	2.5
3	W	383	ASP	2.5
3	W	432	ARG	2.5
3	W	456	GLY	2.5
2	G	162	ALA	2.5
2	N	110	ALA	2.5
2	O	118	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
2	G	186	SER	2.5
1	B	180	TYR	2.5
2	D	290	LEU	2.5
3	W	518	TYR	2.5
2	N	93	ASP	2.5
1	A	674	VAL	2.5
2	H	101	VAL	2.5
3	W	443	VAL	2.5
2	D	72	ASN	2.5
2	H	271	ASN	2.5
3	W	285	PHE	2.4
1	A	347	GLN	2.4
2	D	209	GLU	2.4
1	B	875	ARG	2.4
2	E	58	ASN	2.4
1	A	759	LEU	2.4
2	F	129	PHE	2.4
3	W	634	TYR	2.4
2	E	291	SER	2.4
3	W	792	SER	2.4
3	W	952	SER	2.4
2	I	320	VAL	2.4
2	H	67	GLY	2.4
3	W	992	TYR	2.4
1	A	822	THR	2.4
2	D	48	THR	2.4
1	B	388	SER	2.4
2	F	327	GLU	2.4
2	H	163	SER	2.4
3	W	774	GLU	2.4
3	W	782	VAL	2.4
2	N	111	PRO	2.4
3	W	422	MET	2.4
2	L	52	GLY	2.4
3	W	197	LYS	2.4
2	K	225	LEU	2.4
2	C	107	ASN	2.4
2	K	385	VAL	2.4
2	J	279	THR	2.4
2	M	45	GLU	2.4
3	W	942	PRO	2.4
1	B	407	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
2	I	182	LEU	2.4
2	K	364	GLY	2.4
1	A	758	ALA	2.4
3	W	101	ASP	2.4
2	M	273	TYR	2.4
1	A	189	GLU	2.4
1	A	570	THR	2.4
2	E	56	ILE	2.4
3	W	230	ILE	2.4
2	L	212	VAL	2.4
2	N	117	ARG	2.4
3	W	423	HIS	2.4
2	J	262	GLU	2.4
2	M	163	SER	2.4
3	W	122	ALA	2.4
2	H	15	ARG	2.4
2	I	217	VAL	2.4
2	M	177	MET	2.4
2	E	155	PRO	2.3
2	E	293	GLN	2.3
2	I	379	GLU	2.3
2	J	312	GLN	2.3
2	M	263	PHE	2.3
3	W	1064	ILE	2.3
2	C	132	SER	2.3
2	L	233	SER	2.3
3	W	116	SER	2.3
3	W	182	VAL	2.3
2	H	90	ASP	2.3
2	N	54	LEU	2.3
2	D	251	PRO	2.3
2	D	60	ASN	2.3
2	D	285	PHE	2.3
2	G	72	ASN	2.3
2	J	112	GLN	2.3
2	J	336	ALA	2.3
3	W	802	ILE	2.3
1	B	412	THR	2.3
1	A	638	MET	2.3
2	E	59	TRP	2.3
2	L	259	VAL	2.3
2	K	98	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
2	K	316	HIS	2.3
2	C	379	GLU	2.3
2	E	134	GLU	2.3
2	L	145	ARG	2.3
2	M	215	ARG	2.3
2	E	294	LEU	2.3
3	W	55	LEU	2.3
2	I	192	GLY	2.3
2	L	149	GLY	2.3
1	A	569	GLN	2.3
2	D	310	ASN	2.3
2	M	230	GLU	2.3
3	W	778	THR	2.3
1	A	744	TYR	2.3
3	W	415	ILE	2.3
2	N	86	ASP	2.3
3	W	570	ASP	2.3
2	F	146	GLN	2.3
2	H	47	GLN	2.3
2	L	224	THR	2.3
2	G	249	PHE	2.3
2	I	263	PHE	2.3
2	J	223	ILE	2.3
2	K	221	ALA	2.3
2	L	73	LEU	2.3
2	G	340	GLU	2.3
3	W	781	GLU	2.3
3	W	908	GLN	2.3
2	J	239	ASN	2.3
2	G	361	PHE	2.3
3	W	70	THR	2.3
3	W	659	TYR	2.3
2	H	390	SER	2.3
3	W	736	ILE	2.3
3	W	798	ILE	2.3
3	W	954	HIS	2.3
2	L	86	ASP	2.3
2	M	131	ASN	2.2
2	F	361	PHE	2.2
2	C	205	THR	2.2
2	E	287	THR	2.2
2	H	69	THR	2.2

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Mol	Chain	Res	Type	RSRZ
3	W	325	ILE	2.2
3	W	930	ILE	2.2
2	G	192	GLY	2.2
2	K	217	VAL	2.2
2	I	209	GLU	2.2
2	O	103	GLU	2.2
2	D	314	PHE	2.2
2	D	59	TRP	2.2
2	L	310	ASN	2.2
3	W	83	ASN	2.2
3	W	541	GLY	2.2
2	N	184	ALA	2.2
3	W	787	ALA	2.2
2	D	284	ASN	2.2
2	E	60	ASN	2.2
2	G	94	ASN	2.2
1	A	330	ARG	2.2
2	F	341	THR	2.2
2	I	216	ARG	2.2
2	J	117	ARG	2.2
2	C	234	PHE	2.2
1	A	525	TYR	2.2
1	A	620	ASP	2.2
2	H	230	GLU	2.2
2	L	327	GLU	2.2
3	W	1016	LYS	2.2
2	E	149	GLY	2.2
3	W	207	ALA	2.2
1	B	530	GLN	2.2
2	M	293	GLN	2.2
2	J	289	ARG	2.2
1	B	696	SER	2.2
2	N	331	CYS	2.2
2	D	261	VAL	2.2
2	D	276	ARG	2.2
2	C	201	ALA	2.2
2	G	50	GLY	2.2
2	M	162	ALA	2.2
3	W	84	ALA	2.2
2	E	257	ASN	2.2
2	H	61	PHE	2.2
2	M	136	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
2	O	397	LYS	2.2
3	W	764	LYS	2.2
3	W	953	LEU	2.2
2	K	375	SER	2.2
1	A	444	ARG	2.2
1	B	276	GLU	2.2
2	G	92	VAL	2.2
2	F	325	ARG	2.2
2	G	332	GLU	2.2
2	N	330	VAL	2.2
2	I	59	TRP	2.2
2	K	183	ASN	2.1
2	C	148	THR	2.1
3	W	204	VAL	2.1
2	D	231	ARG	2.1
2	F	255	ARG	2.1
1	B	315	GLU	2.1
2	M	137	GLU	2.1
2	O	318	ALA	2.1
2	F	62	ASP	2.1
3	W	222	ASP	2.1
2	I	261	VAL	2.1
2	J	316	HIS	2.1
1	A	447	TYR	2.1
2	G	144	ARG	2.1
2	H	283	ARG	2.1
2	I	102	ARG	2.1
2	N	102	ARG	2.1
3	W	219	SER	2.1
3	W	503	TYR	2.1
2	O	47	GLN	2.1
3	W	1052	ILE	2.1
1	B	395	ASP	2.1
2	G	16	ASP	2.1
1	A	326	TYR	2.1
2	I	106	ARG	2.1
1	A	467	GLN	2.1
2	D	50	GLY	2.1
2	F	262	GLU	2.1
3	W	812	VAL	2.1
2	H	102	ARG	2.1
2	I	177	MET	2.1

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Mol	Chain	Res	Type	RSRZ
3	W	130	MET	2.1
2	K	156	ASN	2.1
3	W	394	LEU	2.1
2	N	109	ILE	2.1
3	W	731	PHE	2.1
3	W	1059	PRO	2.1
2	F	369	ASP	2.1
2	G	217	VAL	2.1
1	A	302	ASN	2.1
2	J	323	THR	2.1
2	L	118	LYS	2.1
2	K	115	SER	2.1
3	W	955	GLU	2.1
2	I	190	VAL	2.1
2	G	384	ARG	2.1
3	W	1003	CYS	2.1
2	E	44	ASN	2.1
2	J	211	ILE	2.1
3	W	48	ASN	2.1
2	M	105	GLN	2.1
2	D	352	GLU	2.1
2	I	15	ARG	2.0
2	L	116	LEU	2.0
3	W	858	LEU	2.0
2	D	160	TYR	2.0
2	K	67	GLY	2.0
2	O	281	ILE	2.0
2	G	251	PRO	2.0
2	L	213	GLN	2.0
2	M	271	ASN	2.0
3	W	950	VAL	2.0
2	C	123	LYS	2.0
2	G	125	LYS	2.0
3	W	501	LEU	2.0
2	F	160	TYR	2.0
3	W	921	ILE	2.0
2	E	178	GLY	2.0
2	J	275	ALA	2.0
2	N	321	GLY	2.0
1	B	560	CYS	2.0
2	E	212	VAL	2.0
2	G	310	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
3	W	945	GLU	2.0
3	W	305	LYS	2.0
2	C	24	TYR	2.0
2	D	56	ILE	2.0
3	W	1086	PHE	2.0
2	E	318	ALA	2.0
2	F	358	GLY	2.0
2	M	185	GLY	2.0
1	B	152	LYS	2.0
2	F	310	ASN	2.0
2	G	260	GLU	2.0
2	L	131	ASN	2.0
2	L	141	LEU	2.0
2	L	387	THR	2.0
2	I	386	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ZN	O	401	1/1	0.63	0.27	51,51,51,51	0
4	ZN	F	401	1/1	0.98	0.07	51,51,51,51	0
4	ZN	I	401	1/1	0.99	0.07	51,51,51,51	0
4	ZN	L	401	1/1	1.00	0.03	51,51,51,51	0
4	ZN	C	401	1/1	1.00	0.04	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.