



Full wwPDB EM Validation Report ⓘ

Mar 12, 2026 – 11:12 AM UTC

PDB ID : 7AOD / pdb_00007aod
EMDB ID : EMD-11841
Title : Schizosaccharomyces pombe RNA polymerase I (dimer)
Authors : Heiss, F.; Daiss, J.; Becker, P.; Engel, C.
Deposited on : 2020-10-14
Resolution : 4.50 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

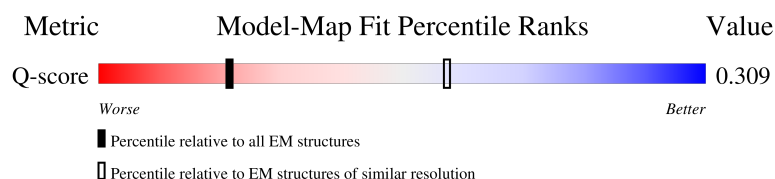
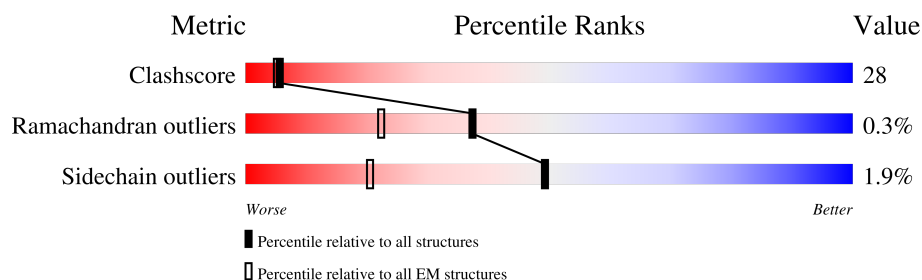
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1689	
1	M	1689	
2	B	1174	
2	N	1174	

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Mol	Chain	Length	Quality of chain
3	C	348	
3	O	348	
4	D	147	
4	P	147	
5	E	210	
5	Q	210	
6	F	142	
6	R	142	
7	G	173	
7	S	173	
8	H	125	
8	T	125	
9	I	119	
9	U	119	
10	J	71	
10	V	71	
11	K	125	
11	W	125	
12	L	63	
12	X	63	

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 59256 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 DNA-directed RNA polymerase I subunit rpa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1384	Total	C	N	O	S	0	0
			10976	6965	1894	2059	58		
1	M	1384	Total	C	N	O	S	0	0
			10976	6965	1894	2059	58		

- Molecule 2 is a protein called Probable DNA-directed RNA polymerase I subunit RPA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1156	Total	C	N	O	S	0	0
			9127	5791	1592	1685	59		
2	N	1156	Total	C	N	O	S	0	0
			9127	5791	1592	1685	59		

- Molecule 3 is a protein called DNA-directed RNA polymerases I and III subunit RPAC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	317	Total	C	N	O	S	0	0
			2533	1621	430	475	7		
3	O	317	Total	C	N	O	S	0	0
			2533	1621	430	475	7		

- Molecule 4 is a protein called DNA-directed RNA polymerase I subunit rpa14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	39	Total	C	N	O	S	0	0
			322	203	57	61	1		
4	P	39	Total	C	N	O	S	0	0
			322	203	57	61	1		

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	207	Total	C	N	O	S	0	0
			1663	1050	301	306	6		
5	Q	207	Total	C	N	O	S	0	0
			1663	1050	301	306	6		

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	82	Total	C	N	O	S	0	0
			650	413	111	123	3		
6	R	82	Total	C	N	O	S	0	0
			650	413	111	123	3		

- Molecule 7 is a protein called DNA-directed RNA polymerase I subunit rpa43.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	160	Total	C	N	O	S	0	0
			1267	817	210	236	4		
7	S	160	Total	C	N	O	S	0	0
			1267	817	210	236	4		

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	123	Total	C	N	O	S	0	0
			990	628	166	193	3		
8	T	123	Total	C	N	O	S	0	0
			990	628	166	193	3		

- Molecule 9 is a protein called DNA-directed RNA polymerase I subunit RPA12.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	57	Total	C	N	O	S	0	0
			431	269	69	89	4		
9	U	57	Total	C	N	O	S	0	0
			431	269	69	89	4		

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	68	Total	C	N	O	S	0	0
			550	350	93	100	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
10	V	68	Total	C	N	O	S	0	0
			550	350	93	100	7		

- Molecule 11 is a protein called DNA-directed RNA polymerases I and III subunit RPAC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	95	Total	C	N	O	S	0	0
			745	472	123	146	4		
11	W	95	Total	C	N	O	S	0	0
			745	472	123	146	4		

- Molecule 12 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	45	Total	C	N	O	S	0	0
			368	225	74	61	8		
12	X	45	Total	C	N	O	S	0	0
			368	225	74	61	8		

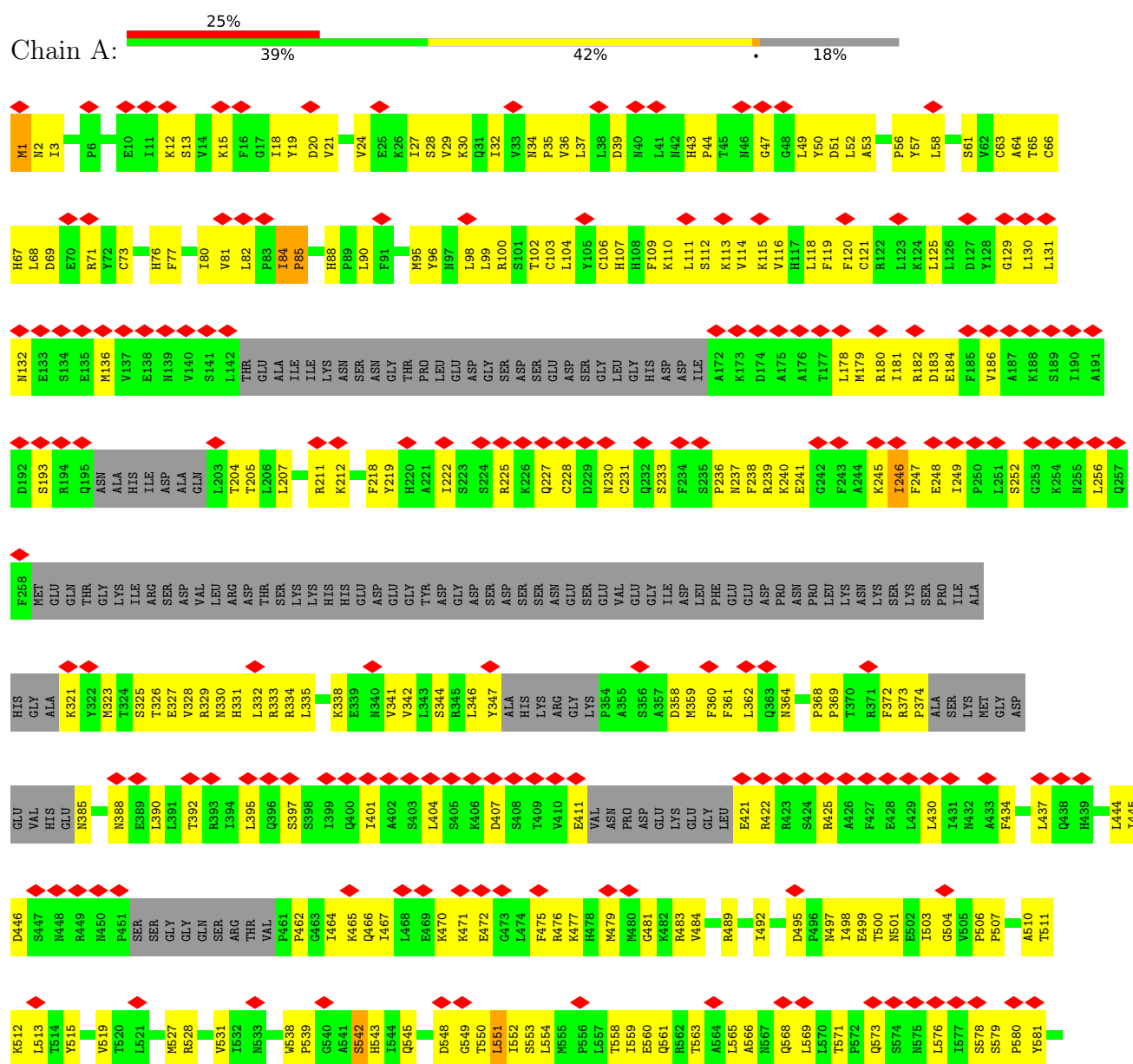
- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
13	A	2	Total	Zn	0
			2	2	
13	B	1	Total	Zn	0
			1	1	
13	I	1	Total	Zn	0
			1	1	
13	J	1	Total	Zn	0
			1	1	
13	L	1	Total	Zn	0
			1	1	
13	M	2	Total	Zn	0
			2	2	
13	N	1	Total	Zn	0
			1	1	
13	U	1	Total	Zn	0
			1	1	
13	V	1	Total	Zn	0
			1	1	
13	X	1	Total	Zn	0
			1	1	

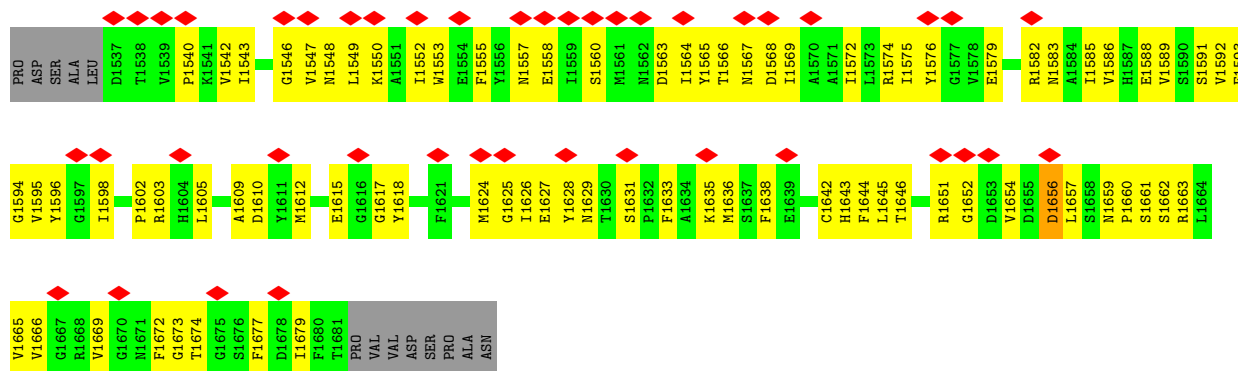
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

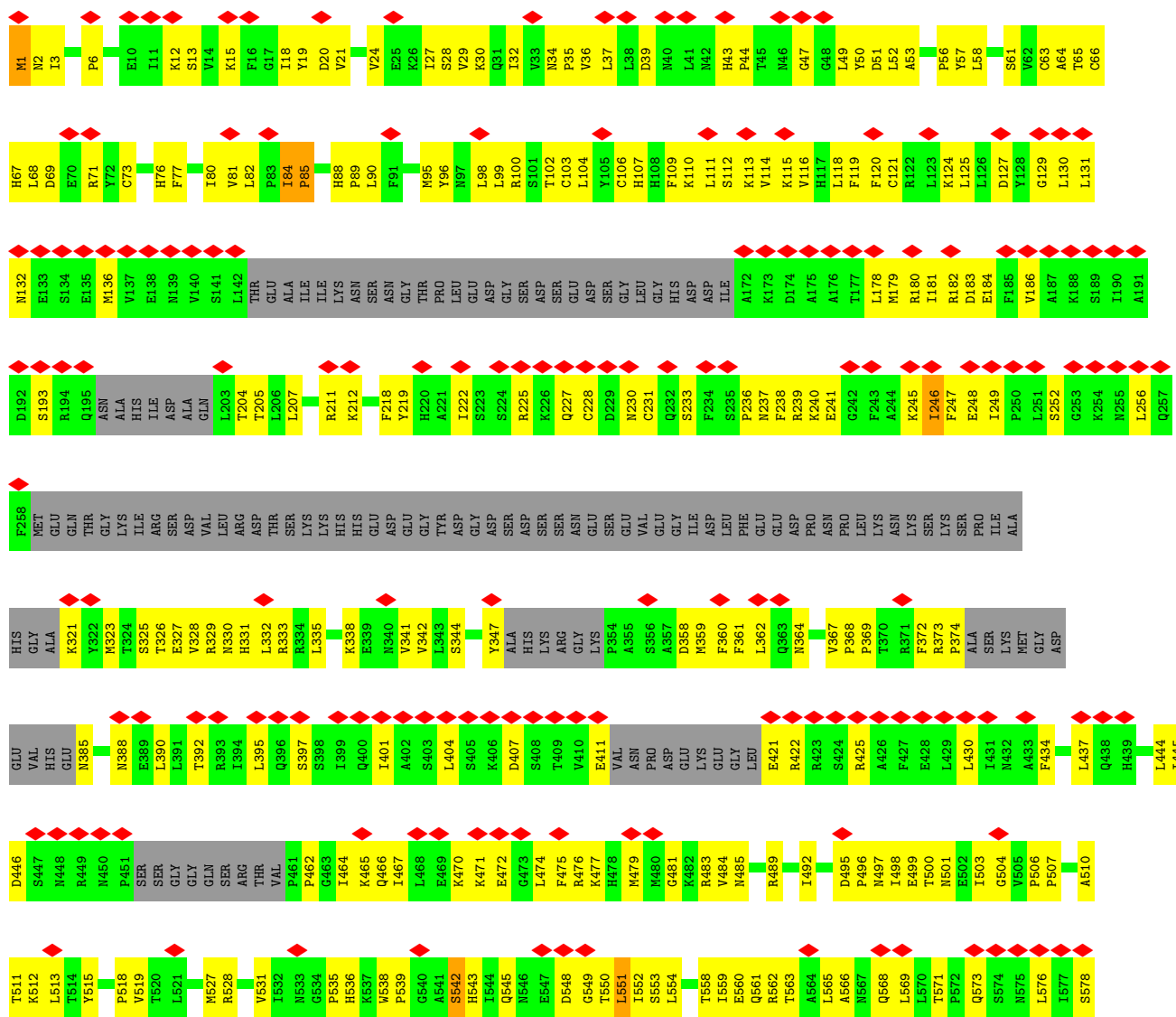
- Molecule 1: DNA-directed RNA polymerase I subunit rpa1



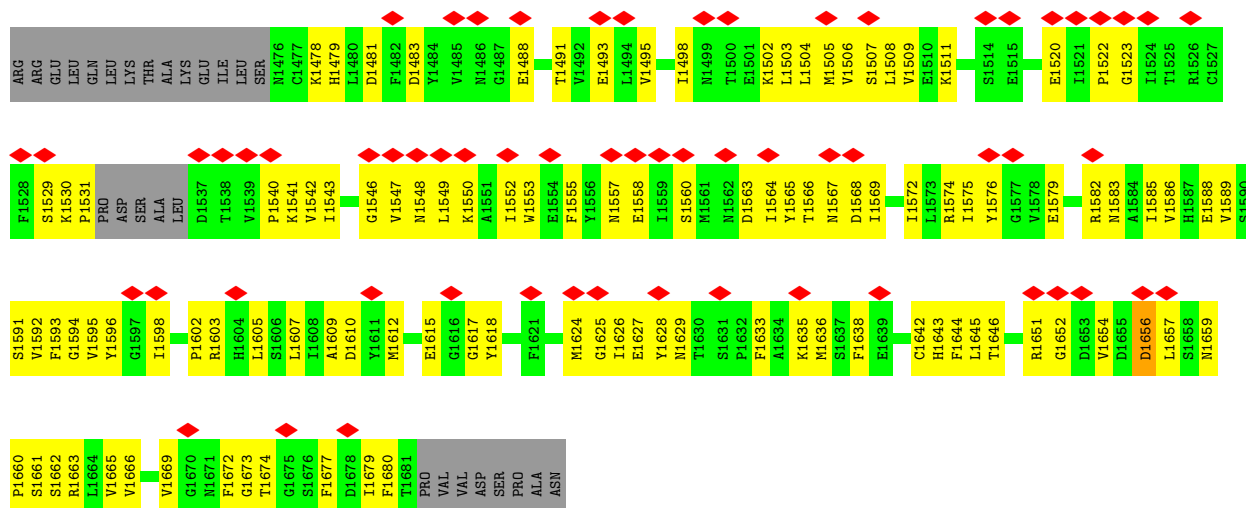




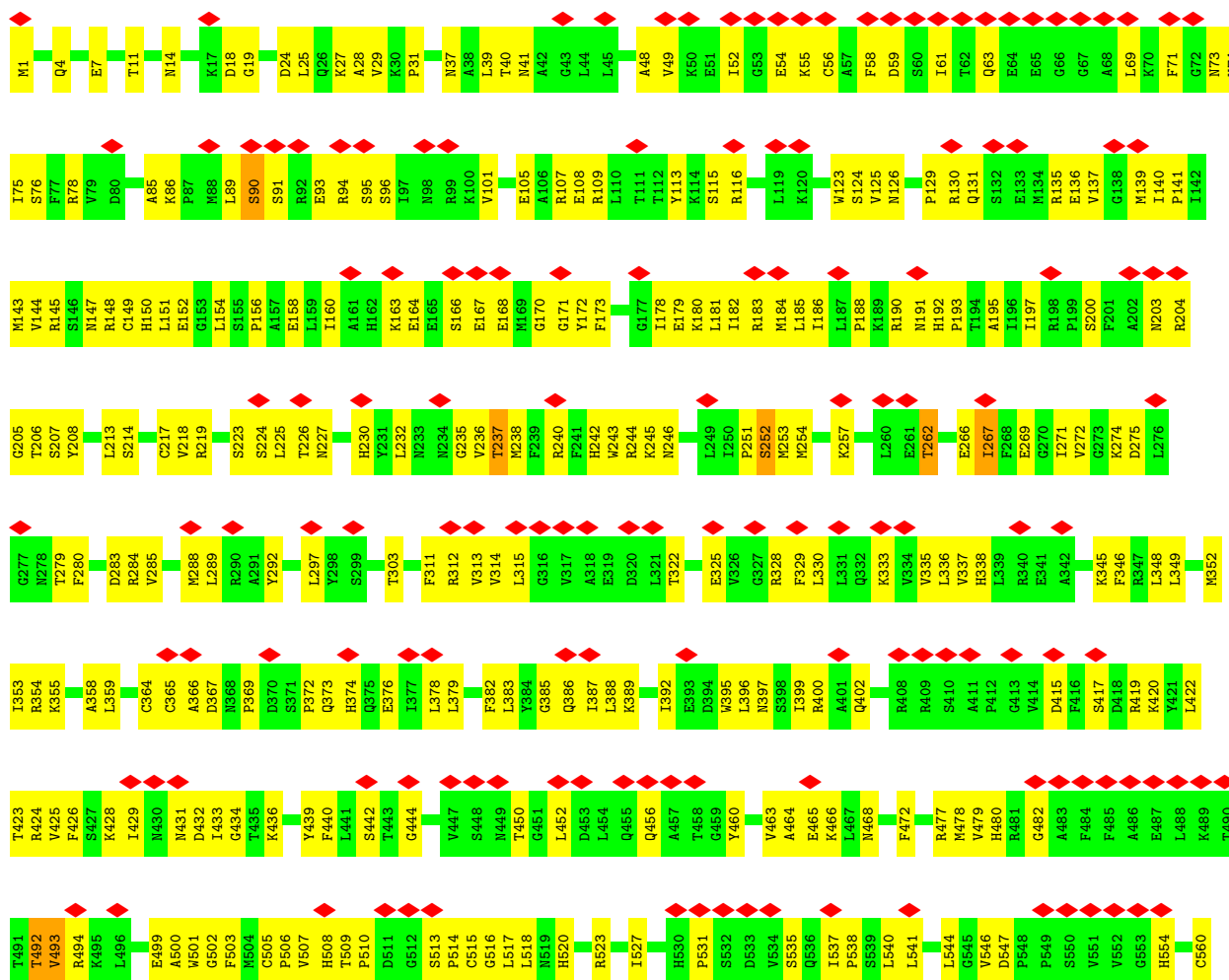
• Molecule 1: DNA-directed RNA polymerase I subunit rpa1



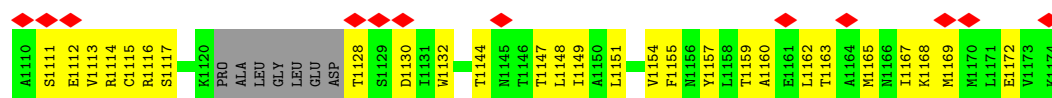




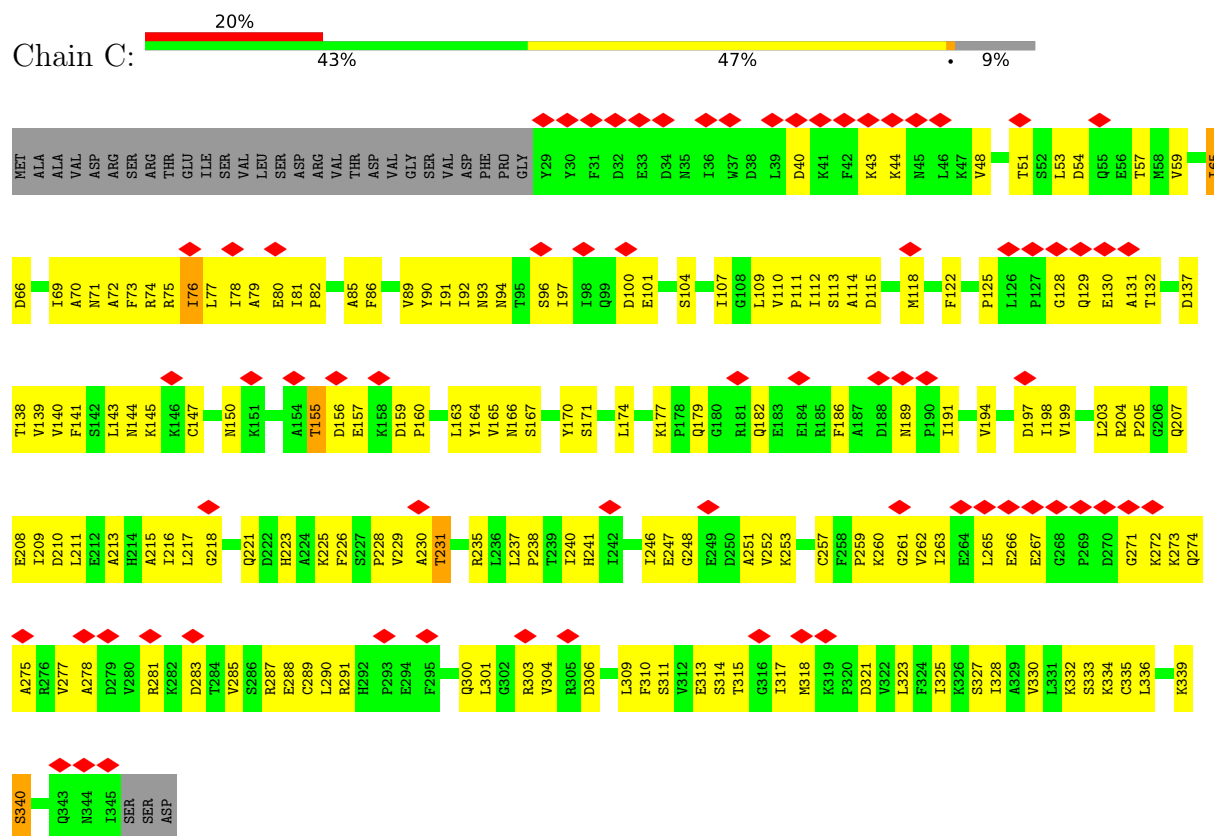
• Molecule 2: Probable DNA-directed RNA polymerase I subunit RPA2



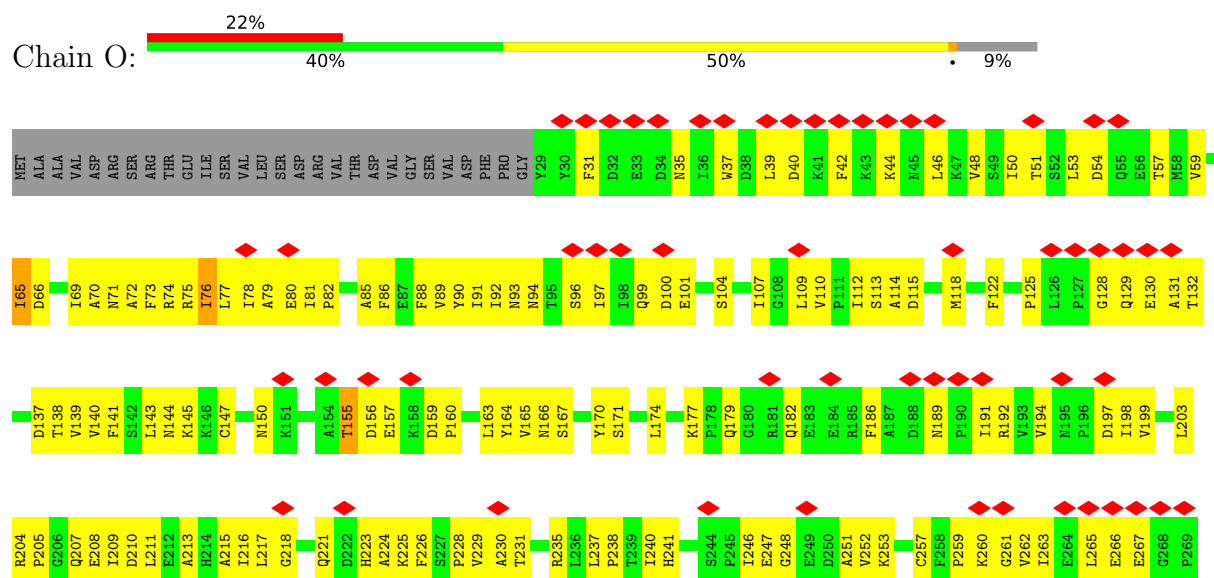
L1040	Y971	P896	F833	M768	M687	M618	D547	G482	S417	L348	L276	G205
Q1043	S972	I897	I834	E769	M688	M619	P848	A483	D418	L349	G277	T206
P1044	E973	D900	G835	D770	T689	G620	P849	F484	R419	M352	N278	S207
V1045	Q974	K901	T836	A771	Y622	D621	S550	F485	K420	I353	T279	Y208
K1046	G875	F902	K837	M772	P623	Y622	V551	A486	Y421	R354	D283	L213
GLY	T976	K902	L838	F691	G624	G624	V552	A487	L422	K355	R284	S214
ARG	A977	R905	E839	L773	L625	L625	G553	L488	T423	L356	V218	C217
LYS	A978	H906	D840	D693	Y626	Y626	H554	L489	R424	A358	R285	V218
ALA	G982	G907	G841	M775	L627	F628	L627	T490	V426	E286	R219	R219
GLY	L985	Q908	D842	S777	S697	S629	C560	T491	K428	L287	Q222	Q222
I1054	Y986	P909	P843	A778	P698	N630	V561	T492	N429	M288	S223	S223
G1055	X987	G910	I844	H779	R699	G636	G562	V493	I430	L289	S224	S224
G1056	G988	I911	V845	E780	M700	P631	L563	R494	N431	R290	L225	L225
G1057	Y990	K915	Y847	G782	M701	A632	D564	R495	D432	Y292	T226	T226
G1058	Y991	W916	D849	F783	Q703	R633	L567	L496	I433	L297	N227	N227
G1059	Y992	P917	E850	G704	Q705	M634	V568	E499	G434	Y298	H230	H230
G1060	H993	T918	S851	Q705	M706	V635	G569	A500	S371	S299	Y231	Y231
G1061	G994	W919	T852	M706	T710	R636	W570	F503	Q373	T303	Y232	Y232
G1062	N995	D920	T852	T710	G715	P637	C571	F504	H374	L307	Y233	Y233
G1063	E996	P922	G853	G791	G715	L641	L575	G502	Q375	F311	N234	N234
G1064	F997	G927	N854	G791	G715	S642	A576	F503	G375	R312	G235	G235
G1065	M998	M928	T857	E792	G715	T643	X577	F504	H374	V313	T237	T237
G1066	H1067	Q929	E858	F794	G715	G644	A580	G505	G376	V314	M238	M238
G1067	G1068	P930	T859	D795	L718	E645	L583	P506	I377	R240	F239	F239
G1068	G1069	D931	H861	K799	R719	L646	L583	V507	L378	R241	R240	R240
G1069	G1070	I932	H862	R800	R721	D647	L583	H508	L379	L315	H242	H242
G1070	G1071	I933	T863	R801	T722	V648	L583	T509	F382	G316	W243	W243
G1071	G1072	I934	E864	R802	R728	G650	M586	D511	L383	V317	R244	R244
G1072	G1073	I935	P865	R803	L729	P651	K987	G512	T384	G385	K245	K245
G1073	G1074	I936	E866	G804	Q730	F652	E589	S513	Y384	A318	N246	N246
G1074	G1075	I937	G867	P805	Q731	E653	Y590	P514	G386	E319	L249	L249
G1075	G1076	I938	F867	P806	G732	G654	V592	C515	Q387	D320	I250	I250
G1076	G1077	I939	H868	H807	Q733	L659	K993	G516	L387	L321	P251	P251
G1077	G1078	I940	D869	H808	T734	A660	L594	L517	L388	T322	S252	S252
G1078	G1079	I941	E870	H809	T734	C661	N596	L518	K389	E325	M253	M253
G1079	G1080	I942	V871	F812	L741	F662	G597	N519	T392	V326	M254	M254
G1080	G1081	M943	R872	A813	H742	P663	T598	H520	E393	G327	K257	K257
G1081	G1082	T944	L873	P814	Y745	L666	A599	H520	D394	R328	L260	L260
G1082	G1083	M947	L874	G815	L747	X669	T600	H520	V395	F329	E261	E261
G1083	G1084	E950	N876	G815	L747	X669	E601	H520	L396	L330	T262	T262
G1084	G1085	S951	D877	G816	L747	X669	E601	H520	N397	Q332	E266	E266
G1085	G1086	D1091	V878	T817	Y750	T672	K604	H530	A464	K333	I267	I267
G1086	G1087	K955	G879	P818	Y750	T672	V605	P531	A464	V334	F268	F268
G1087	G1088	A956	R819	H819	T754	V674	V605	S532	E465	V335	E269	E269
G1088	G1089	G957	D880	R820	M755	E675	P606	D533	K466	G337	G270	G270
G1089	G1090	I951	S881	E821	A756	V757	L607	V534	N468	H338	I271	I271
G1090	G1091	K955	C883	W822	V757	S677	D608	V534	R471	A411	V272	V272
G1091	G1092	A956	L823	W822	V757	S677	D608	V534	F472	P412	G273	G273
G1092	G1093	G957	Q884	Q824	T761	P678	L609	Q536	H475	H339	D275	D275
G1093	G1094	I961	Q885	K825	T761	P678	L609	Q536	R471	R340	K345	K345
G1094	G1095	G961	I886	L826	Y763	V681	D608	V534	H475	E341	F346	F346
G1095	G1096	L962	I887	D827	T764	L682	G612	V534	R471	A342	R347	R347
G1096	G1097	A963	H887	A828	T764	L682	G612	V534	F472	K346	R347	R347
G1097	G1098	Q964	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1098	G1099	S966	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1099	G1100	T967	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1100	G1101	P968	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1101	G1102	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1102	G1103	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1103	G1104	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1104	G1105	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1105	G1106	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1106	G1107	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1107	G1108	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1108	G1109	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347
G1109	G1110	I970	V888	D829	G765	T684	G612	V534	H475	F346	R347	R347

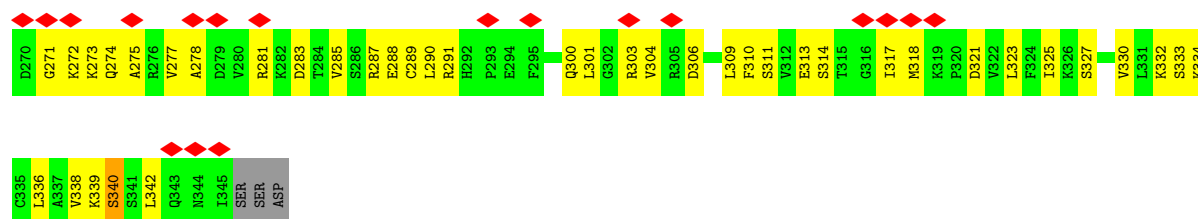


• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

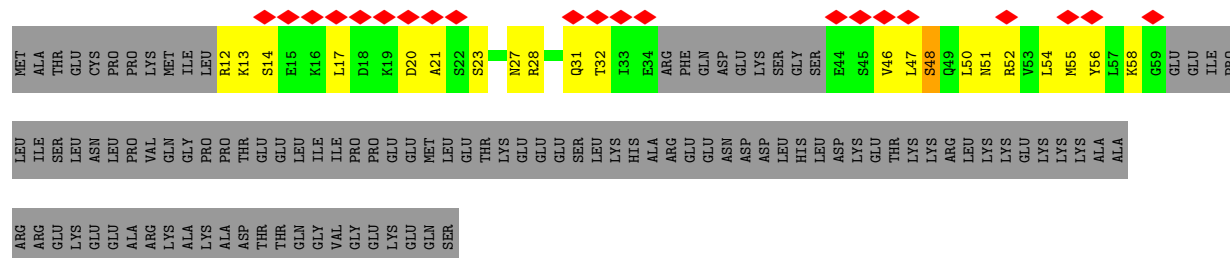


• Molecule 3: DNA-directed RNA polymerases I and III subunit RPAC1

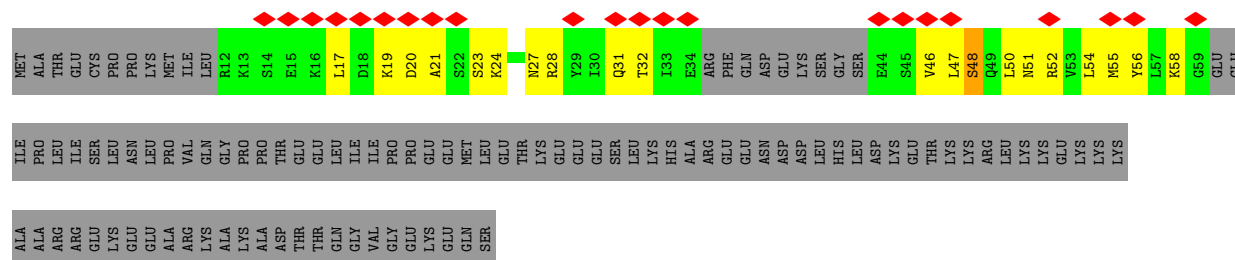




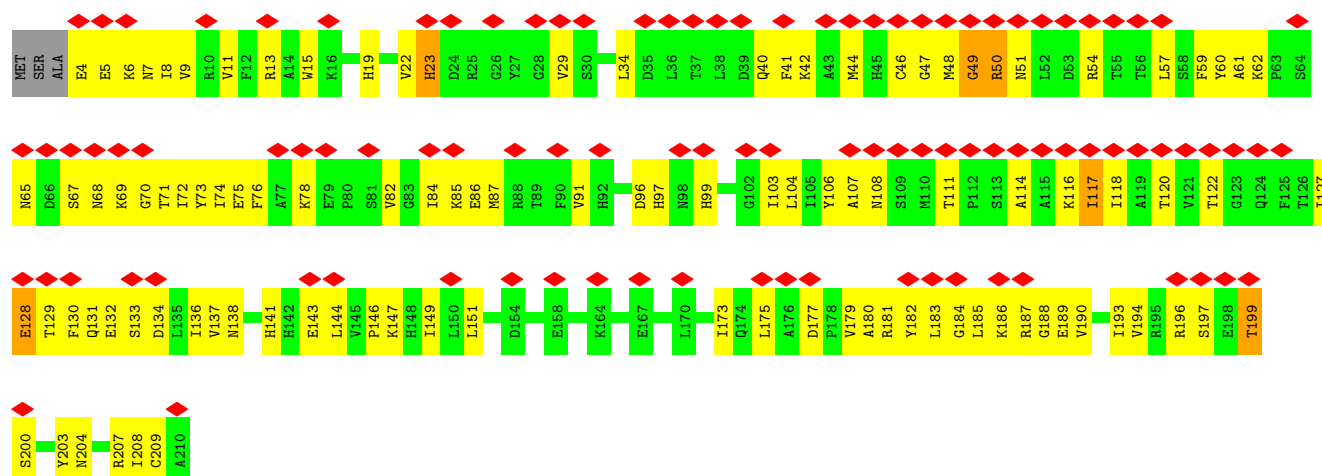
• Molecule 4: DNA-directed RNA polymerase I subunit rpa14



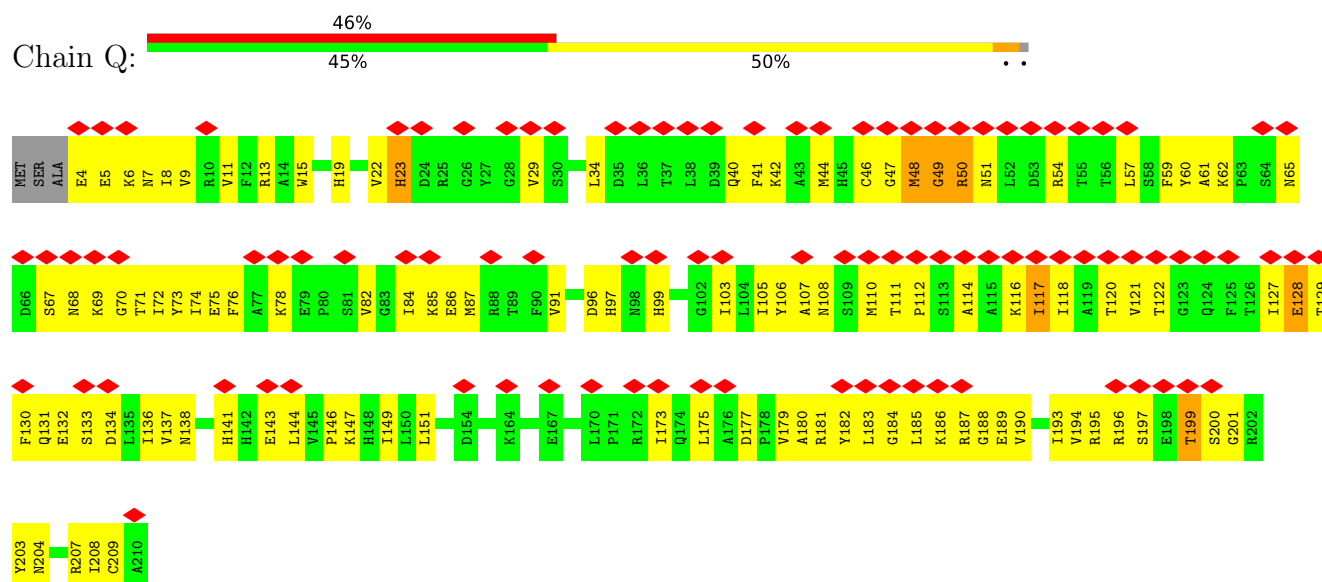
• Molecule 4: DNA-directed RNA polymerase I subunit rpa14



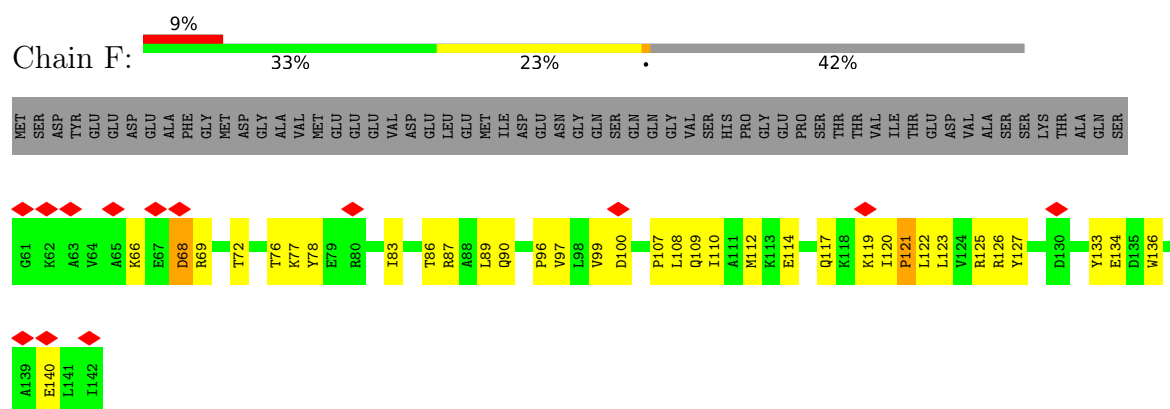
• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



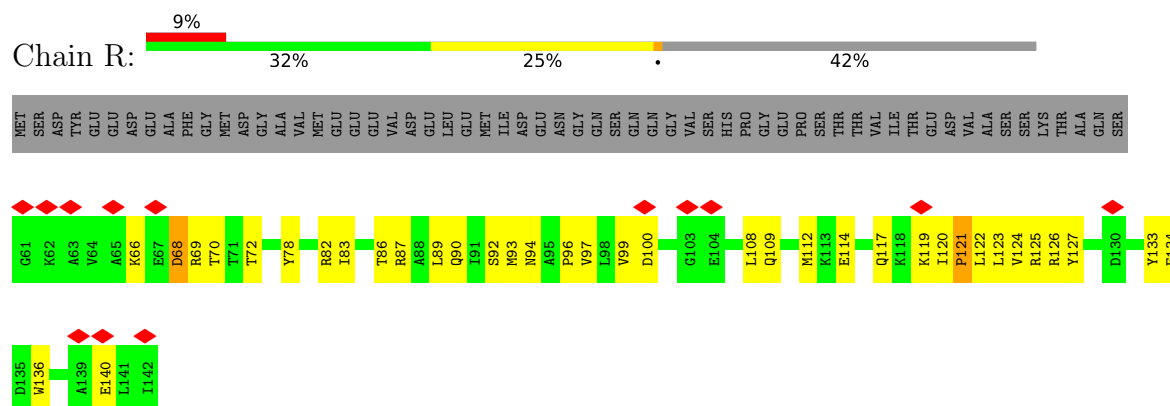
• Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC1



• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

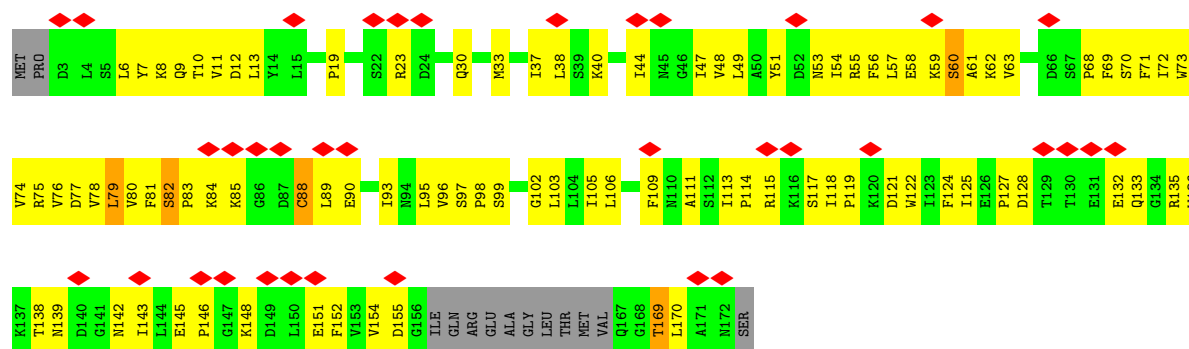


• Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC2

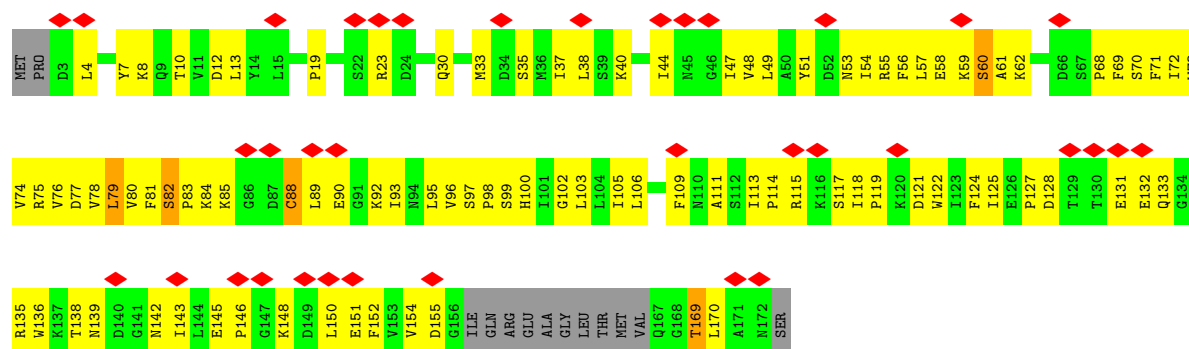


• Molecule 7: DNA-directed RNA polymerase I subunit rpa43

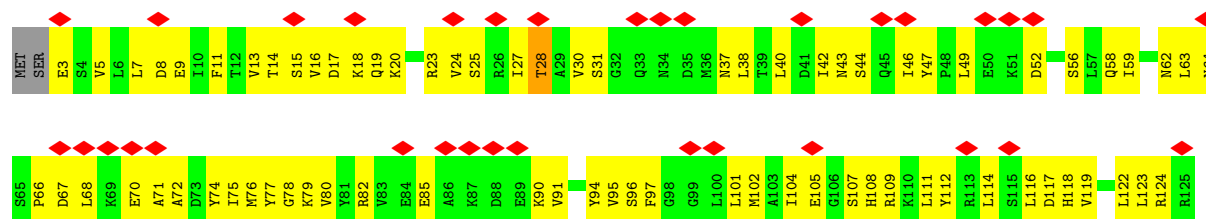




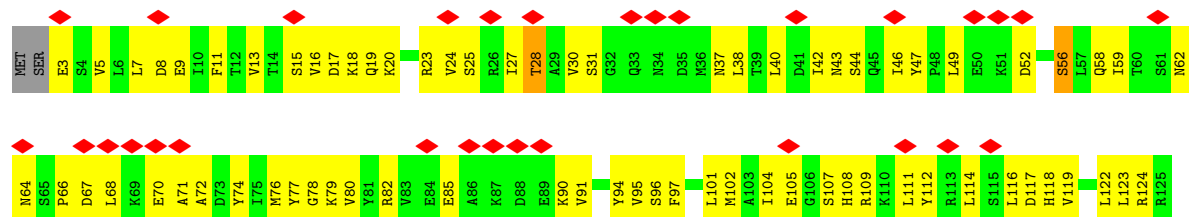
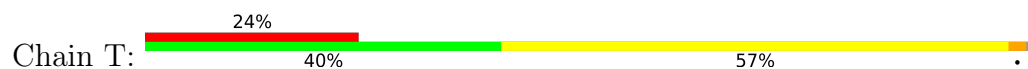
• Molecule 7: DNA-directed RNA polymerase I subunit rpa43



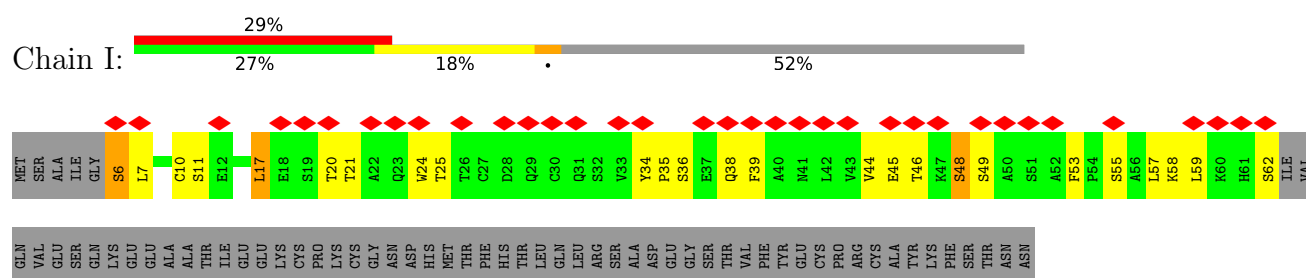
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



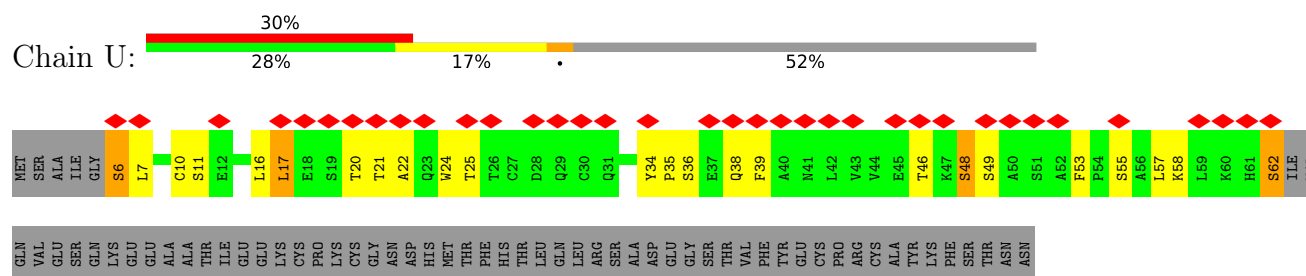
• Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC3



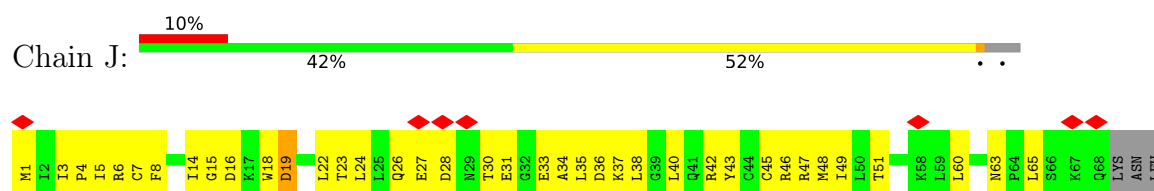
• Molecule 9: DNA-directed RNA polymerase I subunit RPA12



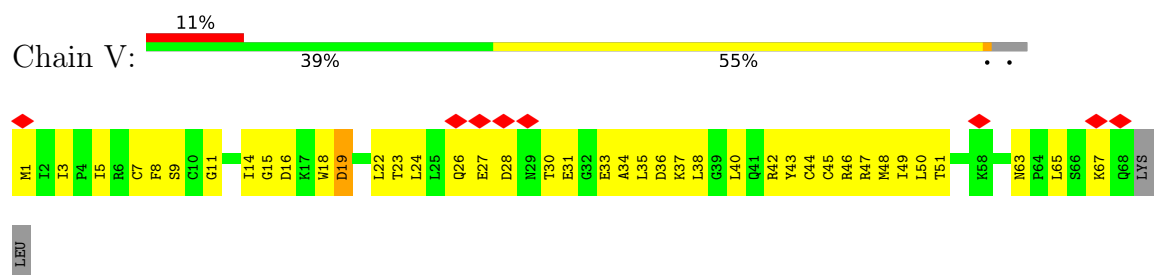
- Molecule 9: DNA-directed RNA polymerase I subunit RPA12



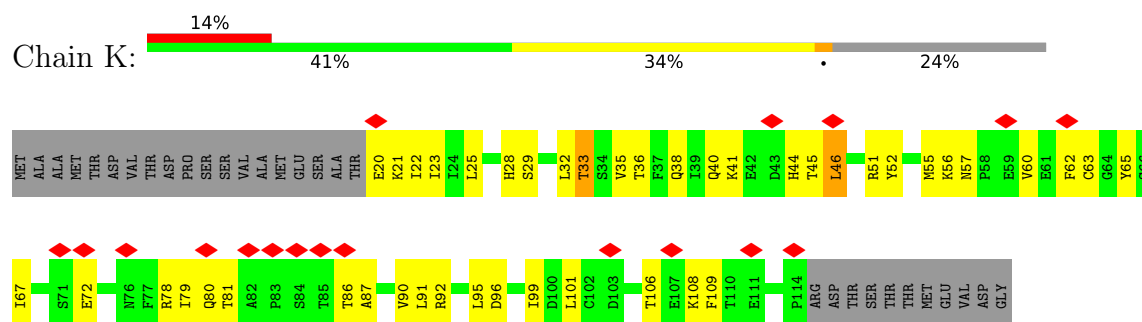
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5



- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC5

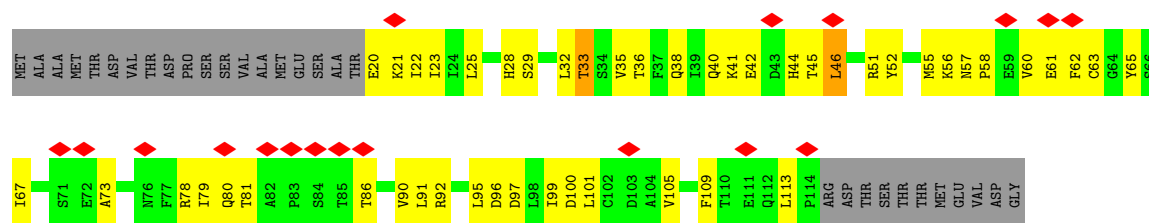


- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

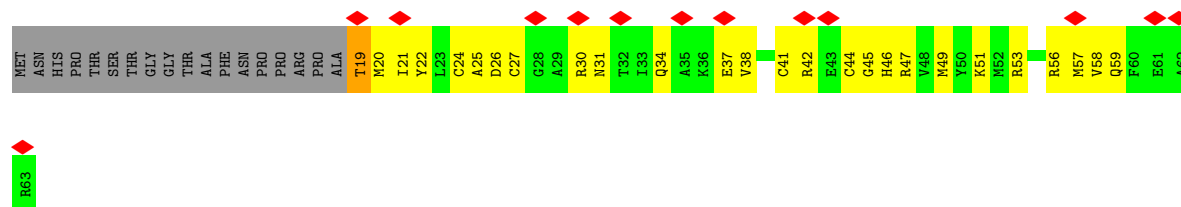


- Molecule 11: DNA-directed RNA polymerases I and III subunit RPAC2

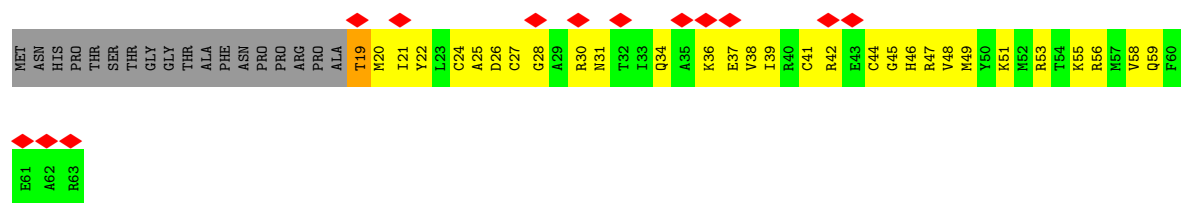
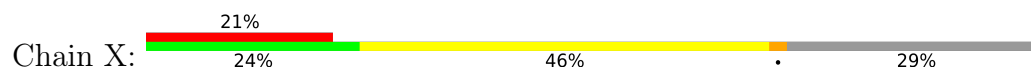




- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 12: DNA-directed RNA polymerases I, II, and III subunit RPABC4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17102	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	86.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.099	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.033	Depositor
Map size ($\text{\AA}$)	382.86002, 382.86002, 382.86002	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0635, 1.0635, 1.0635	Depositor

5 Model quality

5.1 Standard geometry

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	0.31	0/11194	0.53	0/15122
1	M	0.31	0/11194	0.53	0/15122
2	B	0.34	0/9332	0.54	0/12615
2	N	0.34	0/9332	0.54	0/12615
3	C	0.31	0/2588	0.49	0/3505
3	O	0.31	0/2588	0.49	0/3505
4	D	0.25	0/323	0.49	0/427
4	P	0.25	0/323	0.49	0/427
5	E	0.28	0/1695	0.57	3/2287 (0.1%)
5	Q	0.28	0/1695	0.57	3/2287 (0.1%)
6	F	0.41	0/660	0.52	0/893
6	R	0.41	0/660	0.52	0/893
7	G	0.31	0/1295	0.53	0/1755
7	S	0.31	0/1295	0.53	0/1755
8	H	0.29	0/1004	0.59	0/1355
8	T	0.29	0/1004	0.60	0/1355
9	I	0.25	0/439	0.51	0/596
9	U	0.25	0/439	0.51	0/596
10	J	0.37	0/558	0.64	0/751
10	V	0.37	0/558	0.64	0/751
11	K	0.33	0/759	0.48	0/1030
11	W	0.33	0/759	0.48	0/1030
12	L	0.35	0/371	0.56	0/491
12	X	0.35	0/371	0.56	0/491
All	All	0.32	0/60436	0.53	6/81654 (0.0%)

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	4
1	M	0	4
2	B	0	1
2	N	0	1
5	E	0	4
5	Q	0	4
7	G	0	1
7	S	0	1
All	All	0	20

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Q	49	GLY	CA-C-N	5.63	131.83	121.70
5	Q	49	GLY	C-N-CA	5.63	131.83	121.70
5	E	49	GLY	CA-C-N	5.62	131.82	121.70
5	E	49	GLY	C-N-CA	5.62	131.82	121.70
5	E	91	VAL	N-CA-C	-5.16	107.54	111.62
5	Q	91	VAL	N-CA-C	-5.15	107.55	111.62

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1656	ASP	Peptide
1	A	246	ILE	Peptide
1	A	84	ILE	Peptide
1	A	896	TYR	Peptide
2	B	90	SER	Peptide
5	E	128	GLU	Peptide
5	E	23	HIS	Peptide
5	E	50	ARG	Peptide
5	E	68	ASN	Peptide
7	G	60	SER	Peptide
1	M	1656	ASP	Peptide
1	M	246	ILE	Peptide
1	M	84	ILE	Peptide
1	M	896	TYR	Peptide
2	N	90	SER	Peptide
5	Q	128	GLU	Peptide
5	Q	23	HIS	Peptide

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Mol	Chain	Res	Type	Group
5	Q	50	ARG	Peptide
5	Q	68	ASN	Peptide
7	S	60	SER	Peptide

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	10976	0	10980	648	0
1	M	10976	0	10980	660	0
2	B	9127	0	9092	522	0
2	N	9127	0	9092	571	0
3	C	2533	0	2540	155	0
3	O	2533	0	2540	174	0
4	D	322	0	338	21	0
4	P	322	0	338	19	0
5	E	1663	0	1684	79	0
5	Q	1663	0	1684	86	0
6	F	650	0	674	36	0
6	R	650	0	674	38	0
7	G	1267	0	1278	93	0
7	S	1267	0	1278	99	0
8	H	990	0	1001	67	0
8	T	990	0	1001	65	0
9	I	431	0	410	17	0
9	U	431	0	410	21	0
10	J	550	0	564	38	0
10	V	550	0	564	42	0
11	K	745	0	745	42	0
11	W	745	0	745	53	0
12	L	368	0	377	27	0
12	X	368	0	377	52	0
13	A	2	0	0	0	0
13	B	1	0	0	0	0
13	I	1	0	0	0	0
13	J	1	0	0	0	0
13	L	1	0	0	0	0
13	M	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	N	1	0	0	0	0
13	U	1	0	0	0	0
13	V	1	0	0	0	0
13	X	1	0	0	0	0
All	All	59256	0	59366	3265	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 28.

All (3265) 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)
2:N:696:GLN:HG2	2:N:698:PRO:HD2	1.45	0.98
2:B:696:GLN:HG2	2:B:698:PRO:HD2	1.45	0.96
1:A:735:GLN:HE22	8:H:77:TYR:HB2	1.30	0.95
1:A:1279:VAL:O	9:I:48:SER:OG	1.86	0.94
8:H:17:ASP:HA	8:H:18:LYS:HB2	1.51	0.92
1:M:774:TYR:O	8:T:20:LYS:NZ	2.02	0.92
2:B:1089:CYS:HB3	2:B:1092:CYS:SG	2.11	0.91
1:M:103:CYS:SG	1:M:106:CYS:HB3	2.11	0.90
1:A:103:CYS:SG	1:A:106:CYS:HB3	2.11	0.90
2:N:1089:CYS:HB3	2:N:1092:CYS:SG	2.11	0.90
8:T:17:ASP:HA	8:T:18:LYS:HB2	1.51	0.89
1:A:598:ARG:N	1:A:601:ASP:OD2	2.06	0.89
1:M:598:ARG:N	1:M:601:ASP:OD2	2.06	0.88
10:J:5:ILE:HG22	10:J:15:GLY:HA3	1.56	0.88
1:A:1306:ARG:HH21	1:A:1317:GLN:HG2	1.39	0.87
11:K:40:GLN:HG3	11:K:41:LYS:HG2	1.57	0.87
2:N:136:GLU:O	2:N:431:ASN:ND2	2.08	0.86
7:G:93:ILE:HD11	7:G:145:GLU:HA	1.57	0.86
1:M:1306:ARG:HH21	1:M:1317:GLN:HG2	1.40	0.86
2:N:967:THR:HB	2:N:970:ILE:HD11	1.58	0.86
2:B:136:GLU:O	2:B:431:ASN:ND2	2.08	0.85
10:V:5:ILE:HG22	10:V:15:GLY:HA3	1.56	0.85
1:A:1553:TRP:HB3	5:E:136:ILE:HD11	1.57	0.85
10:J:23:THR:OG1	10:J:27:GLU:OE1	1.95	0.85
2:B:967:THR:HB	2:B:970:ILE:HD11	1.58	0.85
1:A:1567:ASN:HB2	1:A:1569:ILE:HG23	1.57	0.85
7:S:93:ILE:HD11	7:S:145:GLU:HA	1.57	0.85
11:W:40:GLN:HG3	11:W:41:LYS:HG2	1.57	0.85
2:N:480:HIS:HD2	2:N:518:LEU:HB3	1.42	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:1567:ASN:HB2	1:M:1569:ILE:HG23	1.57	0.84
12:X:45:GLY:O	12:X:47:ARG:NH1	2.10	0.84
10:V:23:THR:OG1	10:V:27:GLU:OE1	1.95	0.83
3:O:93:ASN:HB2	12:X:55:LYS:HG2	1.60	0.83
1:A:1003:ILE:HD11	1:A:1008:TYR:HD2	1.42	0.83
1:M:1003:ILE:HD11	1:M:1008:TYR:HD2	1.42	0.83
2:B:480:HIS:HD2	2:B:518:LEU:HB3	1.42	0.83
2:B:1089:CYS:CB	2:B:1092:CYS:SG	2.67	0.83
2:N:1089:CYS:CB	2:N:1092:CYS:SG	2.67	0.83
12:L:45:GLY:O	12:L:47:ARG:NH1	2.10	0.82
2:B:630:ASN:O	2:B:633:ARG:NH1	2.13	0.82
2:N:630:ASN:O	2:N:633:ARG:NH1	2.13	0.82
12:L:27:CYS:HB3	12:L:44:CYS:SG	2.20	0.82
12:X:27:CYS:HB3	12:X:44:CYS:SG	2.20	0.82
1:A:88:HIS:N	1:A:360:PHE:O	2.13	0.81
1:M:956:ILE:HA	1:M:999:PHE:HB2	1.62	0.81
1:M:1062:HIS:HB3	1:M:1066:ASP:HB3	1.62	0.81
2:B:927:GLY:O	2:B:929:GLN:NE2	2.13	0.81
1:A:956:ILE:HA	1:A:999:PHE:HB2	1.62	0.81
2:B:944:THR:HG22	2:B:947:MET:HB2	1.62	0.81
2:N:927:GLY:O	2:N:929:GLN:NE2	2.13	0.81
1:A:1062:HIS:HB3	1:A:1066:ASP:HB3	1.63	0.80
1:M:390:LEU:HD23	1:M:444:LEU:HA	1.62	0.80
1:A:390:LEU:HD23	1:A:444:LEU:HA	1.62	0.80
2:N:730:GLN:O	10:V:1:MET:N	2.15	0.79
3:O:91:ILE:HD11	12:X:58:VAL:HB	1.63	0.79
1:M:88:HIS:N	1:M:360:PHE:O	2.13	0.79
2:N:944:THR:HG22	2:N:947:MET:HB2	1.62	0.79
2:N:999:TYR:HA	2:N:1006:GLU:HA	1.65	0.79
1:M:735:GLN:HE22	8:T:77:TYR:HB2	1.48	0.79
5:Q:7:ASN:HD21	5:Q:54:ARG:HH22	1.31	0.79
7:G:96:VAL:HG12	7:G:124:PHE:HE1	1.48	0.79
1:M:717:LYS:NZ	11:W:67:ILE:O	2.13	0.79
7:S:59:LYS:HZ1	7:S:73:TRP:HB2	1.48	0.78
2:B:93:GLU:OE2	7:S:100:HIS:N	2.16	0.78
4:D:12:ARG:HA	7:G:11:VAL:HG23	1.66	0.78
1:A:1246:THR:H	1:A:1566:THR:HB	1.48	0.78
2:N:456:GLN:O	2:N:460:TYR:OH	2.01	0.78
1:A:565:LEU:HA	1:A:568:GLN:HE21	1.48	0.78
1:A:814:GLU:OE1	1:A:1072:LYS:NZ	2.16	0.78
2:B:999:TYR:HA	2:B:1006:GLU:HA	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:814:GLU:OE1	1:M:1072:LYS:NZ	2.16	0.78
1:A:814:GLU:O	1:A:1092:LYS:NZ	2.16	0.78
1:A:858:ARG:NH1	1:A:958:CYS:O	2.16	0.78
2:B:456:GLN:O	2:B:460:TYR:OH	2.01	0.78
1:M:1171:ASN:HB2	1:M:1174:LYS:HB2	1.66	0.78
1:M:1068:LEU:HD13	1:M:1188:VAL:HA	1.65	0.77
1:M:106:CYS:HA	1:M:231:CYS:HB2	1.66	0.77
1:M:565:LEU:HA	1:M:568:GLN:HE21	1.48	0.77
1:M:1060:GLN:NE2	1:M:1610:ASP:OD2	2.16	0.77
2:N:219:ARG:NH1	2:N:223:SER:O	2.17	0.77
2:B:219:ARG:NH1	2:B:223:SER:O	2.17	0.77
1:A:604:ILE:HB	1:A:652:HIS:HB2	1.67	0.77
7:S:96:VAL:HG12	7:S:124:PHE:HE1	1.48	0.77
12:X:19:THR:HB	12:X:34:GLN:HG2	1.66	0.77
1:A:1171:ASN:HB2	1:A:1174:LYS:HB2	1.66	0.77
1:A:1307:ASP:OD1	1:A:1307:ASP:N	2.14	0.77
1:M:1246:THR:H	1:M:1566:THR:HB	1.48	0.77
1:M:1307:ASP:N	1:M:1307:ASP:OD1	2.14	0.77
1:A:1068:LEU:HD13	1:A:1188:VAL:HA	1.65	0.77
5:E:7:ASN:HD21	5:E:54:ARG:HH22	1.31	0.77
1:M:814:GLU:O	1:M:1092:LYS:NZ	2.16	0.76
1:M:858:ARG:NH1	1:M:958:CYS:O	2.16	0.76
2:N:235:GLY:HA2	2:N:284:ARG:HH11	1.50	0.76
12:L:19:THR:HB	12:L:34:GLN:HG2	1.66	0.76
2:N:928:MET:HE3	10:V:42:ARG:HD3	1.67	0.76
1:A:559:ILE:HG12	3:O:130:GLU:HB2	1.68	0.76
1:A:1060:GLN:NE2	1:A:1610:ASP:OD2	2.16	0.76
2:B:235:GLY:HA2	2:B:284:ARG:HH11	1.50	0.76
3:C:75:ARG:HH12	11:K:44:HIS:HB2	1.51	0.76
2:N:1090:ARG:NH2	2:N:1147:THR:OG1	2.18	0.76
3:O:94:ASN:ND2	3:O:100:ASP:OD1	2.19	0.76
7:S:49:LEU:HB2	7:S:79:LEU:HB3	1.68	0.76
2:B:123:TRP:HE1	2:B:422:LEU:HG	1.51	0.76
2:B:849:ASP:OD2	2:B:852:THR:N	2.19	0.76
7:G:59:LYS:HZ1	7:G:73:TRP:HB2	1.50	0.76
1:M:1156:LEU:HD21	1:M:1172:GLU:HA	1.68	0.76
2:N:292:TYR:OH	2:N:297:LEU:O	2.03	0.76
1:A:895:VAL:HG13	1:A:901:LYS:HB3	1.69	0.75
1:M:604:ILE:HB	1:M:652:HIS:HB2	1.67	0.75
12:X:27:CYS:CB	12:X:44:CYS:SG	2.68	0.75
2:B:140:ILE:HG22	2:B:434:GLY:HA2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:292:TYR:OH	2:B:297:LEU:O	2.03	0.75
3:O:155:THR:OG1	3:O:156:ASP:N	2.19	0.75
8:H:63:LEU:HG	8:H:68:LEU:HD12	1.67	0.75
1:M:1103:ASP:O	1:M:1134:LEU:N	2.18	0.75
8:T:63:LEU:HG	8:T:68:LEU:HD12	1.67	0.75
1:A:1114:ALA:HA	1:A:1121:TYR:HB3	1.68	0.75
2:N:880:ASP:HA	12:X:38:VAL:HG22	1.69	0.75
1:A:1156:LEU:HD21	1:A:1172:GLU:HA	1.68	0.75
2:N:123:TRP:HE1	2:N:422:LEU:HG	1.51	0.75
12:L:31:ASN:HD21	12:L:42:ARG:H	1.35	0.75
1:M:1114:ALA:HA	1:M:1121:TYR:HB3	1.68	0.75
1:M:1234:ILE:HG23	1:M:1235:ILE:HG12	1.67	0.75
2:N:849:ASP:OD2	2:N:852:THR:N	2.19	0.75
3:O:48:VAL:HG11	11:W:109:PHE:HD1	1.50	0.75
3:C:94:ASN:ND2	3:C:100:ASP:OD1	2.19	0.75
1:M:1479:HIS:HB2	1:M:1493:GLU:HB3	1.67	0.75
3:C:339:LYS:HZ1	11:K:92:ARG:HA	1.52	0.74
1:M:893:GLU:OE2	2:N:617:SER:OG	2.04	0.74
2:N:143:MET:HE3	2:N:171:GLY:HA2	1.69	0.74
7:G:49:LEU:HB2	7:G:79:LEU:HB3	1.68	0.74
2:N:54:GLU:OE1	2:N:78:ARG:NH2	2.20	0.74
1:A:476:ARG:HG3	2:B:1058:GLU:HG3	1.70	0.74
1:A:1234:ILE:HG23	1:A:1235:ILE:HG12	1.67	0.74
6:F:69:ARG:NH2	6:F:140:GLU:OE2	2.21	0.74
2:N:140:ILE:HG22	2:N:434:GLY:HA2	1.68	0.74
2:N:7:GLU:O	2:N:11:THR:OG1	2.04	0.74
2:N:191:ASN:HD21	2:N:218:VAL:HG12	1.52	0.74
1:A:763:ASN:HA	1:A:787:ASP:HA	1.69	0.74
1:A:1479:HIS:HB2	1:A:1493:GLU:HB3	1.67	0.74
1:M:1281:VAL:O	9:U:46:THR:OG1	2.04	0.74
7:S:118:ILE:HG12	7:S:170:LEU:HD12	1.68	0.74
2:B:54:GLU:OE1	2:B:78:ARG:NH2	2.21	0.74
7:G:128:ASP:O	2:N:116:ARG:NH2	2.17	0.74
7:G:118:ILE:HG12	7:G:170:LEU:HD12	1.68	0.74
1:M:661:SER:HB3	6:R:108:LEU:HD11	1.69	0.74
1:M:763:ASN:HA	1:M:787:ASP:HA	1.69	0.74
3:O:75:ARG:HG2	11:W:45:THR:HB	1.70	0.74
2:B:143:MET:HE3	2:B:171:GLY:HA2	1.69	0.74
2:B:1090:ARG:NH2	2:B:1147:THR:OG1	2.18	0.74
3:C:71:ASN:OD1	3:C:75:ARG:NH2	2.21	0.74
1:A:1065:GLU:HB3	5:E:200:SER:HB2	1.68	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:25:ALA:HB3	12:L:46:HIS:CE1	2.23	0.73
3:O:71:ASN:OD1	3:O:75:ARG:NH2	2.21	0.73
6:R:69:ARG:NH2	6:R:140:GLU:OE2	2.21	0.73
12:X:31:ASN:HD21	12:X:42:ARG:H	1.35	0.73
1:M:895:VAL:HG13	1:M:901:LYS:HB3	1.68	0.73
1:A:1569:ILE:HA	1:A:1572:ILE:HG22	1.71	0.73
1:M:498:ILE:HG13	1:M:499:GLU:H	1.52	0.73
2:B:243:TRP:CD1	2:B:244:ARG:HG2	2.24	0.73
12:L:27:CYS:CB	12:L:44:CYS:SG	2.68	0.73
12:X:25:ALA:HB3	12:X:46:HIS:CE1	2.23	0.73
2:N:54:GLU:HB3	2:N:78:ARG:HB3	1.71	0.73
1:A:705:ARG:HH12	11:K:60:VAL:HG13	1.53	0.73
1:M:1569:ILE:HA	1:M:1572:ILE:HG22	1.71	0.73
1:A:34:ASN:HB2	1:A:36:VAL:HG12	1.71	0.73
2:B:191:ASN:HD21	2:B:218:VAL:HG12	1.52	0.73
2:B:227:ASN:ND2	2:B:335:VAL:O	2.21	0.73
2:B:870:GLU:OE2	2:B:872:ARG:NH2	2.22	0.73
2:N:227:ASN:ND2	2:N:335:VAL:O	2.21	0.73
6:R:89:LEU:HG	7:S:68:PRO:HB3	1.71	0.73
1:A:498:ILE:HG13	1:A:499:GLU:H	1.52	0.72
12:X:21:ILE:HD11	12:X:30:ARG:HB3	1.71	0.72
1:A:106:CYS:HA	1:A:231:CYS:HB2	1.66	0.72
2:N:919:VAL:HB	3:O:78:ILE:HD13	1.71	0.72
2:B:494:ARG:NH2	2:B:513:SER:O	2.22	0.72
5:E:46:CYS:SG	5:E:47:GLY:N	2.61	0.72
1:M:1205:PRO:HB2	1:M:1593:PHE:HE1	1.53	0.72
2:N:834:ILE:HD11	12:X:51:LYS:HD2	1.71	0.72
1:A:1230:ARG:NH1	1:A:1567:ASN:OD1	2.19	0.72
12:L:21:ILE:HD11	12:L:30:ARG:HB3	1.71	0.72
7:S:40:LYS:HG2	7:S:47:ILE:HG12	1.71	0.72
1:M:842:THR:HG21	2:N:1011:ILE:HA	1.71	0.72
1:A:106:CYS:SG	1:A:231:CYS:HB2	2.27	0.72
2:N:494:ARG:NH2	2:N:513:SER:O	2.22	0.72
3:C:130:GLU:HB2	1:M:559:ILE:HG12	1.70	0.72
5:Q:46:CYS:SG	5:Q:47:GLY:N	2.61	0.72
1:A:1103:ASP:O	1:A:1134:LEU:N	2.18	0.72
2:B:781:ARG:NH1	10:J:8:PHE:O	2.22	0.72
4:D:17:LEU:HD21	7:G:7:TYR:HA	1.72	0.72
5:E:65:ASN:OD1	5:E:67:SER:OG	2.08	0.72
1:A:1205:PRO:HB2	1:A:1593:PHE:HE1	1.53	0.71
2:N:243:TRP:CD1	2:N:244:ARG:HG2	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:870:GLU:OE2	2:N:872:ARG:NH2	2.22	0.71
1:A:710:GLN:NE2	11:K:65:TYR:O	2.23	0.71
2:B:54:GLU:HB3	2:B:78:ARG:HB3	1.71	0.71
4:D:20:ASP:OD1	4:D:21:ALA:N	2.24	0.71
7:G:40:LYS:HG2	7:G:47:ILE:HG12	1.71	0.71
2:N:237:THR:O	2:N:252:SER:OG	2.08	0.71
2:N:659:ILE:HG12	2:N:673:HIS:HB2	1.72	0.71
2:B:237:THR:O	2:B:252:SER:OG	2.08	0.71
1:A:786:PHE:HA	1:A:792:LEU:HG	1.71	0.71
2:B:659:ILE:HG12	2:B:673:HIS:HB2	1.72	0.71
1:M:476:ARG:HG3	2:N:1058:GLU:HG3	1.71	0.71
5:Q:65:ASN:OD1	5:Q:67:SER:OG	2.08	0.71
2:B:105:GLU:OE2	2:B:109:ARG:NH2	2.23	0.71
2:N:687:ASN:HD21	2:N:741:LEU:HD12	1.56	0.71
1:M:1504:LEU:HD21	2:N:284:ARG:CZ	2.20	0.71
2:N:440:PHE:O	2:N:444:GLY:N	2.24	0.71
1:M:34:ASN:HB2	1:M:36:VAL:HG12	1.71	0.71
2:B:546:VAL:HG12	2:B:571:CYS:HB3	1.72	0.71
2:B:1101:THR:O	2:B:1111:SER:OG	2.08	0.71
1:M:1657:LEU:HD12	1:M:1663:ARG:HA	1.72	0.71
1:M:604:ILE:HD11	2:N:1072:LEU:HD11	1.73	0.70
1:A:121:CYS:HB3	1:A:186:VAL:HG21	1.73	0.70
2:B:7:GLU:O	2:B:11:THR:OG1	2.04	0.70
2:B:955:LYS:HE3	2:B:985:LEU:HD21	1.72	0.70
2:N:733:GLN:HE21	2:N:755:ASN:H	1.39	0.70
4:P:20:ASP:OD1	4:P:21:ALA:N	2.24	0.70
1:M:1089:LEU:HD23	1:M:1178:LEU:HD11	1.73	0.70
2:N:778:ALA:HB1	10:V:8:PHE:HB3	1.73	0.70
1:A:484:VAL:HG12	2:B:1081:SER:HB2	1.74	0.70
1:A:1657:LEU:HD12	1:A:1663:ARG:HA	1.72	0.70
1:M:248:GLU:HG2	1:M:249:ILE:H	1.57	0.70
2:B:1100:SER:HA	2:B:1113:VAL:HA	1.74	0.70
2:N:179:GLU:HB2	2:N:464:ALA:HB3	1.74	0.70
2:N:190:ARG:HD2	2:N:630:ASN:HD22	1.56	0.70
1:A:99:LEU:O	1:A:102:THR:OG1	2.08	0.70
2:N:955:LYS:HE3	2:N:985:LEU:HD21	1.72	0.70
1:A:1235:ILE:HG23	1:A:1612:MET:HE1	1.74	0.70
2:B:179:GLU:HB2	2:B:464:ALA:HB3	1.74	0.70
5:Q:61:ALA:O	5:Q:71:THR:OG1	2.10	0.70
8:T:40:LEU:HB3	8:T:102:MET:HG2	1.74	0.70
2:B:687:ASN:HD21	2:B:741:LEU:HD12	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:1602:PRO:HA	1:M:1605:LEU:HD13	1.73	0.70
2:N:1100:SER:HA	2:N:1113:VAL:HA	1.74	0.70
1:A:1602:PRO:HA	1:A:1605:LEU:HD13	1.73	0.70
2:B:733:GLN:HE21	2:B:755:ASN:H	1.39	0.70
1:M:121:CYS:HB3	1:M:186:VAL:HG21	1.73	0.70
1:M:786:PHE:HA	1:M:792:LEU:HG	1.72	0.70
2:N:546:VAL:HG12	2:N:571:CYS:HB3	1.72	0.70
1:A:604:ILE:HD11	2:B:1072:LEU:HD11	1.72	0.70
1:A:718:PRO:O	1:A:722:GLY:N	2.22	0.70
1:A:1151:LYS:HG3	1:A:1152:ASN:H	1.57	0.70
3:C:339:LYS:NZ	11:K:92:ARG:HA	2.07	0.70
1:A:248:GLU:HG2	1:A:249:ILE:H	1.57	0.69
2:B:501:TRP:NE1	2:B:675:GLU:OE2	2.25	0.69
1:M:445:ILE:HG12	2:N:1165:MET:HE1	1.73	0.69
1:M:1116:LYS:HG2	1:M:1118:PRO:HD2	1.74	0.69
1:A:1001:THR:HG21	2:B:973:GLU:HA	1.72	0.69
2:B:190:ARG:HD2	2:B:630:ASN:HD22	1.55	0.69
1:M:484:VAL:HG12	2:N:1081:SER:HB2	1.74	0.69
1:M:705:ARG:HH12	11:W:60:VAL:HG13	1.56	0.69
2:N:1101:THR:O	2:N:1111:SER:OG	2.08	0.69
1:A:503:ILE:HD12	1:A:605:LEU:HD11	1.74	0.69
1:A:1089:LEU:HD23	1:A:1178:LEU:HD11	1.73	0.69
1:M:503:ILE:HD12	1:M:605:LEU:HD11	1.75	0.69
1:A:1116:LYS:HG2	1:A:1118:PRO:HD2	1.74	0.69
8:H:40:LEU:HB3	8:H:102:MET:HG2	1.74	0.69
1:A:909:MET:SD	1:A:969:ARG:NH1	2.66	0.69
1:A:1103:ASP:HB3	1:A:1133:TYR:HD2	1.58	0.69
11:K:32:LEU:O	11:K:86:THR:OG1	2.10	0.69
1:M:28:SER:O	2:N:1116:ARG:NH2	2.25	0.69
1:A:1251:LEU:HB2	1:A:1540:PRO:HB2	1.75	0.69
8:H:90:LYS:HE3	8:H:105:GLU:HG2	1.75	0.69
1:M:909:MET:SD	1:M:969:ARG:NH1	2.66	0.69
1:M:678:SER:HA	1:M:1070:VAL:HG11	1.74	0.69
2:N:105:GLU:OE2	2:N:109:ARG:NH2	2.23	0.69
2:N:232:LEU:HD12	2:N:235:GLY:H	1.58	0.69
2:N:501:TRP:NE1	2:N:675:GLU:OE2	2.25	0.69
3:O:262:VAL:HG13	3:O:263:ILE:HG12	1.75	0.69
1:A:88:HIS:HD2	1:A:362:LEU:HD21	1.57	0.69
1:M:1235:ILE:HG23	1:M:1612:MET:HE1	1.74	0.69
7:S:135:ARG:NE	7:S:145:GLU:HB2	2.08	0.69
8:T:90:LYS:HE3	8:T:105:GLU:HG2	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:678:SER:HA	1:A:1070:VAL:HG11	1.74	0.68
1:A:793:CYS:SG	1:A:794:GLY:N	2.66	0.68
3:C:262:VAL:HG13	3:C:263:ILE:HG12	1.75	0.68
1:M:1661:SER:OG	2:N:1061:ARG:NH1	2.26	0.68
1:A:1242:ILE:HG21	1:A:1567:ASN:HD21	1.58	0.68
5:E:61:ALA:O	5:E:71:THR:OG1	2.10	0.68
7:G:135:ARG:NE	7:G:145:GLU:HB2	2.08	0.68
1:M:106:CYS:SG	1:M:231:CYS:HB2	2.27	0.68
1:M:710:GLN:NE2	11:W:65:TYR:O	2.26	0.68
1:M:1242:ILE:HG21	1:M:1567:ASN:HD21	1.58	0.68
2:N:59:ASP:OD2	2:N:73:ASN:ND2	2.24	0.68
2:N:829:ASP:HB2	12:X:20:MET:HE3	1.73	0.68
1:A:180:ARG:NH1	1:A:183:ASP:OD2	2.27	0.68
1:A:604:ILE:N	1:A:652:HIS:O	2.26	0.68
2:B:108:GLU:HA	2:B:722:THR:HG21	1.74	0.68
2:B:232:LEU:HD12	2:B:235:GLY:H	1.58	0.68
2:B:440:PHE:O	2:B:444:GLY:N	2.24	0.68
1:M:604:ILE:N	1:M:652:HIS:O	2.26	0.68
1:M:793:CYS:SG	1:M:794:GLY:N	2.67	0.68
1:M:1151:LYS:HG3	1:M:1152:ASN:H	1.57	0.68
11:W:32:LEU:O	11:W:86:THR:OG1	2.10	0.68
1:A:330:ASN:HA	1:A:333:ARG:HD3	1.76	0.68
1:A:1192:GLU:HG2	1:A:1194:VAL:HG22	1.75	0.68
1:M:99:LEU:O	1:M:102:THR:OG1	2.08	0.68
1:M:330:ASN:HA	1:M:333:ARG:HD3	1.76	0.68
7:S:118:ILE:HA	7:S:170:LEU:HB2	1.75	0.68
7:S:99:SER:HA	7:S:115:ARG:NH1	2.09	0.68
1:M:88:HIS:HD2	1:M:362:LEU:HD21	1.57	0.68
1:A:653:PHE:O	2:B:1076:ARG:NH2	2.27	0.68
2:B:1113:VAL:O	2:B:1114:ARG:NH1	2.27	0.68
7:G:124:PHE:HB2	7:G:136:TRP:CE3	2.29	0.68
2:B:61:ILE:O	2:B:69:LEU:HB2	1.95	0.67
2:B:790:LYS:NZ	2:B:792:GLU:OE2	2.27	0.67
3:C:90:TYR:HE1	1:M:560:GLU:HG2	1.60	0.67
1:M:1103:ASP:HB3	1:M:1133:TYR:HD2	1.58	0.67
7:S:124:PHE:HB2	7:S:136:TRP:CE3	2.29	0.67
2:B:59:ASP:OD2	2:B:73:ASN:ND2	2.24	0.67
3:C:317:ILE:HB	3:C:318:MET:HE2	1.77	0.67
1:M:1324:PHE:O	1:M:1328:PHE:HB3	1.95	0.67
2:N:61:ILE:O	2:N:69:LEU:HB2	1.95	0.67
2:N:955:LYS:NZ	2:N:994:GLY:O	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:781:GLU:O	1:A:783:SER:N	2.28	0.67
3:C:223:HIS:CG	3:C:225:LYS:HE3	2.30	0.67
1:M:718:PRO:O	1:M:722:GLY:N	2.22	0.67
1:M:1279:VAL:O	9:U:48:SER:OG	2.11	0.67
2:N:108:GLU:HA	2:N:722:THR:HG21	1.74	0.67
3:O:223:HIS:CG	3:O:225:LYS:HE3	2.30	0.67
1:A:113:LYS:HG3	1:A:179:MET:HE1	1.76	0.67
3:C:171:SER:N	3:C:198:ILE:O	2.28	0.67
1:M:180:ARG:NH1	1:M:183:ASP:OD2	2.27	0.67
2:N:1090:ARG:HH21	2:N:1147:THR:HG1	1.43	0.67
3:O:94:ASN:O	12:X:53:ARG:NH1	2.25	0.67
3:C:237:LEU:HD12	3:C:238:PRO:HD2	1.76	0.67
7:G:118:ILE:HA	7:G:170:LEU:HB2	1.76	0.67
1:M:113:LYS:HG3	1:M:179:MET:HE1	1.76	0.67
1:A:1504:LEU:HD21	2:B:284:ARG:CZ	2.24	0.67
1:M:1251:LEU:HB2	1:M:1540:PRO:HB2	1.75	0.67
8:H:74:TYR:N	8:H:123:LEU:O	2.28	0.67
11:K:25:LEU:HD11	11:K:38:GLN:HB2	1.76	0.67
1:M:1192:GLU:HG2	1:M:1194:VAL:HG22	1.75	0.67
1:M:998:ARG:HE	1:M:1000:LEU:HD23	1.60	0.67
2:N:144:VAL:HB	2:N:170:GLY:HA2	1.77	0.67
1:A:1522:PRO:HD2	1:A:1550:LYS:HZ1	1.60	0.66
6:F:96:PRO:HB2	7:G:23:ARG:HH11	1.59	0.66
8:H:42:ILE:HD13	8:H:49:LEU:HD12	1.77	0.66
3:O:237:LEU:HD12	3:O:238:PRO:HD2	1.76	0.66
2:B:144:VAL:HB	2:B:170:GLY:HA2	1.77	0.66
7:G:99:SER:HA	7:G:115:ARG:NH1	2.09	0.66
1:M:1230:ARG:NH1	1:M:1567:ASN:OD1	2.19	0.66
11:W:25:LEU:HD11	11:W:38:GLN:HB2	1.76	0.66
1:A:998:ARG:HE	1:A:1000:LEU:HD23	1.60	0.66
2:B:955:LYS:NZ	2:B:994:GLY:O	2.28	0.66
2:N:185:LEU:HB2	2:N:378:LEU:HD21	1.78	0.66
2:N:253:MET:HE3	2:N:257:LYS:HG3	1.78	0.66
2:N:1113:VAL:O	2:N:1114:ARG:NH1	2.27	0.66
3:O:204:ARG:N	3:O:207:GLN:HE21	1.93	0.66
1:A:212:LYS:HD3	1:A:1628:TYR:HE1	1.61	0.66
2:N:790:LYS:NZ	2:N:792:GLU:OE2	2.27	0.66
8:T:42:ILE:HD13	8:T:49:LEU:HD12	1.77	0.66
1:A:247:PHE:O	1:A:321:LYS:N	2.29	0.66
1:M:1660:PRO:HA	1:M:1663:ARG:HB2	1.76	0.66
2:N:480:HIS:CD2	2:N:518:LEU:HB3	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:92:ILE:HG12	3:O:211:LEU:HA	1.78	0.66
1:M:212:LYS:HD3	1:M:1628:TYR:HE1	1.61	0.66
1:M:1038:LYS:HG2	1:M:1638:PHE:CD2	2.30	0.66
2:N:99:ARG:HH22	12:X:46:HIS:HA	1.61	0.66
2:N:672:THR:HG23	2:N:673:HIS:HD1	1.61	0.66
2:B:781:ARG:HD3	10:J:8:PHE:HA	1.76	0.66
3:C:339:LYS:HZ2	11:K:92:ARG:HG3	1.61	0.66
10:J:40:LEU:O	10:J:46:ARG:NH1	2.26	0.66
1:M:131:LEU:HD21	1:M:207:LEU:HG	1.78	0.66
3:O:317:ILE:HB	3:O:318:MET:HE2	1.77	0.66
1:A:634:TYR:CE2	2:B:768:MET:HE2	2.31	0.66
3:C:92:ILE:HG12	3:C:211:LEU:HA	1.78	0.66
5:E:49:GLY:HA2	5:E:50:ARG:HB2	1.78	0.66
1:M:781:GLU:O	1:M:783:SER:N	2.28	0.66
1:A:786:PHE:HB2	1:A:790:GLU:O	1.96	0.65
1:M:247:PHE:O	1:M:321:LYS:N	2.29	0.65
2:N:561:VAL:HG13	2:N:568:VAL:HG23	1.78	0.65
2:N:208:TYR:HA	2:N:232:LEU:HA	1.78	0.65
5:Q:49:GLY:HA2	5:Q:50:ARG:HB2	1.78	0.65
8:T:74:TYR:N	8:T:123:LEU:O	2.28	0.65
10:V:19:ASP:O	10:V:23:THR:HG22	1.96	0.65
1:A:1324:PHE:O	1:A:1328:PHE:HB3	1.95	0.65
1:A:1660:PRO:HA	1:A:1663:ARG:HB2	1.76	0.65
3:C:204:ARG:N	3:C:207:GLN:HE21	1.93	0.65
3:C:315:THR:HG21	10:J:6:ARG:NH2	2.10	0.65
8:H:79:LYS:HA	8:H:118:HIS:HA	1.78	0.65
10:J:19:ASP:O	10:J:23:THR:HG22	1.96	0.65
1:M:102:THR:HG22	1:M:335:LEU:HD22	1.79	0.65
2:B:185:LEU:HB2	2:B:378:LEU:HD21	1.78	0.65
2:B:672:THR:HG23	2:B:673:HIS:HD1	1.61	0.65
2:B:719:ARG:O	2:B:872:ARG:NH2	2.30	0.65
1:A:77:PHE:CE1	1:A:369:PRO:HD3	2.32	0.65
1:A:131:LEU:HD21	1:A:207:LEU:HG	1.78	0.65
1:A:1051:VAL:HG21	1:A:1063:TYR:HB2	1.79	0.65
2:B:253:MET:HE3	2:B:257:LYS:HG3	1.78	0.65
2:B:761:ILE:HD13	2:B:1011:ILE:HD12	1.78	0.65
1:M:77:PHE:CE1	1:M:369:PRO:HD3	2.32	0.65
3:O:240:ILE:HB	3:O:277:VAL:HG11	1.79	0.65
1:A:1228:ILE:HG13	1:A:1229:PRO:HD3	1.77	0.65
1:M:1228:ILE:HG13	1:M:1229:PRO:HD3	1.77	0.65
2:N:719:ARG:O	2:N:872:ARG:NH2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:164:GLU:N	2:B:164:GLU:OE1	2.30	0.65
2:B:208:TYR:HA	2:B:232:LEU:HA	1.78	0.65
2:N:595:ARG:NH1	2:N:645:GLU:OE2	2.29	0.65
1:A:607:ARG:HH12	1:A:609:PRO:HD2	1.62	0.65
1:A:612:HIS:CD2	1:A:614:PRO:HD2	2.32	0.65
3:C:240:ILE:HB	3:C:277:VAL:HG11	1.79	0.65
1:M:1553:TRP:HB3	5:Q:136:ILE:HD11	1.78	0.65
3:O:101:GLU:OE1	3:O:101:GLU:N	2.28	0.65
1:A:1038:LYS:HG2	1:A:1638:PHE:CD2	2.31	0.65
1:A:1661:SER:OG	2:B:1061:ARG:NH1	2.29	0.65
1:M:607:ARG:HB2	1:M:649:MET:HE2	1.78	0.65
1:A:1673:GLY:HA2	6:F:78:TYR:CD1	2.32	0.64
2:N:164:GLU:OE1	2:N:164:GLU:N	2.30	0.64
6:R:68:ASP:OD2	6:R:68:ASP:N	2.28	0.64
1:A:39:ASP:OD1	1:A:43:HIS:N	2.29	0.64
1:A:1242:ILE:HD13	1:A:1568:ASP:H	1.63	0.64
2:B:864:GLU:HG2	2:B:865:PRO:HD2	1.79	0.64
1:M:687:GLN:HB2	2:N:937:HIS:CD2	2.32	0.64
2:N:63:GLN:HB3	2:N:69:LEU:HB3	1.80	0.64
2:N:1160:ALA:O	2:N:1163:THR:OG1	2.15	0.64
4:P:47:LEU:O	4:P:51:ASN:ND2	2.31	0.64
1:A:687:GLN:HB2	2:B:937:HIS:CD2	2.33	0.64
3:C:101:GLU:OE1	3:C:101:GLU:N	2.28	0.64
1:M:786:PHE:HB2	1:M:790:GLU:O	1.96	0.64
2:N:761:ILE:HD13	2:N:1011:ILE:HD12	1.78	0.64
2:N:906:HIS:NE2	2:N:950:GLU:OE1	2.30	0.64
12:X:19:THR:OG1	12:X:20:MET:N	2.26	0.64
1:A:607:ARG:HB2	1:A:649:MET:HE2	1.79	0.64
2:B:906:HIS:NE2	2:B:950:GLU:OE1	2.30	0.64
10:J:27:GLU:O	10:J:27:GLU:HG2	1.97	0.64
1:M:717:LYS:HZ1	11:W:67:ILE:C	2.03	0.64
1:A:102:THR:HG22	1:A:335:LEU:HD22	1.79	0.64
1:A:797:ASP:N	1:A:800:SER:OG	2.30	0.64
4:D:13:LYS:HE3	7:G:10:THR:OG1	1.98	0.64
7:G:30:GLN:HA	7:G:33:MET:HB2	1.79	0.64
10:V:27:GLU:O	10:V:27:GLU:HG2	1.96	0.64
1:A:515:TYR:OH	1:A:595:ARG:NH1	2.31	0.64
1:A:1138:SER:HB3	1:A:1141:PHE:HB2	1.80	0.64
2:B:728:ARG:NH2	2:B:789:TYR:OH	2.31	0.64
7:G:115:ARG:HA	7:G:118:ILE:HD12	1.80	0.64
1:A:404:LEU:HG	1:A:430:LEU:HD23	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:561:VAL:HG13	2:B:568:VAL:HG23	1.78	0.64
2:B:905:ARG:NH2	2:B:950:GLU:OE2	2.26	0.64
2:N:205:GLY:O	2:N:208:TYR:N	2.28	0.64
7:S:30:GLN:HA	7:S:33:MET:HB2	1.79	0.64
1:A:820:ILE:HD13	1:A:823:ARG:HD3	1.80	0.64
1:A:989:ALA:HB1	1:A:994:PHE:HB3	1.80	0.64
2:B:205:GLY:O	2:B:208:TYR:N	2.28	0.64
1:M:471:LYS:HZ2	1:M:476:ARG:HH21	1.46	0.64
1:M:612:HIS:CD2	1:M:614:PRO:HD2	2.32	0.64
1:M:989:ALA:HB1	1:M:994:PHE:HB3	1.80	0.64
1:M:1636:MET:HE2	1:M:1645:LEU:HA	1.79	0.64
2:N:728:ARG:NH2	2:N:789:TYR:OH	2.31	0.64
2:B:595:ARG:NH1	2:B:645:GLU:OE2	2.30	0.64
2:B:1160:ALA:O	2:B:1163:THR:OG1	2.15	0.64
1:M:607:ARG:HH12	1:M:609:PRO:HD2	1.62	0.64
1:M:1051:VAL:HG21	1:M:1063:TYR:HB2	1.79	0.64
2:N:864:GLU:HG2	2:N:865:PRO:HD2	1.79	0.64
2:B:480:HIS:CD2	2:B:518:LEU:HB3	2.28	0.64
1:M:13:SER:OG	2:N:1172:GLU:OE2	2.14	0.64
1:A:53:ALA:O	1:A:65:THR:OG1	2.13	0.63
2:B:40:THR:OG1	2:B:148:ARG:NH1	2.31	0.63
1:M:812:VAL:HG11	1:M:824:LEU:HD13	1.79	0.63
2:N:149:CYS:SG	2:N:150:HIS:N	2.71	0.63
2:N:691:PHE:N	2:N:966:SER:OG	2.31	0.63
1:A:661:SER:HB3	6:F:108:LEU:HD11	1.80	0.63
3:C:125:PRO:HB3	3:C:132:THR:HG21	1.80	0.63
6:F:89:LEU:HG	7:G:68:PRO:HB3	1.79	0.63
6:F:125:ARG:HB3	6:F:127:TYR:HE2	1.63	0.63
2:N:905:ARG:NH2	2:N:950:GLU:OE2	2.26	0.63
6:R:125:ARG:HB3	6:R:127:TYR:HE2	1.63	0.63
2:B:63:GLN:HB3	2:B:69:LEU:HB3	1.79	0.63
2:B:149:CYS:SG	2:B:150:HIS:N	2.71	0.63
4:D:47:LEU:O	4:D:51:ASN:ND2	2.31	0.63
1:M:56:PRO:HG3	1:M:63:CYS:HB2	1.80	0.63
8:T:79:LYS:HA	8:T:118:HIS:HA	1.78	0.63
1:A:842:THR:HG21	2:B:1011:ILE:HA	1.81	0.63
2:B:636:ARG:HH22	2:B:675:GLU:CD	2.07	0.63
1:M:515:TYR:OH	1:M:595:ARG:NH1	2.31	0.63
1:M:1001:THR:HG21	2:N:973:GLU:HA	1.80	0.63
2:N:40:THR:OG1	2:N:148:ARG:NH1	2.31	0.63
2:N:636:ARG:HH22	2:N:675:GLU:CD	2.07	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:125:PRO:HB3	3:O:132:THR:HG21	1.80	0.63
1:A:1636:MET:HE2	1:A:1645:LEU:HA	1.79	0.63
3:C:65:ILE:HD11	3:C:69:ILE:HB	1.81	0.63
3:C:155:THR:OG1	3:C:156:ASP:N	2.19	0.63
1:M:1281:VAL:HG21	1:M:1505:MET:HG2	1.80	0.63
2:N:1097:SER:OG	2:N:1115:CYS:SG	2.56	0.63
5:E:177:ASP:OD1	5:E:179:VAL:N	2.31	0.63
6:F:87:ARG:NH1	6:F:90:GLN:OE1	2.32	0.63
12:L:19:THR:OG1	12:L:20:MET:N	2.26	0.63
3:O:334:LYS:HE2	11:W:46:LEU:HD12	1.81	0.63
5:Q:177:ASP:OD1	5:Q:179:VAL:N	2.31	0.63
1:A:895:VAL:HA	1:A:901:LYS:HD3	1.81	0.63
1:M:820:ILE:HD13	1:M:823:ARG:HD3	1.80	0.63
1:M:1132:ARG:NH2	6:R:70:THR:HG23	2.13	0.63
1:A:812:VAL:HG11	1:A:824:LEU:HD13	1.79	0.63
1:M:1242:ILE:HD13	1:M:1568:ASP:H	1.63	0.63
2:N:433:ILE:HG22	2:N:436:LYS:HZ3	1.63	0.63
1:A:893:GLU:OE2	2:B:617:SER:OG	2.17	0.62
2:B:718:LEU:HA	2:B:721:ARG:HG3	1.80	0.62
1:M:765:LYS:HB2	1:M:785:LEU:HD13	1.81	0.62
1:A:446:ASP:OD1	1:A:465:LYS:NZ	2.32	0.62
1:A:471:LYS:HZ2	1:A:476:ARG:HH21	1.45	0.62
1:M:1138:SER:HB3	1:M:1141:PHE:HB2	1.80	0.62
2:N:718:LEU:HA	2:N:721:ARG:HG3	1.80	0.62
1:A:1588:GLU:O	1:A:1591:SER:OG	2.16	0.62
5:E:182:TYR:HD2	5:E:183:LEU:HD22	1.64	0.62
1:M:29:VAL:HG12	1:M:30:LYS:HG2	1.81	0.62
2:N:55:LYS:NZ	2:N:397:ASN:OD1	2.31	0.62
1:A:1572:ILE:O	1:A:1576:TYR:HB2	1.99	0.62
2:B:733:GLN:NE2	2:B:754:THR:OG1	2.31	0.62
5:E:42:LYS:O	5:E:46:CYS:HB2	2.00	0.62
1:M:404:LEU:HG	1:M:430:LEU:HD23	1.80	0.62
3:O:171:SER:N	3:O:198:ILE:O	2.28	0.62
1:A:56:PRO:HG3	1:A:63:CYS:HB2	1.80	0.62
1:M:39:ASP:OD1	1:M:43:HIS:N	2.29	0.62
2:N:1112:GLU:HG2	2:N:1114:ARG:HH12	1.64	0.62
5:Q:74:ILE:HG22	5:Q:103:ILE:HD12	1.81	0.62
5:E:59:PHE:HB2	5:E:74:ILE:HD11	1.82	0.62
1:M:82:LEU:HB2	1:M:84:ILE:HD13	1.82	0.62
1:M:1563:ASP:N	1:M:1563:ASP:OD1	2.32	0.62
1:M:1635:LYS:HB3	1:M:1644:PHE:CD2	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:42:LYS:O	5:Q:46:CYS:HB2	2.00	0.62
5:E:74:ILE:HG22	5:E:103:ILE:HD12	1.81	0.62
2:N:818:PRO:HB3	2:N:820:ARG:NH1	2.15	0.62
6:R:125:ARG:HB3	6:R:127:TYR:CE2	2.35	0.62
1:A:1281:VAL:HG21	1:A:1505:MET:HG2	1.80	0.62
2:B:336:LEU:HB2	2:B:345:LYS:HD3	1.82	0.62
1:M:797:ASP:N	1:M:800:SER:OG	2.30	0.62
8:H:24:VAL:HG22	8:H:43:ASN:HA	1.82	0.62
2:N:99:ARG:HH22	12:X:47:ARG:NH1	1.97	0.62
3:O:50:ILE:HD12	11:W:113:LEU:HB3	1.82	0.62
9:U:6:SER:O	9:U:6:SER:OG	2.15	0.62
1:A:15:LYS:HB2	1:A:1654:VAL:HG22	1.81	0.62
1:A:634:TYR:CZ	2:B:768:MET:HB2	2.35	0.62
1:A:886:ALA:HA	1:A:889:ASN:HD22	1.63	0.62
2:B:54:GLU:HB3	2:B:78:ARG:HD3	1.82	0.62
2:B:1112:GLU:HG2	2:B:1114:ARG:HH12	1.64	0.62
6:F:125:ARG:HB3	6:F:127:TYR:CE2	2.35	0.62
1:M:27:ILE:O	2:N:1116:ARG:NE	2.32	0.62
1:M:717:LYS:HD3	1:M:720:GLU:HG3	1.82	0.62
1:M:895:VAL:HA	1:M:901:LYS:HD3	1.81	0.62
1:M:1065:GLU:HB3	5:Q:200:SER:HB2	1.80	0.62
2:N:244:ARG:O	2:N:246:ASN:ND2	2.33	0.62
2:N:336:LEU:HB2	2:N:345:LYS:HD3	1.82	0.62
7:G:12:ASP:OD2	7:G:75:ARG:NE	2.25	0.61
1:M:1070:VAL:HA	1:M:1073:GLN:HE21	1.65	0.61
3:O:65:ILE:HD11	3:O:69:ILE:HB	1.81	0.61
10:J:35:LEU:HA	10:J:38:LEU:HD13	1.82	0.61
1:M:886:ALA:HA	1:M:889:ASN:HD22	1.64	0.61
2:B:691:PHE:N	2:B:966:SER:OG	2.32	0.61
2:B:829:ASP:OD2	12:L:22:TYR:OH	2.18	0.61
2:N:780:GLU:OE1	3:O:224:ALA:N	2.26	0.61
7:S:115:ARG:HA	7:S:118:ILE:HD12	1.80	0.61
1:A:774:TYR:O	8:H:20:LYS:NZ	2.26	0.61
2:B:818:PRO:HB3	2:B:820:ARG:NH1	2.15	0.61
1:M:962:GLN:NE2	1:M:992:GLY:O	2.17	0.61
1:M:1572:ILE:O	1:M:1576:TYR:HB2	1.99	0.61
2:N:733:GLN:NE2	2:N:754:THR:OG1	2.31	0.61
5:Q:182:TYR:HD2	5:Q:183:LEU:HD22	1.64	0.61
1:A:29:VAL:HG12	1:A:30:LYS:HG2	1.82	0.61
2:N:715:GLY:HA2	2:N:750:TYR:HE1	1.66	0.61
2:N:891:ARG:NH1	3:O:101:GLU:OE1	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:223:HIS:HD2	3:O:225:LYS:H	1.49	0.61
12:X:26:ASP:OD1	12:X:27:CYS:N	2.32	0.61
1:A:717:LYS:HD3	1:A:720:GLU:HG3	1.82	0.61
1:A:1602:PRO:HB2	5:E:199:THR:HG21	1.82	0.61
1:M:1588:GLU:O	1:M:1591:SER:OG	2.16	0.61
3:O:88:PHE:HB3	12:X:59:GLN:NE2	2.15	0.61
10:V:40:LEU:O	10:V:46:ARG:NH1	2.26	0.61
1:A:67:HIS:ND1	2:B:1102:ILE:HD11	2.16	0.61
1:M:15:LYS:HB2	1:M:1654:VAL:HG22	1.81	0.61
1:M:1038:LYS:HZ2	1:M:1626:ILE:HA	1.65	0.61
5:Q:59:PHE:HB2	5:Q:74:ILE:HD11	1.82	0.61
1:M:1251:LEU:HD13	1:M:1558:GLU:HB3	1.83	0.61
1:A:82:LEU:HB2	1:A:84:ILE:HD13	1.82	0.61
1:A:668:ASN:N	1:A:668:ASN:OD1	2.34	0.61
1:A:1635:LYS:HB3	1:A:1644:PHE:CD2	2.35	0.61
11:K:36:THR:HG22	11:K:78:ARG:HD3	1.83	0.61
1:M:1246:THR:OG1	1:M:1566:THR:OG1	2.11	0.61
2:B:571:CYS:HB2	2:B:575:LEU:HD23	1.82	0.61
1:M:446:ASP:OD1	1:M:465:LYS:NZ	2.32	0.61
3:O:91:ILE:HG12	12:X:58:VAL:O	2.00	0.61
8:T:24:VAL:HG22	8:T:43:ASN:HA	1.81	0.61
11:W:36:THR:HG22	11:W:78:ARG:HD3	1.83	0.61
1:A:1226:LEU:HD21	1:A:1595:VAL:HG21	1.83	0.60
1:M:81:VAL:HA	1:M:364:ASN:HB3	1.83	0.60
1:A:1038:LYS:HZ2	1:A:1626:ILE:HA	1.64	0.60
2:B:715:GLY:HA2	2:B:750:TYR:HE1	1.66	0.60
2:B:995:ASN:HB3	2:B:1010:ASP:HB3	1.83	0.60
1:M:968:ARG:HG3	1:M:969:ARG:H	1.65	0.60
5:Q:84:ILE:HG23	5:Q:85:LYS:HE3	1.83	0.60
10:V:35:LEU:HA	10:V:38:LEU:HD13	1.82	0.60
1:A:52:LEU:O	1:A:64:ALA:N	2.30	0.60
1:A:411:GLU:HB3	1:A:422:ARG:NH2	2.16	0.60
1:A:765:LYS:HB2	1:A:785:LEU:HD13	1.81	0.60
1:A:916:LEU:O	1:A:919:SER:OG	2.12	0.60
1:A:968:ARG:HG3	1:A:969:ARG:H	1.65	0.60
1:A:1044:CYS:SG	1:A:1046:GLN:NE2	2.74	0.60
2:B:156:PRO:HB3	2:B:166:SER:OG	2.02	0.60
2:B:279:THR:HG23	9:I:46:THR:HG22	1.83	0.60
1:M:411:GLU:HB3	1:M:422:ARG:NH2	2.16	0.60
2:N:571:CYS:HB2	2:N:575:LEU:HD23	1.82	0.60
1:A:19:TYR:CD2	2:B:1168:LYS:HD2	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:LYS:C	1:A:472:GLU:H	2.09	0.60
1:A:612:HIS:CE1	1:A:1204:GLU:HG3	2.36	0.60
1:A:612:HIS:ND1	1:A:1204:GLU:HG3	2.17	0.60
2:B:116:ARG:HD3	7:S:131:GLU:OE1	2.00	0.60
7:G:97:SER:HB2	2:N:93:GLU:CD	2.26	0.60
1:M:612:HIS:ND1	1:M:1204:GLU:HG3	2.17	0.60
2:N:54:GLU:HB3	2:N:78:ARG:HD3	1.82	0.60
2:N:99:ARG:NH2	12:X:47:ARG:HH12	1.99	0.60
1:A:77:PHE:CE1	1:A:368:PRO:HA	2.37	0.60
1:A:560:GLU:HG2	3:O:90:TYR:HE1	1.64	0.60
1:A:1305:SER:O	1:A:1309:TYR:N	2.35	0.60
7:G:56:PHE:HB3	7:G:74:VAL:HG22	1.84	0.60
1:M:3:ILE:HG21	6:R:89:LEU:HD11	1.82	0.60
1:M:760:PRO:HD2	1:M:1088:SER:HA	1.84	0.60
1:M:1238:ALA:HB1	1:M:1618:TYR:CE2	2.36	0.60
2:N:593:LYS:HB3	2:N:598:THR:HG21	1.83	0.60
1:A:462:PRO:HA	1:A:466:GLN:OE1	2.02	0.60
1:A:1044:CYS:O	1:A:1046:GLN:NE2	2.34	0.60
2:B:587:LYS:HD2	2:B:607:LEU:HA	1.84	0.60
1:M:1045:VAL:O	1:M:1191:GLY:N	2.34	0.60
2:N:587:LYS:HD2	2:N:607:LEU:HA	1.84	0.60
2:N:822:TRP:HB3	2:N:826:LEU:HD12	1.84	0.60
1:A:613:LYS:NZ	1:A:672:GLN:OE1	2.35	0.60
1:M:470:LYS:C	1:M:472:GLU:H	2.09	0.60
1:M:660:ARG:NH1	6:R:108:LEU:HD13	2.17	0.60
1:M:1044:CYS:SG	1:M:1046:GLN:NE2	2.74	0.60
1:M:1271:VAL:HG12	1:M:1273:SER:H	1.66	0.60
1:A:512:LYS:HD3	2:B:1031:VAL:HG11	1.82	0.60
1:A:1563:ASP:OD1	1:A:1563:ASP:N	2.32	0.60
2:B:205:GLY:HA3	2:B:208:TYR:CD2	2.36	0.60
2:B:217:CYS:HB2	2:B:338:HIS:ND1	2.17	0.60
3:C:167:SER:OG	3:C:203:LEU:O	2.17	0.60
1:M:499:GLU:O	1:M:633:HIS:HB2	2.02	0.60
1:M:634:TYR:CE2	2:N:768:MET:HE2	2.36	0.60
1:A:445:ILE:HG12	2:B:1165:MET:HE1	1.83	0.60
1:A:1070:VAL:HA	1:A:1073:GLN:HE21	1.65	0.60
1:A:1238:ALA:HB1	1:A:1618:TYR:CE2	2.36	0.60
1:A:1251:LEU:HD13	1:A:1558:GLU:HB3	1.83	0.60
1:A:1582:ARG:NH1	5:E:197:SER:OG	2.34	0.60
2:B:244:ARG:O	2:B:246:ASN:ND2	2.33	0.60
2:B:1032:ARG:HE	2:B:1044:PRO:HB3	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:1032:ARG:HE	2:N:1044:PRO:HB3	1.67	0.60
1:A:1309:TYR:O	1:A:1313:TYR:HB2	2.02	0.60
2:B:593:LYS:HB3	2:B:598:THR:HG21	1.83	0.60
1:M:613:LYS:NZ	1:M:672:GLN:OE1	2.35	0.60
1:M:1226:LEU:HD21	1:M:1595:VAL:HG21	1.83	0.60
2:N:205:GLY:HA3	2:N:208:TYR:CD2	2.36	0.60
2:B:1097:SER:HB2	2:B:1117:SER:H	1.67	0.59
6:F:96:PRO:CB	7:G:23:ARG:HH11	2.15	0.59
1:M:612:HIS:CE1	1:M:1204:GLU:HG3	2.36	0.59
1:M:1044:CYS:O	1:M:1046:GLN:NE2	2.34	0.59
2:N:156:PRO:HB3	2:N:166:SER:OG	2.02	0.59
2:N:777:SER:OG	2:N:781:ARG:NH1	2.35	0.59
3:O:128:GLY:N	3:O:129:GLN:OE1	2.34	0.59
1:A:543:HIS:HB2	1:A:552:ILE:O	2.02	0.59
2:B:1097:SER:OG	2:B:1115:CYS:SG	2.56	0.59
3:C:90:TYR:HA	12:L:59:GLN:OE1	2.02	0.59
9:I:6:SER:O	9:I:6:SER:OG	2.16	0.59
3:O:229:VAL:HA	3:O:314:SER:HA	1.83	0.59
1:A:1045:VAL:O	1:A:1191:GLY:N	2.34	0.59
2:B:14:ASN:OD1	2:B:14:ASN:N	2.35	0.59
2:B:232:LEU:HG	2:B:236:VAL:O	2.02	0.59
3:C:223:HIS:HD2	3:C:225:LYS:H	1.49	0.59
4:D:28:ARG:O	4:D:32:THR:HG23	2.02	0.59
5:E:84:ILE:HG23	5:E:85:LYS:HE3	1.83	0.59
7:G:105:ILE:HG23	7:G:109:PHE:HB2	1.84	0.59
1:M:850:LEU:HA	1:M:929:LEU:HA	1.83	0.59
1:A:736:ARG:HD3	8:H:75:ILE:HD12	1.85	0.59
3:C:128:GLY:N	3:C:129:GLN:OE1	2.34	0.59
1:M:77:PHE:CE1	1:M:368:PRO:HA	2.37	0.59
1:A:850:LEU:HA	1:A:929:LEU:HA	1.83	0.59
1:A:1271:VAL:HG12	1:A:1273:SER:H	1.66	0.59
6:F:68:ASP:OD2	6:F:68:ASP:N	2.28	0.59
2:N:733:GLN:NE2	2:N:755:ASN:H	2.01	0.59
1:A:734:ILE:HD11	1:A:740:TYR:HB2	1.83	0.59
1:M:462:PRO:HA	1:M:466:GLN:OE1	2.02	0.59
1:M:885:ILE:HG22	1:M:889:ASN:HD21	1.67	0.59
1:M:1522:PRO:HD2	1:M:1550:LYS:HZ1	1.66	0.59
2:N:217:CYS:HB2	2:N:338:HIS:ND1	2.17	0.59
4:P:27:ASN:OD1	4:P:31:GLN:NE2	2.36	0.59
7:S:105:ILE:HG23	7:S:109:PHE:HB2	1.84	0.59
1:M:734:ILE:HD11	1:M:740:TYR:HB2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:1305:SER:O	1:M:1309:TYR:N	2.35	0.59
1:A:81:VAL:HA	1:A:364:ASN:HB3	1.83	0.59
1:A:240:LYS:HA	1:A:246:ILE:HG22	1.85	0.59
1:A:499:GLU:O	1:A:633:HIS:HB2	2.02	0.59
1:A:1038:LYS:HE3	1:A:1626:ILE:HG23	1.85	0.59
2:B:433:ILE:HG22	2:B:436:LYS:HZ3	1.66	0.59
2:B:733:GLN:NE2	2:B:755:ASN:H	2.01	0.59
3:C:334:LYS:HE2	11:K:46:LEU:HD12	1.82	0.59
2:N:232:LEU:HG	2:N:236:VAL:O	2.02	0.59
2:N:1097:SER:HB2	2:N:1117:SER:H	1.67	0.59
4:P:17:LEU:O	7:S:4:LEU:HD21	2.03	0.59
6:R:93:MET:HG3	7:S:68:PRO:HG3	1.83	0.59
8:T:38:LEU:HD21	8:T:40:LEU:HD22	1.85	0.59
1:A:760:PRO:HD2	1:A:1088:SER:HA	1.84	0.59
2:B:822:TRP:HB3	2:B:826:LEU:HD12	1.84	0.59
3:C:75:ARG:HG2	11:K:45:THR:HB	1.84	0.59
6:F:97:VAL:HG22	6:F:99:VAL:H	1.67	0.59
7:G:44:ILE:HG21	7:G:80:VAL:HG11	1.85	0.59
2:N:728:ARG:HH22	3:O:99:GLN:HE22	1.50	0.59
7:S:70:SER:OG	7:S:71:PHE:N	2.36	0.59
2:B:208:TYR:CD1	2:B:232:LEU:HB3	2.38	0.59
2:B:218:VAL:HA	2:B:224:SER:HA	1.85	0.59
2:B:777:SER:OG	2:B:781:ARG:NH1	2.36	0.59
3:C:336:LEU:O	3:C:340:SER:OG	2.21	0.59
4:D:27:ASN:OD1	4:D:31:GLN:NE2	2.36	0.59
6:F:114:GLU:OE1	6:F:119:LYS:HB2	2.03	0.59
1:M:543:HIS:HB2	1:M:552:ILE:O	2.02	0.59
1:M:1038:LYS:HE3	1:M:1626:ILE:HG23	1.84	0.59
3:O:59:VAL:HG12	3:O:311:SER:HA	1.85	0.59
3:O:336:LEU:O	3:O:340:SER:OG	2.21	0.59
1:A:12:LYS:HB3	2:B:1172:GLU:OE2	2.02	0.58
1:M:1309:TYR:O	1:M:1313:TYR:HB2	2.02	0.58
2:N:918:THR:HG23	3:O:78:ILE:HD11	1.85	0.58
2:N:995:ASN:HB3	2:N:1010:ASP:HB3	1.83	0.58
6:R:97:VAL:HG22	6:R:99:VAL:H	1.67	0.58
1:A:1569:ILE:HG21	1:A:1585:ILE:HG22	1.85	0.58
7:G:128:ASP:C	2:N:116:ARG:HH22	2.10	0.58
8:H:43:ASN:OD1	8:H:46:ILE:N	2.23	0.58
1:M:240:LYS:HA	1:M:246:ILE:HG22	1.85	0.58
5:Q:188:GLY:N	5:Q:209:CYS:O	2.36	0.58
1:A:880:SER:OG	1:A:882:ASP:OD1	2.20	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:59:VAL:HG12	3:C:311:SER:HA	1.85	0.58
9:I:55:SER:HB3	9:I:58:LYS:HB2	1.84	0.58
1:M:178:LEU:HA	1:M:181:ILE:HD12	1.86	0.58
1:M:734:ILE:HG22	8:T:76:MET:HG2	1.84	0.58
2:N:237:THR:OG1	2:N:252:SER:OG	2.13	0.58
3:O:339:LYS:NZ	11:W:92:ARG:HA	2.18	0.58
2:B:200:SER:HA	2:B:203:ASN:HD21	1.68	0.58
2:B:235:GLY:HA2	2:B:284:ARG:NH1	2.17	0.58
3:C:229:VAL:HA	3:C:314:SER:HA	1.83	0.58
2:N:37:ASN:HB3	2:N:41:ASN:HD21	1.68	0.58
2:N:793:SER:OG	2:N:887:HIS:ND1	2.33	0.58
3:O:35:ASN:O	11:W:56:LYS:HD2	2.03	0.58
7:S:44:ILE:HG21	7:S:80:VAL:HG11	1.85	0.58
7:S:56:PHE:HB3	7:S:74:VAL:HG22	1.84	0.58
1:A:870:LEU:HD12	1:A:987:THR:HG21	1.85	0.58
1:M:917:THR:HG23	1:M:959:LEU:HD11	1.85	0.58
1:M:1569:ILE:HG21	1:M:1585:ILE:HG22	1.85	0.58
3:O:338:VAL:HG13	11:W:22:ILE:HG21	1.84	0.58
4:P:28:ARG:O	4:P:32:THR:HG23	2.03	0.58
6:R:87:ARG:NH1	6:R:90:GLN:OE1	2.32	0.58
9:U:55:SER:HB3	9:U:58:LYS:HB2	1.84	0.58
2:B:55:LYS:NZ	2:B:397:ASN:OD1	2.31	0.58
12:L:26:ASP:OD1	12:L:27:CYS:N	2.32	0.58
2:N:208:TYR:CD1	2:N:232:LEU:HB3	2.38	0.58
7:S:117:SER:HB2	7:S:169:THR:HA	1.86	0.58
1:A:885:ILE:HG22	1:A:889:ASN:HD21	1.67	0.58
2:B:824:GLN:O	12:L:56:ARG:NH2	2.37	0.58
8:H:38:LEU:HD21	8:H:40:LEU:HD22	1.85	0.58
1:M:1064:GLY:O	1:M:1603:ARG:HG2	2.04	0.58
11:W:79:ILE:HD11	11:W:91:LEU:HD13	1.86	0.58
1:A:558:THR:N	1:A:561:GLN:OE1	2.22	0.58
2:B:37:ASN:HB3	2:B:41:ASN:HD21	1.68	0.58
3:C:91:ILE:HA	3:C:211:LEU:HB3	1.86	0.58
7:G:121:ASP:N	7:G:121:ASP:OD1	2.36	0.58
1:M:870:LEU:HD12	1:M:987:THR:HG21	1.85	0.58
1:M:1003:ILE:HD11	1:M:1008:TYR:CD2	2.32	0.58
1:M:1270:LEU:HD22	1:M:1313:TYR:CD1	2.39	0.58
2:N:200:SER:HA	2:N:203:ASN:HD21	1.68	0.58
6:R:96:PRO:HG3	7:S:23:ARG:HG2	1.84	0.58
1:A:178:LEU:HA	1:A:181:ILE:HD12	1.86	0.58
2:N:880:ASP:HA	12:X:38:VAL:CG2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:T:24:VAL:HG13	8:T:42:ILE:C	2.29	0.58
1:A:77:PHE:CD1	1:A:368:PRO:HA	2.39	0.57
1:A:917:THR:HG23	1:A:959:LEU:HD11	1.85	0.57
1:A:1038:LYS:HZ1	1:A:1629:ASN:HD22	1.51	0.57
1:A:1673:GLY:HA2	6:F:78:TYR:CE1	2.39	0.57
11:K:57:ASN:O	11:K:60:VAL:HG12	2.05	0.57
1:M:558:THR:N	1:M:561:GLN:OE1	2.22	0.57
2:N:283:ASP:OD1	2:N:284:ARG:N	2.37	0.57
8:T:96:SER:HA	8:T:101:LEU:HD23	1.86	0.57
1:A:1:MET:HB2	2:B:1079:ASN:HB3	1.85	0.57
1:A:774:TYR:HB3	1:A:933:PHE:CD2	2.39	0.57
1:A:1270:LEU:HD22	1:A:1313:TYR:CD1	2.39	0.57
8:H:80:VAL:HB	8:H:95:VAL:HG22	1.87	0.57
1:M:19:TYR:CD2	2:N:1168:LYS:HD2	2.38	0.57
1:M:388:ASN:O	1:M:392:THR:HG23	2.04	0.57
1:M:668:ASN:OD1	1:M:668:ASN:N	2.34	0.57
2:N:218:VAL:HA	2:N:224:SER:HA	1.85	0.57
2:N:439:TYR:O	2:N:442:SER:OG	2.21	0.57
4:P:56:TYR:CE1	7:S:106:LEU:HD23	2.39	0.57
1:A:1550:LYS:HA	1:A:1553:TRP:HD1	1.69	0.57
2:B:85:ALA:O	2:B:115:SER:OG	2.20	0.57
8:H:24:VAL:HG13	8:H:42:ILE:C	2.29	0.57
1:M:979:LEU:HD22	1:M:1010:PHE:CZ	2.39	0.57
2:N:123:TRP:HE3	2:N:131:GLN:O	1.88	0.57
5:Q:173:ILE:N	5:Q:208:ILE:O	2.37	0.57
1:A:388:ASN:O	1:A:392:THR:HG23	2.04	0.57
1:M:53:ALA:O	1:M:65:THR:OG1	2.13	0.57
1:M:1498:ILE:HD11	9:U:22:ALA:HB2	1.87	0.57
3:O:137:ASP:HB3	3:O:138:THR:HG23	1.86	0.57
1:A:1064:GLY:O	1:A:1603:ARG:HG2	2.04	0.57
2:B:58:PHE:HB3	2:B:74:LYS:HA	1.86	0.57
2:B:123:TRP:HE3	2:B:131:GLN:O	1.88	0.57
2:B:225:LEU:HD12	2:B:226:THR:H	1.69	0.57
2:B:373:GLN:HA	2:B:651:PRO:O	2.05	0.57
2:B:518:LEU:HD23	2:B:518:LEU:H	1.69	0.57
7:G:145:GLU:HB3	7:G:146:PRO:HD3	1.86	0.57
1:M:130:LEU:HD21	1:M:193:SER:HB3	1.87	0.57
8:T:80:VAL:HB	8:T:95:VAL:HG22	1.87	0.57
1:A:211:ARG:NH2	1:A:1651:ARG:HD2	2.20	0.57
1:A:705:ARG:NH1	11:K:60:VAL:O	2.37	0.57
2:B:208:TYR:HD1	2:B:232:LEU:HB3	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:253:MET:HE1	2:B:267:ILE:HG12	1.86	0.57
1:M:77:PHE:CD1	1:M:368:PRO:HA	2.39	0.57
2:N:58:PHE:HB3	2:N:74:LYS:HA	1.86	0.57
2:B:184:MET:HB2	2:B:479:VAL:HG22	1.87	0.57
2:B:1034:THR:HG22	2:B:1035:GLY:H	1.69	0.57
3:C:137:ASP:HB3	3:C:138:THR:HG23	1.86	0.57
5:E:188:GLY:N	5:E:209:CYS:O	2.36	0.57
7:G:19:PRO:HD3	7:G:69:PHE:HB3	1.86	0.57
7:G:70:SER:OG	7:G:71:PHE:N	2.35	0.57
7:G:117:SER:HB2	7:G:169:THR:HA	1.86	0.57
1:M:1550:LYS:HA	1:M:1553:TRP:HD1	1.69	0.57
2:N:18:ASP:OD2	2:N:19:GLY:N	2.38	0.57
2:N:824:GLN:O	12:X:56:ARG:NH2	2.38	0.57
5:E:54:ARG:HB3	5:E:78:LYS:HD3	1.86	0.57
1:M:1038:LYS:HZ1	1:M:1629:ASN:HD22	1.52	0.57
2:B:831:LEU:HD13	2:B:845:VAL:HG12	1.87	0.57
5:E:15:TRP:O	5:E:19:HIS:N	2.38	0.57
2:N:531:PRO:HB3	2:N:631:PRO:HD3	1.87	0.57
6:R:114:GLU:OE1	6:R:119:LYS:HB2	2.03	0.57
1:A:736:ARG:NH2	8:H:68:LEU:O	2.38	0.57
1:A:979:LEU:HD22	1:A:1010:PHE:CZ	2.39	0.57
1:A:1233:GLU:HA	1:A:1237:THR:HG22	1.87	0.57
3:C:77:LEU:HG	3:C:229:VAL:HG11	1.87	0.57
8:H:96:SER:HA	8:H:101:LEU:HD23	1.86	0.57
11:K:79:ILE:HD11	11:K:91:LEU:HD13	1.86	0.57
2:N:14:ASN:OD1	2:N:14:ASN:N	2.35	0.57
11:W:57:ASN:O	11:W:60:VAL:HG12	2.04	0.57
1:A:696:LEU:HB2	1:A:835:TYR:CE2	2.40	0.56
1:A:962:GLN:NE2	1:A:992:GLY:O	2.17	0.56
2:B:271:ILE:HG23	2:B:272:VAL:HG13	1.87	0.56
2:B:687:ASN:ND2	2:B:741:LEU:HD12	2.20	0.56
5:E:173:ILE:N	5:E:208:ILE:O	2.37	0.56
7:G:37:ILE:HG13	7:G:38:LEU:HD23	1.87	0.56
1:M:774:TYR:HB3	1:M:933:PHE:CD2	2.39	0.56
7:S:37:ILE:HG13	7:S:38:LEU:HD23	1.87	0.56
8:T:7:LEU:HB2	8:T:59:ILE:HG12	1.87	0.56
1:A:130:LEU:HD21	1:A:193:SER:HB3	1.87	0.56
1:A:826:SER:O	1:A:829:SER:OG	2.21	0.56
2:B:283:ASP:OD1	2:B:284:ARG:N	2.37	0.56
2:B:502:GLY:HA2	2:B:681:VAL:HA	1.87	0.56
3:C:96:SER:OG	3:C:97:ILE:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:40:GLN:OE1	5:E:44:MET:HE3	2.05	0.56
8:H:7:LEU:HB2	8:H:59:ILE:HG12	1.87	0.56
1:M:685:LEU:HB3	1:M:689:HIS:HB2	1.87	0.56
2:N:225:LEU:HD12	2:N:226:THR:H	1.69	0.56
2:N:587:LYS:HA	2:N:605:VAL:HG23	1.87	0.56
3:O:91:ILE:HA	3:O:211:LEU:HB3	1.86	0.56
1:A:528:ARG:HG3	1:A:566:ALA:HB1	1.87	0.56
1:A:542:SER:OG	1:A:543:HIS:N	2.38	0.56
2:B:18:ASP:OD2	2:B:19:GLY:N	2.38	0.56
2:B:336:LEU:HB3	2:B:338:HIS:CE1	2.40	0.56
2:B:399:ILE:HG22	2:B:429:ILE:HG21	1.88	0.56
2:B:439:TYR:O	2:B:442:SER:OG	2.21	0.56
2:B:921:MET:HE1	2:B:933:ILE:HG13	1.87	0.56
4:D:48:SER:HA	4:D:51:ASN:HD22	1.71	0.56
1:M:77:PHE:CD2	2:N:1096:ILE:HG12	2.41	0.56
1:M:852:GLU:O	1:M:856:ASN:ND2	2.38	0.56
2:N:184:MET:HB2	2:N:479:VAL:HG22	1.87	0.56
2:N:235:GLY:HA2	2:N:284:ARG:NH1	2.17	0.56
2:N:523:ARG:NE	2:N:741:LEU:HD13	2.20	0.56
2:N:852:THR:OG1	2:N:854:GLN:HG2	2.06	0.56
2:N:928:MET:HE3	10:V:42:ARG:CD	2.35	0.56
5:Q:15:TRP:O	5:Q:19:HIS:N	2.38	0.56
7:S:19:PRO:HD3	7:S:69:PHE:HB3	1.86	0.56
8:T:43:ASN:OD1	8:T:46:ILE:N	2.23	0.56
1:A:492:ILE:HG13	1:A:630:ILE:HD11	1.88	0.56
2:B:135:ARG:NH2	2:B:426:PHE:HB3	2.20	0.56
1:M:542:SER:O	1:M:554:LEU:HB2	2.06	0.56
1:M:606:ASN:OD1	1:M:607:ARG:N	2.39	0.56
2:N:253:MET:HE1	2:N:267:ILE:HG12	1.86	0.56
2:N:336:LEU:HB3	2:N:338:HIS:CE1	2.40	0.56
3:O:75:ARG:HH12	11:W:44:HIS:HB2	1.70	0.56
3:O:143:LEU:HD23	3:O:174:LEU:HG	1.88	0.56
5:Q:54:ARG:HB3	5:Q:78:LYS:HD3	1.86	0.56
1:A:498:ILE:HG13	1:A:499:GLU:N	2.21	0.56
2:B:523:ARG:NE	2:B:741:LEU:HD13	2.20	0.56
2:B:793:SER:OG	2:B:887:HIS:ND1	2.32	0.56
2:N:518:LEU:HD23	2:N:518:LEU:H	1.69	0.56
3:O:79:ALA:HB1	3:O:221:GLN:N	2.21	0.56
5:Q:40:GLN:OE1	5:Q:44:MET:HE3	2.05	0.56
7:S:145:GLU:HB3	7:S:146:PRO:HD3	1.86	0.56
2:B:844:ILE:HG22	2:B:845:VAL:HG13	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:230:ALA:N	3:C:313:GLU:O	2.39	0.56
3:C:315:THR:HG21	10:J:6:ARG:HH22	1.69	0.56
1:M:498:ILE:HG13	1:M:499:GLU:N	2.21	0.56
2:N:399:ILE:HG22	2:N:429:ILE:HG21	1.88	0.56
2:N:921:MET:HE1	2:N:933:ILE:HG13	1.87	0.56
2:N:1034:THR:HG22	2:N:1035:GLY:H	1.69	0.56
4:P:52:ARG:HA	4:P:55:MET:HE2	1.88	0.56
1:A:852:GLU:O	1:A:856:ASN:ND2	2.38	0.56
2:B:531:PRO:HB3	2:B:631:PRO:HD3	1.87	0.56
3:C:79:ALA:HB1	3:C:221:GLN:N	2.21	0.56
7:G:61:ALA:HB2	7:G:72:ILE:HB	1.87	0.56
1:M:1335:ILE:HD11	1:M:1511:LYS:HE3	1.87	0.56
2:N:135:ARG:NH2	2:N:426:PHE:HB3	2.20	0.56
2:N:315:LEU:HD21	2:N:330:LEU:HD21	1.87	0.56
2:N:844:ILE:HG22	2:N:845:VAL:HG13	1.87	0.56
3:O:241:HIS:CE1	3:O:300:GLN:HB3	2.41	0.56
1:A:542:SER:O	1:A:554:LEU:HB2	2.06	0.56
2:B:315:LEU:HD21	2:B:330:LEU:HD21	1.87	0.56
3:C:204:ARG:HB2	10:J:63:ASN:HD21	1.71	0.56
5:E:146:PRO:HB3	5:E:194:VAL:O	2.06	0.56
1:M:211:ARG:NH2	1:M:1651:ARG:HD2	2.20	0.56
1:M:726:ARG:HA	11:W:78:ARG:HH21	1.71	0.56
2:N:364:CYS:SG	2:N:622:TYR:N	2.79	0.56
2:N:373:GLN:HA	2:N:651:PRO:O	2.05	0.56
3:O:96:SER:OG	3:O:97:ILE:N	2.38	0.56
1:A:481:GLY:HA2	2:B:1057:GLY:HA3	1.88	0.56
1:A:612:HIS:HA	1:A:1200:GLN:CD	2.31	0.56
1:A:955:GLN:HA	1:A:959:LEU:O	2.06	0.56
1:M:955:GLN:HA	1:M:959:LEU:O	2.06	0.56
2:N:540:LEU:O	2:N:544:LEU:HB2	2.06	0.56
3:O:35:ASN:O	11:W:56:LYS:HA	2.06	0.56
2:B:109:ARG:HD2	2:B:875:GLY:O	2.06	0.56
2:B:540:LEU:O	2:B:544:LEU:HB2	2.06	0.56
2:B:1087:TRP:HA	2:B:1147:THR:O	2.06	0.56
1:M:111:LEU:HD11	1:M:222:ILE:HG22	1.88	0.56
1:M:219:TYR:HA	1:M:222:ILE:HG12	1.87	0.56
1:M:559:ILE:O	1:M:563:THR:OG1	2.22	0.56
1:M:1001:THR:HG23	2:N:976:THR:HG23	1.89	0.56
2:N:365:CYS:N	2:N:620:GLY:O	2.27	0.56
2:N:831:LEU:HD13	2:N:845:VAL:HG12	1.87	0.56
3:O:77:LEU:HG	3:O:229:VAL:HG11	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:TYR:HA	1:A:222:ILE:HG12	1.88	0.55
2:B:285:VAL:O	2:B:289:LEU:HG	2.06	0.55
2:B:364:CYS:SG	2:B:622:TYR:N	2.79	0.55
1:M:116:VAL:HG12	1:M:342:VAL:HG21	1.88	0.55
2:N:891:ARG:HD3	3:O:99:GLN:HG2	1.88	0.55
8:T:95:VAL:HG11	8:T:119:VAL:HG21	1.87	0.55
1:A:116:VAL:HG12	1:A:342:VAL:HG21	1.88	0.55
1:A:606:ASN:OD1	1:A:607:ARG:N	2.39	0.55
1:A:712:LEU:HD11	1:A:753:ASN:ND2	2.22	0.55
2:B:587:LYS:HA	2:B:605:VAL:HG23	1.87	0.55
3:C:143:LEU:HD23	3:C:174:LEU:HG	1.88	0.55
3:C:145:LYS:HD3	3:C:166:ASN:HB3	1.88	0.55
4:D:17:LEU:CD2	7:G:7:TYR:HA	2.35	0.55
6:F:96:PRO:HG3	7:G:23:ARG:HG2	1.88	0.55
8:H:95:VAL:HG11	8:H:119:VAL:HG21	1.87	0.55
1:M:492:ILE:HG13	1:M:630:ILE:HD11	1.88	0.55
1:M:507:PRO:O	1:M:511:THR:HG23	2.07	0.55
5:Q:49:GLY:HA3	5:Q:51:ASN:H	1.70	0.55
7:S:121:ASP:OD1	7:S:121:ASP:N	2.37	0.55
1:A:685:LEU:HB3	1:A:689:HIS:HB2	1.87	0.55
1:A:759:ARG:NH2	1:A:1092:LYS:HB2	2.22	0.55
5:E:49:GLY:HA3	5:E:51:ASN:H	1.71	0.55
1:M:528:ARG:HG3	1:M:566:ALA:HB1	1.87	0.55
1:M:696:LEU:HB2	1:M:835:TYR:CE2	2.40	0.55
1:M:1233:GLU:HA	1:M:1237:THR:HG22	1.87	0.55
2:N:1087:TRP:HA	2:N:1147:THR:O	2.06	0.55
3:O:230:ALA:N	3:O:313:GLU:O	2.39	0.55
7:S:122:TRP:CD1	7:S:139:ASN:H	2.24	0.55
1:A:88:HIS:CD2	1:A:362:LEU:HD21	2.41	0.55
1:A:507:PRO:O	1:A:511:THR:HG23	2.07	0.55
1:A:1263:PHE:HE1	1:A:1555:PHE:CG	2.24	0.55
1:A:1335:ILE:HD11	1:A:1511:LYS:HE3	1.87	0.55
2:B:123:TRP:NE1	2:B:422:LEU:HG	2.22	0.55
2:B:365:CYS:N	2:B:620:GLY:O	2.27	0.55
5:E:13:ARG:HE	5:E:137:VAL:HG12	1.71	0.55
1:M:916:LEU:O	1:M:919:SER:OG	2.12	0.55
1:M:1680:PHE:O	6:R:122:LEU:HA	2.06	0.55
2:N:109:ARG:HD2	2:N:875:GLY:O	2.06	0.55
2:N:271:ILE:HG23	2:N:272:VAL:HG13	1.87	0.55
2:B:386:GLN:HE21	2:B:452:LEU:HD22	1.72	0.55
3:C:262:VAL:HG21	3:C:283:ASP:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:335:CYS:HB3	11:K:99:ILE:HG12	1.88	0.55
1:M:52:LEU:O	1:M:64:ALA:N	2.30	0.55
1:M:1020:ILE:HG22	2:N:515:CYS:SG	2.47	0.55
2:B:145:ARG:HB3	2:B:170:GLY:HA3	1.89	0.55
1:M:612:HIS:HA	1:M:1200:GLN:CD	2.31	0.55
2:B:852:THR:OG1	2:B:854:GLN:HG2	2.06	0.55
3:C:241:HIS:CE1	3:C:300:GLN:HB3	2.41	0.55
1:M:542:SER:OG	1:M:543:HIS:N	2.38	0.55
1:M:1263:PHE:HE1	1:M:1555:PHE:CG	2.24	0.55
1:M:1522:PRO:HD2	1:M:1550:LYS:NZ	2.22	0.55
2:N:502:GLY:HA2	2:N:681:VAL:HA	1.87	0.55
7:S:12:ASP:OD2	7:S:75:ARG:NE	2.25	0.55
2:N:208:TYR:HD1	2:N:232:LEU:HB3	1.70	0.55
2:N:285:VAL:O	2:N:289:LEU:HG	2.06	0.55
1:A:862:LEU:HD13	1:A:996:ALA:HB1	1.89	0.55
1:A:1139:GLU:O	1:A:1143:ARG:HG2	2.07	0.55
2:B:614:VAL:HB	2:B:624:GLY:H	1.72	0.55
1:M:712:LEU:HD11	1:M:753:ASN:ND2	2.22	0.55
1:M:1602:PRO:HB2	5:Q:199:THR:HG21	1.89	0.55
5:Q:13:ARG:HE	5:Q:137:VAL:HG12	1.71	0.55
2:B:874:LEU:HD11	2:B:887:HIS:HB2	1.89	0.55
1:M:32:ILE:HA	1:M:47:GLY:O	2.07	0.55
1:M:653:PHE:O	2:N:1076:ARG:NH2	2.40	0.55
1:M:862:LEU:HD13	1:M:996:ALA:HB1	1.89	0.55
2:N:183:ARG:HD2	2:N:478:MET:HE3	1.89	0.55
2:N:503:PHE:CE1	2:N:636:ARG:HB3	2.42	0.55
7:G:122:TRP:CD1	7:G:139:ASN:H	2.24	0.54
1:M:949:SER:OG	1:M:951:VAL:HG22	2.07	0.54
1:M:1249:LEU:HD12	1:M:1542:VAL:CG1	2.38	0.54
3:O:144:ASN:HA	3:O:209:ILE:O	2.07	0.54
5:Q:146:PRO:HB3	5:Q:194:VAL:O	2.06	0.54
1:A:32:ILE:HA	1:A:47:GLY:O	2.07	0.54
2:B:183:ARG:HD2	2:B:478:MET:HE3	1.89	0.54
5:E:73:TYR:CE2	5:E:75:GLU:HB3	2.42	0.54
11:K:81:THR:HG21	11:K:90:VAL:HG21	1.89	0.54
1:M:1062:HIS:CB	1:M:1066:ASP:HB3	2.36	0.54
3:O:88:PHE:HB3	12:X:59:GLN:HE21	1.71	0.54
3:O:262:VAL:HG21	3:O:283:ASP:HB2	1.89	0.54
3:O:288:GLU:OE2	3:O:291:ARG:NH2	2.40	0.54
1:A:1003:ILE:HD11	1:A:1008:TYR:CD2	2.32	0.54
1:A:1246:THR:OG1	1:A:1566:THR:OG1	2.11	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1249:LEU:HD12	1:A:1542:VAL:CG1	2.38	0.54
1:A:1522:PRO:HD2	1:A:1550:LYS:NZ	2.22	0.54
2:B:237:THR:HG21	2:B:353:ILE:HD13	1.90	0.54
2:B:957:GLY:N	2:B:964:GLN:HE21	2.05	0.54
2:B:1085:GLN:HB3	2:B:1148:LEU:HD21	1.90	0.54
2:N:145:ARG:HB3	2:N:170:GLY:HA3	1.89	0.54
1:A:111:LEU:HD11	1:A:222:ILE:HG22	1.88	0.54
1:M:35:PRO:HG3	1:M:395:LEU:HG	1.89	0.54
1:M:1248:THR:HB	1:M:1564:ILE:HB	1.89	0.54
1:M:1279:VAL:HG13	1:M:1301:LEU:HA	1.88	0.54
2:N:386:GLN:HE21	2:N:452:LEU:HD22	1.72	0.54
5:Q:73:TYR:CE2	5:Q:75:GLU:HB3	2.42	0.54
7:S:61:ALA:HB2	7:S:72:ILE:HB	1.87	0.54
11:W:81:THR:HG21	11:W:90:VAL:HG21	1.89	0.54
1:A:910:LYS:NZ	1:A:967:GLY:O	2.41	0.54
1:A:1279:VAL:HG13	1:A:1301:LEU:HA	1.88	0.54
2:B:882:GLU:HB2	2:B:884:GLN:HE21	1.71	0.54
2:B:985:LEU:HG	2:B:990:TYR:HB2	1.89	0.54
4:D:52:ARG:HA	4:D:55:MET:HE2	1.88	0.54
10:J:24:LEU:O	10:J:28:ASP:HB2	2.08	0.54
1:M:67:HIS:ND1	2:N:1102:ILE:HD11	2.22	0.54
1:M:1009:TYR:OH	2:N:500:ALA:HB3	2.08	0.54
1:M:1139:GLU:O	1:M:1143:ARG:HG2	2.07	0.54
2:N:614:VAL:HB	2:N:624:GLY:H	1.72	0.54
2:N:677:SER:OG	2:N:679:THR:HB	2.07	0.54
2:N:875:GLY:HA2	12:X:39:ILE:HG21	1.89	0.54
3:O:145:LYS:HD3	3:O:166:ASN:HB3	1.88	0.54
4:P:48:SER:HA	4:P:51:ASN:HD22	1.71	0.54
1:A:949:SER:OG	1:A:951:VAL:HG22	2.07	0.54
2:B:116:ARG:HA	2:B:139:MET:HG2	1.90	0.54
3:C:144:ASN:HA	3:C:209:ILE:O	2.07	0.54
6:F:96:PRO:HB2	7:G:23:ARG:NH1	2.23	0.54
1:M:1478:LYS:HG3	1:M:1495:VAL:HG23	1.90	0.54
2:N:99:ARG:HH22	12:X:47:ARG:HH12	1.52	0.54
2:N:147:ASN:HA	2:N:152:GLU:OE1	2.08	0.54
2:N:882:GLU:HB2	2:N:884:GLN:HE21	1.71	0.54
2:N:957:GLY:N	2:N:964:GLN:HE21	2.05	0.54
3:O:167:SER:OG	3:O:203:LEU:O	2.17	0.54
1:A:35:PRO:HG3	1:A:395:LEU:HG	1.89	0.54
2:B:677:SER:OG	2:B:679:THR:HB	2.07	0.54
5:E:71:THR:HG23	5:E:99:HIS:HD2	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:7:TYR:HD2	7:G:82:SER:HB3	1.73	0.54
1:M:88:HIS:CD2	1:M:362:LEU:HD21	2.41	0.54
1:M:759:ARG:NH2	1:M:1092:LYS:HB2	2.22	0.54
1:M:846:ASP:HB3	2:N:993:HIS:CG	2.42	0.54
3:O:204:ARG:H	3:O:207:GLN:HE21	1.55	0.54
1:A:329:ARG:O	1:A:332:LEU:HG	2.08	0.54
1:A:372:PHE:CE1	2:B:1157:TYR:HA	2.43	0.54
1:A:1277:ARG:HG2	1:A:1278:GLN:H	1.73	0.54
7:G:57:LEU:O	7:G:59:LYS:HG3	2.08	0.54
1:M:13:SER:HA	1:M:1656:ASP:O	2.08	0.54
1:M:329:ARG:O	1:M:332:LEU:HG	2.08	0.54
1:M:704:THR:HG22	1:M:705:ARG:H	1.72	0.54
1:M:1277:ARG:HG2	1:M:1278:GLN:H	1.73	0.54
1:M:1582:ARG:NH1	5:Q:197:SER:OG	2.39	0.54
2:N:116:ARG:HA	2:N:139:MET:HG2	1.90	0.54
2:B:935:ASN:OD1	2:B:937:HIS:ND1	2.41	0.54
1:M:464:ILE:O	1:M:467:ILE:HG12	2.07	0.54
2:N:985:LEU:HG	2:N:990:TYR:HB2	1.89	0.54
1:A:247:PHE:N	1:A:321:LYS:O	2.41	0.54
2:B:93:GLU:CD	7:S:97:SER:HB2	2.33	0.54
2:B:503:PHE:CE1	2:B:636:ARG:HB3	2.42	0.54
2:B:901:LYS:HB2	2:B:1021:LEU:HD22	1.89	0.54
2:B:976:THR:HG22	2:B:978:ALA:H	1.72	0.54
9:I:24:TRP:NE1	9:I:34:TYR:O	2.41	0.54
2:N:237:THR:HG21	2:N:353:ILE:HD13	1.90	0.54
2:N:976:THR:HG22	2:N:978:ALA:H	1.72	0.54
7:S:114:PRO:HD2	7:S:117:SER:OG	2.08	0.54
1:A:98:LEU:HD23	1:A:360:PHE:HE2	1.74	0.53
1:A:1151:LYS:HG3	1:A:1152:ASN:N	2.22	0.53
2:B:693:ASP:OD1	2:B:693:ASP:N	2.32	0.53
1:M:80:ILE:HD11	1:M:395:LEU:HD13	1.90	0.53
2:N:415:ASP:OD2	2:N:417:SER:OG	2.23	0.53
2:N:687:ASN:ND2	2:N:741:LEU:HD12	2.20	0.53
2:N:919:VAL:HG21	3:O:75:ARG:HD3	1.89	0.53
5:Q:180:ALA:HA	5:Q:185:LEU:HD12	1.90	0.53
1:A:464:ILE:O	1:A:467:ILE:HG12	2.07	0.53
2:B:107:ARG:NH1	2:B:721:ARG:HH22	2.06	0.53
2:B:243:TRP:HD1	2:B:244:ARG:HG2	1.72	0.53
7:G:114:PRO:HD2	7:G:117:SER:OG	2.08	0.53
9:I:20:THR:OG1	9:I:36:SER:HB3	2.08	0.53
9:I:24:TRP:HA	9:I:36:SER:OG	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:247:PHE:N	1:M:321:LYS:O	2.41	0.53
1:M:997:SER:OG	1:M:1003:ILE:HG22	2.08	0.53
2:N:154:LEU:HD22	2:N:158:GLU:HG3	1.89	0.53
2:N:971:TYR:CG	2:N:977:ALA:HB2	2.44	0.53
9:U:20:THR:OG1	9:U:36:SER:HB3	2.08	0.53
12:X:24:CYS:HA	12:X:49:MET:HG2	1.89	0.53
2:B:842:ASP:OD1	2:B:843:PRO:HD2	2.08	0.53
2:N:372:PRO:HB2	2:N:499:GLU:OE1	2.08	0.53
2:N:874:LEU:HD11	2:N:887:HIS:HB2	1.89	0.53
1:A:471:LYS:NZ	1:A:476:ARG:HH21	2.07	0.53
1:A:704:THR:HG22	1:A:705:ARG:H	1.72	0.53
2:B:93:GLU:OE2	7:S:99:SER:OG	2.15	0.53
2:B:820:ARG:HG2	2:B:821:GLU:HG3	1.91	0.53
3:C:204:ARG:HG3	10:J:60:LEU:HD22	1.91	0.53
5:E:106:TYR:O	5:E:131:GLN:HB2	2.09	0.53
6:F:72:THR:O	6:F:126:ARG:NH1	2.30	0.53
11:K:52:TYR:O	11:K:56:LYS:HG2	2.09	0.53
1:M:893:GLU:HB2	1:M:985:TYR:CZ	2.44	0.53
2:N:820:ARG:HG2	2:N:821:GLU:HG3	1.91	0.53
2:B:147:ASN:HA	2:B:152:GLU:OE1	2.08	0.53
2:B:253:MET:HB2	2:B:288:MET:SD	2.48	0.53
1:M:844:ARG:HD2	2:N:995:ASN:HD21	1.74	0.53
2:N:253:MET:HB2	2:N:288:MET:SD	2.48	0.53
3:O:114:ALA:HB2	3:O:191:ILE:HG23	1.90	0.53
10:V:47:ARG:NH1	10:V:48:MET:SD	2.82	0.53
1:A:113:LYS:HB3	1:A:230:ASN:HD21	1.74	0.53
1:A:902:LEU:HD22	1:A:968:ARG:HH21	1.74	0.53
1:A:1248:THR:HB	1:A:1564:ILE:HB	1.90	0.53
3:C:86:PHE:CD2	3:C:215:ALA:HB2	2.44	0.53
4:D:54:LEU:O	4:D:58:LYS:HG2	2.08	0.53
12:L:24:CYS:HA	12:L:49:MET:HG2	1.89	0.53
1:M:582:SER:OG	7:S:35:SER:O	2.26	0.53
1:M:1309:TYR:OH	1:M:1315:VAL:HG23	2.09	0.53
2:N:935:ASN:OD1	2:N:937:HIS:ND1	2.41	0.53
4:P:47:LEU:HA	4:P:50:LEU:HD12	1.90	0.53
11:W:52:TYR:O	11:W:56:LYS:HG2	2.09	0.53
1:A:660:ARG:NH1	6:F:108:LEU:HD13	2.23	0.53
1:A:997:SER:OG	1:A:1003:ILE:HG22	2.08	0.53
1:A:1306:ARG:HA	1:A:1309:TYR:HB3	1.91	0.53
2:B:985:LEU:HD12	2:B:988:ALA:HB3	1.90	0.53
4:D:47:LEU:HA	4:D:50:LEU:HD12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:60:VAL:HA	11:K:81:THR:HG22	1.91	0.53
1:M:844:ARG:HD2	2:N:995:ASN:ND2	2.23	0.53
2:N:312:ARG:NH1	2:N:322:THR:O	2.40	0.53
2:N:505:CYS:SG	2:N:683:SER:N	2.77	0.53
2:N:891:ARG:CD	3:O:99:GLN:HG2	2.38	0.53
6:R:72:THR:O	6:R:126:ARG:NH1	2.30	0.53
9:U:24:TRP:HA	9:U:36:SER:OG	2.08	0.53
9:U:24:TRP:NE1	9:U:34:TYR:O	2.41	0.53
10:V:67:LYS:HG3	12:X:28:GLY:O	2.09	0.53
1:A:13:SER:HA	1:A:1656:ASP:O	2.08	0.53
1:A:80:ILE:HD11	1:A:395:LEU:HD13	1.90	0.53
1:A:219:TYR:HH	1:A:347:TYR:HH	1.56	0.53
1:A:1309:TYR:OH	1:A:1315:VAL:HG23	2.09	0.53
2:B:154:LEU:HD22	2:B:158:GLU:HG3	1.90	0.53
2:B:763:TYR:CE2	2:B:922:PRO:HD3	2.44	0.53
8:H:108:HIS:ND1	8:H:108:HIS:O	2.42	0.53
11:K:51:ARG:HG3	11:K:63:CYS:SG	2.49	0.53
1:M:910:LYS:NZ	1:M:967:GLY:O	2.41	0.53
3:O:76:ILE:HA	3:O:80:GLU:HB2	1.91	0.53
3:O:167:SER:O	3:O:203:LEU:N	2.23	0.53
1:A:136:MET:HE2	5:E:187:ARG:HD2	1.91	0.53
1:A:852:GLU:HA	1:A:855:ASP:HB3	1.89	0.53
2:B:325:GLU:CD	2:B:328:ARG:HE	2.17	0.53
2:B:971:TYR:CG	2:B:977:ALA:HB2	2.44	0.53
10:J:47:ARG:NH1	10:J:48:MET:SD	2.82	0.53
1:M:326:THR:HG23	1:M:329:ARG:NH1	2.24	0.53
1:M:518:PRO:HB2	6:R:92:SER:O	2.08	0.53
1:M:1306:ARG:HA	1:M:1309:TYR:HB3	1.91	0.53
1:M:1663:ARG:HD2	1:M:1669:VAL:O	2.09	0.53
2:N:279:THR:HG23	9:U:46:THR:HG22	1.91	0.53
3:O:86:PHE:CD2	3:O:215:ALA:HB2	2.44	0.53
3:O:204:ARG:HB2	10:V:63:ASN:HD21	1.74	0.53
1:A:743:GLY:HA2	1:A:746:ILE:HD12	1.90	0.53
1:A:1062:HIS:CB	1:A:1066:ASP:HB3	2.36	0.53
1:A:1478:LYS:HG3	1:A:1495:VAL:HG23	1.90	0.53
2:B:372:PRO:HB2	2:B:499:GLU:OE1	2.08	0.53
2:B:919:VAL:HB	3:C:78:ILE:HD13	1.91	0.53
3:C:167:SER:O	3:C:203:LEU:N	2.23	0.53
3:C:247:GLU:HA	3:C:273:LYS:O	2.09	0.53
3:C:288:GLU:OE2	3:C:291:ARG:NH2	2.40	0.53
8:H:66:PRO:O	8:H:70:GLU:HG2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:31:GLU:OE1	10:J:31:GLU:N	2.33	0.53
1:M:113:LYS:HB3	1:M:230:ASN:HD21	1.74	0.53
1:M:731:PRO:O	1:M:745:GLN:NE2	2.42	0.53
1:M:1005:PRO:HG3	2:N:969:PHE:CG	2.44	0.53
1:M:1075:HIS:HB2	1:M:1182:ARG:NH2	2.24	0.53
2:N:901:LYS:HB2	2:N:1021:LEU:HD22	1.89	0.53
2:N:1163:THR:HG22	2:N:1168:LYS:HG2	1.89	0.53
5:Q:106:TYR:O	5:Q:131:GLN:HB2	2.09	0.53
2:B:514:PRO:HA	2:B:517:LEU:HD12	1.91	0.52
1:M:852:GLU:HA	1:M:855:ASP:HB3	1.89	0.52
1:M:1151:LYS:HG3	1:M:1152:ASN:N	2.22	0.52
2:N:107:ARG:NH1	2:N:721:ARG:HH22	2.06	0.52
2:N:1085:GLN:HB3	2:N:1148:LEU:HD21	1.90	0.52
7:S:57:LEU:O	7:S:59:LYS:HG3	2.08	0.52
1:A:504:GLY:HA2	1:A:622:ARG:O	2.09	0.52
1:A:637:CYS:O	1:A:641:ASN:N	2.42	0.52
1:A:1663:ARG:HD2	1:A:1669:VAL:O	2.09	0.52
3:C:77:LEU:HD11	3:C:323:LEU:HB3	1.91	0.52
2:N:509:THR:CG2	2:N:516:GLY:H	2.23	0.52
2:N:733:GLN:HB2	10:V:51:THR:O	2.10	0.52
2:N:809:HIS:NE2	12:X:36:LYS:HE3	2.23	0.52
10:V:24:LEU:O	10:V:28:ASP:HB2	2.08	0.52
1:A:28:SER:O	2:B:1116:ARG:NH2	2.42	0.52
3:C:76:ILE:HA	3:C:80:GLU:HB2	1.91	0.52
5:E:177:ASP:OD1	5:E:179:VAL:HG22	2.09	0.52
6:F:69:ARG:HD2	6:F:136:TRP:NE1	2.25	0.52
8:H:70:GLU:HG3	8:H:71:ALA:N	2.24	0.52
1:M:401:ILE:HG13	1:M:437:LEU:HD13	1.91	0.52
1:M:639:SER:HA	1:M:682:LEU:HD11	1.91	0.52
1:M:880:SER:OG	1:M:882:ASP:OD1	2.20	0.52
2:N:217:CYS:SG	2:N:337:VAL:HG22	2.49	0.52
2:N:286:GLU:HB2	9:U:7:LEU:HD11	1.91	0.52
2:N:325:GLU:CD	2:N:328:ARG:HE	2.17	0.52
2:N:842:ASP:OD1	2:N:843:PRO:HD2	2.08	0.52
4:P:54:LEU:O	4:P:58:LYS:HG2	2.08	0.52
5:Q:71:THR:HG23	5:Q:99:HIS:HD2	1.73	0.52
5:Q:96:ASP:OD2	5:Q:97:HIS:ND1	2.43	0.52
5:Q:147:LYS:HE3	5:Q:149:ILE:HD11	1.91	0.52
8:T:108:HIS:O	8:T:108:HIS:ND1	2.42	0.52
11:W:21:LYS:HG3	11:W:22:ILE:HG23	1.91	0.52
1:A:66:CYS:HB3	1:A:76:HIS:CE1	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:722:GLY:O	1:A:724:TYR:HD1	1.92	0.52
2:B:523:ARG:HE	2:B:745:TYR:HE2	1.58	0.52
11:K:21:LYS:HG3	11:K:22:ILE:HG23	1.92	0.52
1:M:611:LEU:HD23	1:M:1204:GLU:HA	1.91	0.52
1:M:1522:PRO:O	1:M:1548:ASN:ND2	2.42	0.52
2:N:728:ARG:HH22	3:O:99:GLN:NE2	2.08	0.52
2:N:985:LEU:HD12	2:N:988:ALA:HB3	1.90	0.52
2:B:91:SER:O	7:S:132:GLU:HG3	2.09	0.52
2:B:1060:GLU:OE1	2:B:1060:GLU:N	2.36	0.52
2:B:1163:THR:HG22	2:B:1168:LYS:HG2	1.90	0.52
3:C:246:ILE:HD12	3:C:251:ALA:HA	1.91	0.52
5:E:96:ASP:OD2	5:E:97:HIS:ND1	2.43	0.52
7:S:58:GLU:OE2	7:S:60:SER:N	2.43	0.52
11:W:60:VAL:HA	11:W:81:THR:HG22	1.91	0.52
1:A:109:PHE:CZ	1:A:335:LEU:HD21	2.45	0.52
1:A:326:THR:HG23	1:A:329:ARG:NH1	2.24	0.52
2:B:217:CYS:SG	2:B:337:VAL:HG22	2.49	0.52
3:C:114:ALA:HB2	3:C:191:ILE:HG23	1.91	0.52
5:E:180:ALA:HA	5:E:185:LEU:HD12	1.90	0.52
1:M:218:PHE:O	1:M:222:ILE:HG23	2.10	0.52
1:M:481:GLY:HA2	2:N:1057:GLY:HA3	1.91	0.52
1:M:722:GLY:O	1:M:724:TYR:HD1	1.92	0.52
1:M:1279:VAL:HG23	9:U:53:PHE:CE2	2.45	0.52
2:N:523:ARG:HE	2:N:745:TYR:HE2	1.58	0.52
2:N:755:ASN:OD1	2:N:1017:TYR:HD1	1.93	0.52
1:A:106:CYS:SG	1:A:231:CYS:N	2.83	0.52
2:B:509:THR:CG2	2:B:516:GLY:H	2.23	0.52
2:B:715:GLY:HA2	2:B:750:TYR:CE1	2.45	0.52
1:M:109:PHE:CZ	1:M:335:LEU:HD21	2.45	0.52
1:M:634:TYR:O	1:M:637:CYS:N	2.38	0.52
2:N:836:ILE:HD13	12:X:56:ARG:HE	1.75	0.52
2:N:1032:ARG:HH12	2:N:1035:GLY:HA3	1.75	0.52
6:R:69:ARG:HD2	6:R:136:TRP:NE1	2.25	0.52
7:S:98:PRO:HD3	7:S:124:PHE:CE2	2.45	0.52
8:T:13:VAL:HB	8:T:52:ASP:N	2.25	0.52
1:A:401:ILE:HG13	1:A:437:LEU:HD13	1.91	0.52
1:A:639:SER:HA	1:A:682:LEU:HD11	1.91	0.52
2:B:613:TYR:CE2	2:B:615:PRO:HG3	2.45	0.52
2:B:742:HIS:NE2	2:B:747:LEU:HB3	2.25	0.52
3:C:122:PHE:HA	3:C:137:ASP:OD1	2.10	0.52
8:H:14:THR:OG1	8:H:28:THR:O	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:12:LYS:HB3	2:N:1172:GLU:OE2	2.10	0.52
1:M:98:LEU:HD23	1:M:360:PHE:HE2	1.73	0.52
1:M:545:GLN:HE21	1:M:549:GLY:HA2	1.75	0.52
1:M:1038:LYS:HG2	1:M:1638:PHE:HD2	1.74	0.52
1:M:1282:THR:OG1	1:M:1298:ALA:O	2.28	0.52
2:N:245:LYS:HG2	2:N:450:THR:HA	1.91	0.52
1:A:475:PHE:HE2	1:A:1636:MET:HB3	1.75	0.52
1:M:902:LEU:HD22	1:M:968:ARG:HH21	1.74	0.52
2:N:514:PRO:HA	2:N:517:LEU:HD12	1.91	0.52
3:O:89:VAL:N	12:X:59:GLN:HE22	2.07	0.52
3:O:109:LEU:HD23	3:O:225:LYS:HB3	1.92	0.52
3:O:247:GLU:HA	3:O:273:LYS:O	2.10	0.52
5:Q:60:TYR:HB2	5:Q:72:ILE:O	2.10	0.52
8:T:66:PRO:O	8:T:70:GLU:HG2	2.09	0.52
11:W:51:ARG:HG3	11:W:63:CYS:SG	2.49	0.52
1:A:576:LEU:HD23	1:A:579:SER:HA	1.92	0.52
1:A:731:PRO:O	1:A:745:GLN:NE2	2.42	0.52
1:A:1075:HIS:HB2	1:A:1182:ARG:NH2	2.24	0.52
3:C:285:VAL:O	3:C:287:ARG:HG3	2.10	0.52
5:E:60:TYR:HB2	5:E:72:ILE:O	2.10	0.52
7:G:98:PRO:HD3	7:G:124:PHE:CE2	2.45	0.52
1:M:743:GLY:HA2	1:M:746:ILE:HD12	1.91	0.52
3:O:246:ILE:HD12	3:O:251:ALA:HA	1.91	0.52
7:S:7:TYR:HD2	7:S:82:SER:HB3	1.73	0.52
7:S:10:THR:HG22	7:S:77:ASP:HB3	1.92	0.52
1:A:560:GLU:HG2	3:O:90:TYR:CE1	2.44	0.51
1:A:893:GLU:HB2	1:A:985:TYR:CZ	2.44	0.51
7:G:99:SER:HA	7:G:115:ARG:HH11	1.75	0.51
8:H:13:VAL:HB	8:H:52:ASP:N	2.25	0.51
9:I:10:CYS:SG	9:I:11:SER:N	2.83	0.51
12:L:22:TYR:HD2	12:L:51:LYS:HA	1.75	0.51
1:M:88:HIS:CE1	1:M:90:LEU:HB2	2.45	0.51
3:O:48:VAL:HG11	11:W:109:PHE:CD1	2.40	0.51
3:O:140:VAL:HA	3:O:213:ALA:O	2.11	0.51
9:U:10:CYS:SG	9:U:11:SER:N	2.83	0.51
9:U:25:THR:HG21	9:U:39:PHE:HZ	1.75	0.51
1:A:113:LYS:HE2	1:A:179:MET:HE1	1.91	0.51
2:B:689:THR:HB	2:B:692:SER:HB3	1.93	0.51
1:M:6:PRO:HA	7:S:69:PHE:HE2	1.74	0.51
1:M:634:TYR:CZ	2:N:768:MET:HB2	2.45	0.51
1:M:637:CYS:O	1:M:641:ASN:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:1128:THR:N	7:S:84:LYS:HZ1	2.08	0.51
4:P:56:TYR:CD1	7:S:106:LEU:HA	2.46	0.51
5:Q:177:ASP:OD1	5:Q:179:VAL:HG22	2.09	0.51
1:A:110:LYS:HB2	1:A:225:ARG:HB2	1.91	0.51
1:A:611:LEU:HD23	1:A:1204:GLU:HA	1.91	0.51
1:A:797:ASP:H	1:A:800:SER:HG	1.56	0.51
3:C:204:ARG:H	3:C:207:GLN:HE21	1.55	0.51
7:G:58:GLU:OE2	7:G:60:SER:N	2.43	0.51
9:I:25:THR:HG21	9:I:39:PHE:HZ	1.75	0.51
1:M:110:LYS:HB2	1:M:225:ARG:HB2	1.91	0.51
2:N:39:LEU:HD11	2:N:385:GLY:HA3	1.92	0.51
2:N:613:TYR:CE2	2:N:615:PRO:HG3	2.45	0.51
2:N:763:TYR:CE2	2:N:922:PRO:HD3	2.44	0.51
2:N:928:MET:HB3	10:V:42:ARG:HD3	1.91	0.51
1:A:88:HIS:CE1	1:A:90:LEU:HB2	2.46	0.51
1:A:513:LEU:HD22	1:A:597:VAL:HG11	1.92	0.51
1:A:634:TYR:O	1:A:637:CYS:N	2.38	0.51
1:A:733:ALA:O	8:H:77:TYR:N	2.43	0.51
3:C:111:PRO:HB3	10:J:6:ARG:HH21	1.75	0.51
3:C:140:VAL:HA	3:C:213:ALA:O	2.11	0.51
5:E:147:LYS:HE3	5:E:149:ILE:HD11	1.91	0.51
1:M:715:ALA:O	1:M:827:VAL:HG23	2.11	0.51
1:M:826:SER:O	1:M:829:SER:OG	2.21	0.51
2:N:9:GLU:HG3	10:V:22:LEU:HD21	1.91	0.51
2:N:232:LEU:HD23	2:N:238:MET:HG2	1.92	0.51
2:N:354:ARG:HH12	2:N:358:ALA:HB2	1.76	0.51
2:N:689:THR:HB	2:N:692:SER:HB3	1.93	0.51
3:O:77:LEU:HD11	3:O:323:LEU:HB3	1.91	0.51
6:R:100:ASP:N	6:R:100:ASP:OD1	2.42	0.51
1:A:545:GLN:HE21	1:A:549:GLY:HA2	1.75	0.51
1:A:1126:ASP:OD2	5:E:204:ASN:HB2	2.10	0.51
2:B:312:ARG:NH1	2:B:322:THR:O	2.40	0.51
2:B:877:ASP:OD1	2:B:881:SER:OG	2.18	0.51
5:E:128:GLU:HA	5:E:129:THR:OG1	2.10	0.51
5:E:128:GLU:OE2	5:E:184:GLY:HA2	2.11	0.51
1:M:113:LYS:HE2	1:M:179:MET:HE1	1.91	0.51
1:M:504:GLY:HA2	1:M:622:ARG:O	2.09	0.51
1:M:680:ASP:N	1:M:680:ASP:OD2	2.44	0.51
1:M:998:ARG:NE	1:M:1000:LEU:HD23	2.26	0.51
1:M:1674:THR:HB	6:R:82:ARG:HB2	1.91	0.51
2:N:999:TYR:HB3	2:N:1004:GLY:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:Q:128:GLU:OE2	5:Q:184:GLY:HA2	2.11	0.51
8:T:70:GLU:HG3	8:T:71:ALA:N	2.24	0.51
1:A:605:LEU:HD12	1:A:619:HIS:ND1	2.26	0.51
2:B:39:LEU:HD11	2:B:385:GLY:HA3	1.92	0.51
2:B:191:ASN:ND2	2:B:218:VAL:HG12	2.24	0.51
2:B:562:GLN:HB2	2:B:626:TYR:HD1	1.76	0.51
2:B:882:GLU:OE1	2:B:882:GLU:N	2.43	0.51
3:C:140:VAL:HG23	3:C:177:LYS:HB2	1.93	0.51
8:H:47:TYR:CD1	8:H:74:TYR:HB2	2.46	0.51
1:M:106:CYS:SG	1:M:231:CYS:N	2.83	0.51
1:M:374:PRO:O	1:M:385:ASN:ND2	2.44	0.51
1:M:1245:PRO:O	1:M:1546:GLY:N	2.42	0.51
2:N:40:THR:HG23	2:N:41:ASN:H	1.75	0.51
2:N:123:TRP:NE1	2:N:422:LEU:HG	2.22	0.51
8:T:82:ARG:HB3	8:T:94:TYR:HB2	1.93	0.51
1:A:1642:CYS:SG	1:A:1643:HIS:N	2.83	0.51
2:B:4:GLN:HB3	2:B:7:GLU:HB2	1.93	0.51
3:C:51:THR:OG1	3:C:59:VAL:O	2.23	0.51
3:C:109:LEU:HD23	3:C:225:LYS:HB3	1.92	0.51
6:F:100:ASP:OD1	6:F:100:ASP:N	2.42	0.51
7:G:10:THR:HG22	7:G:77:ASP:HB3	1.92	0.51
11:K:20:GLU:HB3	11:K:23:ILE:HD11	1.93	0.51
1:M:841:PHE:O	2:N:761:ILE:HD12	2.11	0.51
1:M:1642:CYS:SG	1:M:1643:HIS:N	2.83	0.51
2:N:271:ILE:HD13	2:N:353:ILE:HG23	1.92	0.51
2:N:290:ARG:HD3	9:U:16:LEU:HD22	1.93	0.51
3:O:122:PHE:HA	3:O:137:ASP:OD1	2.10	0.51
3:O:285:VAL:O	3:O:287:ARG:HG3	2.10	0.51
1:A:328:VAL:HA	1:A:331:HIS:ND1	2.26	0.51
2:B:271:ILE:HD13	2:B:353:ILE:HG23	1.92	0.51
2:B:354:ARG:HH12	2:B:358:ALA:HB2	1.76	0.51
2:B:653:GLU:N	2:B:653:GLU:OE1	2.44	0.51
2:B:755:ASN:OD1	2:B:1017:TYR:HD1	1.93	0.51
2:B:1032:ARG:HH12	2:B:1035:GLY:HA3	1.75	0.51
2:B:1043:GLN:HE21	2:B:1154:VAL:HG21	1.76	0.51
3:C:246:ILE:HD11	3:C:275:ALA:HB3	1.93	0.51
1:M:471:LYS:NZ	1:M:476:ARG:HH21	2.07	0.51
2:N:562:GLN:HB2	2:N:626:TYR:HD1	1.76	0.51
2:B:40:THR:HG23	2:B:41:ASN:H	1.75	0.51
2:B:767:ASP:HA	2:B:771:ALA:HB3	1.93	0.51
2:N:742:HIS:NE2	2:N:747:LEU:HB3	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:ALA:HA	1:A:597:VAL:HG22	1.93	0.51
1:A:1522:PRO:O	1:A:1548:ASN:ND2	2.42	0.51
1:A:1642:CYS:O	1:A:1646:THR:HG23	2.10	0.51
2:B:24:ASP:HA	2:B:27:LYS:HE2	1.92	0.51
2:B:245:LYS:HG2	2:B:450:THR:HA	1.91	0.51
3:C:223:HIS:CD2	3:C:225:LYS:HG2	2.46	0.51
1:M:605:LEU:HD12	1:M:619:HIS:ND1	2.26	0.51
1:M:613:LYS:HG2	1:M:614:PRO:HD3	1.93	0.51
2:N:163:LYS:HB3	2:N:720:TYR:CD1	2.46	0.51
2:N:191:ASN:ND2	2:N:218:VAL:HG12	2.24	0.51
2:N:818:PRO:O	2:N:822:TRP:HB2	2.11	0.51
3:O:140:VAL:HG23	3:O:177:LYS:HB2	1.93	0.51
5:Q:143:GLU:HB2	5:Q:144:LEU:HD12	1.92	0.51
12:X:22:TYR:HD2	12:X:51:LYS:HA	1.75	0.51
1:A:19:TYR:O	2:B:1166:ASN:ND2	2.42	0.50
1:A:182:ARG:O	1:A:186:VAL:HG23	2.11	0.50
1:A:218:PHE:O	1:A:222:ILE:HG23	2.10	0.50
1:A:715:ALA:O	1:A:827:VAL:HG23	2.11	0.50
1:A:1073:GLN:HA	1:A:1076:LEU:HG	1.92	0.50
2:B:999:TYR:HB3	2:B:1004:GLY:O	2.11	0.50
7:G:10:THR:HA	7:G:77:ASP:HA	1.92	0.50
1:M:107:HIS:O	1:M:338:LYS:HD2	2.11	0.50
2:N:547:ASP:OD1	2:N:547:ASP:N	2.43	0.50
3:O:37:TRP:NE1	11:W:97:ASP:HB3	2.26	0.50
5:Q:128:GLU:HA	5:Q:129:THR:OG1	2.10	0.50
2:B:415:ASP:OD2	2:B:417:SER:OG	2.22	0.50
2:B:502:GLY:N	2:B:681:VAL:HG23	2.26	0.50
3:C:266:GLU:HB2	3:C:274:GLN:HB2	1.93	0.50
5:E:8:ILE:HG13	5:E:41:PHE:HE2	1.76	0.50
1:M:576:LEU:HD23	1:M:579:SER:HA	1.92	0.50
2:N:1043:GLN:HE21	2:N:1154:VAL:HG21	1.76	0.50
2:N:1112:GLU:CD	2:N:1114:ARG:HH22	2.19	0.50
5:Q:8:ILE:HG13	5:Q:41:PHE:HE2	1.76	0.50
7:S:51:TYR:HA	7:S:77:ASP:O	2.11	0.50
1:A:129:GLY:HA2	1:A:207:LEU:HD21	1.94	0.50
1:A:239:ARG:HD2	1:A:240:LYS:O	2.11	0.50
1:A:559:ILE:O	1:A:563:THR:OG1	2.22	0.50
1:A:613:LYS:HG2	1:A:614:PRO:HD3	1.93	0.50
1:A:998:ARG:NE	1:A:1000:LEU:HD23	2.26	0.50
2:B:1112:GLU:CD	2:B:1114:ARG:HH22	2.19	0.50
3:C:259:PRO:O	3:C:262:VAL:HG12	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:66:CYS:HB3	1:M:76:HIS:CE1	2.43	0.50
1:M:475:PHE:HA	1:M:479:MET:HB3	1.93	0.50
1:M:1238:ALA:HB1	1:M:1618:TYR:HE2	1.76	0.50
1:M:1642:CYS:O	1:M:1646:THR:HG23	2.10	0.50
2:N:208:TYR:OH	2:N:238:MET:HG3	2.11	0.50
8:T:47:TYR:CD1	8:T:74:TYR:HB2	2.46	0.50
8:T:109:ARG:C	8:T:111:LEU:H	2.20	0.50
1:A:212:LYS:HD3	1:A:1628:TYR:CE1	2.44	0.50
1:A:372:PHE:HE1	2:B:1157:TYR:HA	1.74	0.50
1:A:687:GLN:HG2	1:A:688:ASP:H	1.75	0.50
1:A:1154:ASP:N	1:A:1154:ASP:OD1	2.45	0.50
1:A:1574:ARG:HG2	1:A:1575:ILE:HG23	1.93	0.50
1:A:1579:GLU:HB3	5:E:146:PRO:HD2	1.92	0.50
2:B:232:LEU:HD23	2:B:238:MET:HG2	1.92	0.50
2:B:818:PRO:O	2:B:822:TRP:HB2	2.11	0.50
7:G:51:TYR:HA	7:G:77:ASP:O	2.11	0.50
7:G:98:PRO:HB3	7:G:124:PHE:CB	2.42	0.50
1:M:67:HIS:CG	2:N:1102:ILE:HD11	2.46	0.50
1:M:1038:LYS:NZ	1:M:1626:ILE:HA	2.27	0.50
1:M:1615:GLU:HG3	1:M:1617:GLY:H	1.76	0.50
2:N:4:GLN:HB3	2:N:7:GLU:HB2	1.93	0.50
2:N:205:GLY:O	2:N:207:SER:N	2.44	0.50
2:N:502:GLY:N	2:N:681:VAL:HG23	2.26	0.50
5:Q:130:PHE:HE1	5:Q:181:ARG:HG3	1.77	0.50
1:A:106:CYS:HA	1:A:231:CYS:CB	2.39	0.50
1:A:374:PRO:O	1:A:385:ASN:ND2	2.44	0.50
1:A:581:TYR:CE2	2:B:1110:ALA:HB2	2.47	0.50
1:A:1481:ASP:HB2	1:A:1491:THR:HB	1.93	0.50
2:B:205:GLY:O	2:B:207:SER:N	2.44	0.50
5:E:143:GLU:HB2	5:E:144:LEU:HD12	1.92	0.50
1:M:182:ARG:O	1:M:186:VAL:HG23	2.11	0.50
1:M:687:GLN:HG2	1:M:688:ASP:H	1.75	0.50
2:N:505:CYS:HB2	2:N:683:SER:HB2	1.93	0.50
2:N:715:GLY:HA2	2:N:750:TYR:CE1	2.45	0.50
3:O:223:HIS:CD2	3:O:225:LYS:HG2	2.46	0.50
10:V:43:TYR:HA	10:V:46:ARG:HB3	1.94	0.50
1:A:368:PRO:HD2	1:A:373:ARG:HD3	1.93	0.50
1:A:1282:THR:OG1	1:A:1298:ALA:O	2.28	0.50
2:B:91:SER:OG	7:S:132:GLU:HG2	2.11	0.50
2:B:180:LYS:NZ	2:B:463:VAL:HB	2.26	0.50
2:B:492:THR:OG1	2:B:493:VAL:N	2.33	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:991:ASN:OD1	2:B:992:TYR:N	2.44	0.50
5:E:132:GLU:C	5:E:134:ASP:H	2.20	0.50
8:H:109:ARG:C	8:H:111:LEU:H	2.20	0.50
2:N:502:GLY:H	2:N:681:VAL:HG23	1.76	0.50
5:Q:131:GLN:HE21	5:Q:134:ASP:HB2	1.76	0.50
6:R:134:GLU:OE1	6:R:134:GLU:N	2.45	0.50
1:A:744:LYS:HA	1:A:791:LEU:HD23	1.94	0.50
3:C:122:PHE:HE2	3:C:125:PRO:HD3	1.77	0.50
5:E:131:GLN:HE21	5:E:134:ASP:HB2	1.76	0.50
7:G:135:ARG:NH2	7:G:145:GLU:OE1	2.45	0.50
10:J:3:ILE:HD11	10:J:49:ILE:HG22	1.92	0.50
1:M:475:PHE:HE2	1:M:1636:MET:HB3	1.75	0.50
1:M:1073:GLN:HA	1:M:1076:LEU:HG	1.92	0.50
1:M:1574:ARG:HG2	1:M:1575:ILE:HG23	1.93	0.50
2:N:99:ARG:NH2	12:X:47:ARG:NH1	2.59	0.50
3:O:259:PRO:O	3:O:262:VAL:HG12	2.12	0.50
7:S:10:THR:HA	7:S:77:ASP:HA	1.92	0.50
7:S:62:LYS:C	7:S:70:SER:HG	2.15	0.50
7:S:98:PRO:HB3	7:S:124:PHE:CB	2.42	0.50
1:A:483:ARG:HA	2:B:1054:ILE:O	2.10	0.50
1:A:1086:TYR:HD1	1:A:1178:LEU:HD22	1.77	0.50
1:A:1238:ALA:HB1	1:A:1618:TYR:HE2	1.76	0.50
1:A:1550:LYS:HA	1:A:1553:TRP:CD1	2.46	0.50
2:B:547:ASP:N	2:B:547:ASP:OD1	2.43	0.50
2:B:876:ASN:CG	2:B:884:GLN:HB2	2.37	0.50
7:G:145:GLU:OE2	7:G:148:LYS:NZ	2.45	0.50
1:M:106:CYS:HA	1:M:231:CYS:CB	2.39	0.50
1:M:510:ALA:HA	1:M:597:VAL:HG22	1.94	0.50
1:M:513:LEU:HD22	1:M:597:VAL:HG11	1.93	0.50
1:M:1052:ARG:NH1	1:M:1056:GLY:O	2.45	0.50
2:N:24:ASP:HA	2:N:27:LYS:HE2	1.92	0.50
2:N:577:LYS:HB2	2:N:613:TYR:CZ	2.47	0.50
2:N:767:ASP:HA	2:N:771:ALA:HB3	1.93	0.50
2:N:801:ARG:HG2	2:N:802:ARG:N	2.27	0.50
2:N:991:ASN:OD1	2:N:992:TYR:N	2.44	0.50
1:A:680:ASP:OD2	1:A:680:ASP:N	2.44	0.50
1:A:759:ARG:NH2	1:A:815:LEU:O	2.45	0.50
1:A:1549:LEU:HA	1:A:1552:ILE:HG12	1.94	0.50
2:B:208:TYR:OH	2:B:238:MET:HG3	2.11	0.50
2:B:505:CYS:SG	2:B:683:SER:N	2.77	0.50
7:G:113:ILE:HG21	7:G:170:LEU:HG	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:3:ILE:HD13	10:J:18:TRP:HB2	1.94	0.50
1:M:328:VAL:HA	1:M:331:HIS:ND1	2.26	0.50
1:M:1244:THR:O	1:M:1566:THR:HG21	2.12	0.50
2:N:876:ASN:CG	2:N:884:GLN:HB2	2.37	0.50
10:V:3:ILE:HD11	10:V:49:ILE:HG22	1.92	0.50
1:A:1045:VAL:HB	1:A:1191:GLY:H	1.76	0.49
1:A:1052:ARG:HG2	1:A:1058:ILE:HA	1.94	0.49
2:B:502:GLY:H	2:B:681:VAL:HG23	1.76	0.49
5:E:136:ILE:HG13	5:E:137:VAL:HG13	1.94	0.49
10:J:43:TYR:HA	10:J:46:ARG:HB3	1.94	0.49
1:M:739:ILE:HD12	1:M:741:TRP:CH2	2.47	0.49
1:M:763:ASN:ND2	1:M:1084:LYS:HG3	2.27	0.49
1:M:1277:ARG:HB3	1:M:1302:ASP:HB3	1.94	0.49
1:M:1679:ILE:HD12	6:R:83:ILE:HG12	1.93	0.49
2:N:180:LYS:NZ	2:N:463:VAL:HB	2.26	0.49
2:N:583:LEU:HD23	2:N:611:ILE:HG12	1.94	0.49
2:N:653:GLU:OE1	2:N:653:GLU:N	2.44	0.49
2:N:683:SER:OG	2:N:684:ILE:N	2.45	0.49
8:T:9:GLU:HB2	8:T:11:PHE:CE2	2.47	0.49
1:A:545:GLN:OE1	1:A:592:LYS:HD2	2.12	0.49
1:A:701:THR:CG2	1:A:743:GLY:H	2.25	0.49
1:A:763:ASN:ND2	1:A:1084:LYS:HG3	2.27	0.49
1:A:1244:THR:O	1:A:1566:THR:HG21	2.12	0.49
1:A:1615:GLU:HG3	1:A:1617:GLY:H	1.76	0.49
2:B:395:TRP:HE3	2:B:396:LEU:HD12	1.76	0.49
2:B:577:LYS:HB2	2:B:613:TYR:CZ	2.47	0.49
1:M:96:TYR:OH	1:M:100:ARG:NH2	2.33	0.49
1:M:701:THR:CG2	1:M:743:GLY:H	2.25	0.49
1:M:759:ARG:NH2	1:M:815:LEU:O	2.45	0.49
1:M:1596:TYR:HB2	1:M:1598:ILE:HG22	1.95	0.49
1:M:1672:PHE:CD1	2:N:1068:GLY:HA2	2.47	0.49
2:N:85:ALA:O	2:N:115:SER:OG	2.20	0.49
3:O:208:GLU:OE1	3:O:210:ASP:HB2	2.12	0.49
5:Q:132:GLU:C	5:Q:134:ASP:H	2.20	0.49
6:R:109:GLN:HG2	6:R:112:MET:HE2	1.94	0.49
1:A:1596:TYR:HB2	1:A:1598:ILE:HG22	1.94	0.49
2:B:589:GLU:O	2:B:592:VAL:HG12	2.13	0.49
5:E:118:ILE:O	5:E:122:THR:HG23	2.12	0.49
1:M:483:ARG:HA	2:N:1054:ILE:O	2.12	0.49
1:M:1065:GLU:O	1:M:1067:SER:N	2.46	0.49
2:N:48:ALA:O	2:N:52:ILE:HG13	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:125:VAL:HG23	2:N:129:PRO:HG3	1.94	0.49
2:N:849:ASP:HB3	2:N:852:THR:OG1	2.12	0.49
6:R:125:ARG:HA	6:R:134:GLU:O	2.12	0.49
11:W:20:GLU:HB3	11:W:23:ILE:HD11	1.93	0.49
1:A:666:ILE:O	1:A:671:SER:OG	2.30	0.49
2:B:48:ALA:O	2:B:52:ILE:HG13	2.12	0.49
2:B:93:GLU:OE1	7:S:97:SER:HB2	2.12	0.49
2:B:163:LYS:HB3	2:B:720:TYR:CD1	2.46	0.49
2:B:468:ASN:ND2	2:B:710:THR:HB	2.27	0.49
2:B:822:TRP:N	2:B:822:TRP:CD1	2.80	0.49
4:D:56:TYR:CE1	7:G:106:LEU:HD23	2.47	0.49
8:H:82:ARG:HB3	8:H:94:TYR:HB2	1.93	0.49
1:M:239:ARG:HD2	1:M:240:LYS:O	2.12	0.49
1:M:666:ILE:O	1:M:671:SER:OG	2.30	0.49
1:M:1223:ASN:OD1	1:M:1224:VAL:N	2.46	0.49
3:O:238:PRO:HA	3:O:303:ARG:HA	1.95	0.49
5:Q:118:ILE:O	5:Q:122:THR:HG23	2.12	0.49
10:V:63:ASN:HB3	10:V:65:LEU:HD23	1.95	0.49
1:A:1148:TYR:HA	1:A:1151:LYS:HG2	1.93	0.49
1:A:1579:GLU:CB	5:E:146:PRO:HD2	2.42	0.49
2:B:280:PHE:O	2:B:284:ARG:HG2	2.12	0.49
2:B:335:VAL:HG23	2:B:336:LEU:N	2.28	0.49
2:B:433:ILE:O	2:B:436:LYS:N	2.44	0.49
6:F:125:ARG:HA	6:F:134:GLU:O	2.12	0.49
6:F:134:GLU:N	6:F:134:GLU:OE1	2.45	0.49
9:I:10:CYS:HB2	9:I:17:LEU:HD21	1.95	0.49
1:M:775:TRP:O	8:T:20:LYS:HD2	2.12	0.49
2:N:191:ASN:HD22	2:N:217:CYS:HA	1.78	0.49
2:N:335:VAL:HG23	2:N:336:LEU:N	2.28	0.49
2:N:468:ASN:ND2	2:N:710:THR:HB	2.27	0.49
2:N:966:SER:OG	2:N:966:SER:O	2.30	0.49
3:O:122:PHE:HE2	3:O:125:PRO:HD3	1.77	0.49
3:O:141:PHE:HB3	3:O:174:LEU:HD22	1.95	0.49
3:O:246:ILE:HD11	3:O:275:ALA:HB3	1.93	0.49
3:O:266:GLU:HB2	3:O:274:GLN:HB2	1.93	0.49
3:O:339:LYS:HZ1	11:W:92:ARG:HA	1.77	0.49
5:Q:138:ASN:HD22	5:Q:141:HIS:CE1	2.30	0.49
6:R:96:PRO:HB2	7:S:23:ARG:HH11	1.78	0.49
10:V:16:ASP:OD1	10:V:16:ASP:N	2.46	0.49
1:A:1245:PRO:O	1:A:1546:GLY:N	2.42	0.49
1:A:1277:ARG:HB3	1:A:1302:ASP:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:505:CYS:HB2	2:B:683:SER:HB2	1.93	0.49
6:F:90:GLN:HE22	6:F:122:LEU:HD11	1.78	0.49
1:M:744:LYS:HA	1:M:791:LEU:HD23	1.94	0.49
1:M:1045:VAL:HB	1:M:1191:GLY:H	1.76	0.49
1:M:1129:PRO:HD2	1:M:1133:TYR:CE1	2.48	0.49
1:M:1481:ASP:HB2	1:M:1491:THR:HB	1.93	0.49
3:O:125:PRO:HB2	3:O:129:GLN:HB2	1.95	0.49
5:Q:136:ILE:HG13	5:Q:137:VAL:HG13	1.94	0.49
6:R:90:GLN:HE22	6:R:122:LEU:HD11	1.78	0.49
7:S:85:LYS:HB3	7:S:155:ASP:C	2.38	0.49
1:A:1052:ARG:NH1	1:A:1056:GLY:O	2.45	0.49
2:B:86:LYS:HB3	2:B:150:HIS:CE1	2.48	0.49
2:B:349:LEU:O	2:B:353:ILE:HG22	2.12	0.49
4:D:17:LEU:HD21	7:G:6:LEU:O	2.12	0.49
5:E:130:PHE:HE1	5:E:181:ARG:HG3	1.77	0.49
1:M:368:PRO:HD2	1:M:373:ARG:HD3	1.93	0.49
1:M:746:ILE:O	1:M:749:SER:OG	2.22	0.49
1:M:1052:ARG:HG2	1:M:1058:ILE:HA	1.94	0.49
1:A:67:HIS:CG	2:B:1102:ILE:HD11	2.47	0.49
1:A:739:ILE:HD12	1:A:741:TRP:CH2	2.47	0.49
1:A:1038:LYS:NZ	1:A:1626:ILE:HA	2.27	0.49
1:A:1672:PHE:CD1	2:B:1068:GLY:HA2	2.47	0.49
2:B:849:ASP:HB3	2:B:852:THR:OG1	2.12	0.49
3:C:318:MET:HB2	3:C:323:LEU:HD22	1.94	0.49
6:F:109:GLN:HG2	6:F:112:MET:HE2	1.94	0.49
10:J:63:ASN:HB3	10:J:65:LEU:HD23	1.94	0.49
2:N:86:LYS:HB3	2:N:150:HIS:CE1	2.48	0.49
2:N:108:GLU:HG2	12:X:48:VAL:HG11	1.94	0.49
2:N:163:LYS:HD2	2:N:720:TYR:CD2	2.48	0.49
2:N:395:TRP:HE3	2:N:396:LEU:HD12	1.77	0.49
2:N:589:GLU:O	2:N:592:VAL:HG12	2.13	0.49
2:N:672:THR:HG23	2:N:673:HIS:ND1	2.27	0.49
7:S:113:ILE:HG21	7:S:170:LEU:HG	1.94	0.49
7:S:135:ARG:NH2	7:S:145:GLU:OE1	2.45	0.49
8:T:78:GLY:HA3	8:T:97:PHE:HD1	1.78	0.49
1:M:227:GLN:OE1	1:M:227:GLN:N	2.46	0.49
1:M:952:ASN:CG	2:N:943:MET:HE1	2.37	0.49
1:M:1148:TYR:HA	1:M:1151:LYS:HG2	1.94	0.49
1:A:96:TYR:OH	1:A:100:ARG:NH2	2.33	0.49
1:A:853:GLN:HA	1:A:856:ASN:HD21	1.77	0.49
2:B:503:PHE:HE1	2:B:636:ARG:HB3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:78:GLY:HA3	8:H:97:PHE:HD1	1.78	0.49
1:M:129:GLY:HA2	1:M:207:LEU:HD21	1.94	0.49
1:M:1306:ARG:NH2	1:M:1317:GLN:HG2	2.20	0.49
2:N:466:LYS:HE2	2:N:472:PHE:CE1	2.48	0.49
2:N:634:MET:HE3	2:N:651:PRO:HG3	1.94	0.49
2:N:742:HIS:CE1	2:N:747:LEU:HB3	2.48	0.49
3:O:51:THR:OG1	3:O:59:VAL:O	2.23	0.49
9:U:35:PRO:HB2	9:U:38:GLN:HG3	1.95	0.49
1:A:475:PHE:HA	1:A:479:MET:HB3	1.93	0.48
1:A:1065:GLU:O	1:A:1067:SER:N	2.46	0.48
2:B:156:PRO:O	2:B:160:ILE:HG12	2.13	0.48
2:B:163:LYS:HD2	2:B:720:TYR:CD2	2.48	0.48
2:B:583:LEU:HD23	2:B:611:ILE:HG12	1.94	0.48
2:B:772:MET:SD	2:B:902:PHE:HB2	2.53	0.48
1:M:212:LYS:HD3	1:M:1628:TYR:CE1	2.44	0.48
1:M:1086:TYR:HD1	1:M:1178:LEU:HD22	1.77	0.48
1:M:1585:ILE:HD11	1:M:1609:ALA:HA	1.95	0.48
2:N:156:PRO:O	2:N:160:ILE:HG12	2.13	0.48
2:N:280:PHE:O	2:N:284:ARG:HG2	2.12	0.48
2:N:776:LYS:O	2:N:780:GLU:HG3	2.13	0.48
2:N:882:GLU:OE1	2:N:882:GLU:N	2.43	0.48
3:O:51:THR:OG1	3:O:59:VAL:HG23	2.13	0.48
1:A:227:GLN:OE1	1:A:227:GLN:N	2.46	0.48
1:A:228:CYS:HB2	1:A:233:SER:H	1.78	0.48
1:A:844:ARG:HD2	2:B:995:ASN:HD21	1.77	0.48
1:A:1066:ASP:OD1	1:A:1183:TYR:OH	2.29	0.48
2:B:125:VAL:HG23	2:B:129:PRO:HG3	1.94	0.48
2:B:830:GLY:O	2:B:845:VAL:HA	2.13	0.48
3:C:125:PRO:HB2	3:C:129:GLN:HB2	1.95	0.48
5:E:131:GLN:NE2	5:E:132:GLU:O	2.46	0.48
7:G:85:LYS:HB3	7:G:155:ASP:C	2.38	0.48
8:H:9:GLU:HB2	8:H:11:PHE:CE2	2.47	0.48
1:M:228:CYS:CB	1:M:231:CYS:HB3	2.44	0.48
1:M:1154:ASP:OD1	1:M:1154:ASP:N	2.45	0.48
1:M:1256:SER:O	1:M:1260:ALA:N	2.38	0.48
2:N:509:THR:HG21	2:N:516:GLY:H	1.78	0.48
2:N:592:VAL:O	2:N:596:ASN:ND2	2.46	0.48
2:N:880:ASP:H	12:X:38:VAL:HG13	1.78	0.48
2:N:928:MET:HG3	10:V:44:CYS:HB3	1.95	0.48
3:O:145:LYS:O	3:O:208:GLU:HG2	2.13	0.48
7:S:145:GLU:OE2	7:S:148:LYS:NZ	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:U:10:CYS:HB2	9:U:17:LEU:HD21	1.95	0.48
10:V:3:ILE:HD13	10:V:18:TRP:HB2	1.94	0.48
12:X:31:ASN:ND2	12:X:42:ARG:H	2.08	0.48
1:A:112:SER:OG	1:A:114:VAL:HG12	2.13	0.48
1:A:1019:LEU:O	1:A:1022:THR:OG1	2.26	0.48
1:A:1129:PRO:HD2	1:A:1133:TYR:CE1	2.48	0.48
1:A:1520:GLU:OE1	1:A:1523:GLY:N	2.40	0.48
2:B:466:LYS:HE2	2:B:472:PHE:CE1	2.48	0.48
2:B:592:VAL:O	2:B:596:ASN:ND2	2.46	0.48
2:B:801:ARG:HG2	2:B:802:ARG:N	2.27	0.48
3:C:85:ALA:HB3	3:C:226:PHE:CE1	2.49	0.48
3:C:141:PHE:HB3	3:C:174:LEU:HD22	1.95	0.48
5:E:138:ASN:HD22	5:E:141:HIS:CE1	2.30	0.48
7:G:62:LYS:C	7:G:70:SER:HG	2.15	0.48
1:M:125:LEU:HD11	1:M:130:LEU:HD22	1.95	0.48
1:M:1549:LEU:HA	1:M:1552:ILE:HG12	1.94	0.48
2:N:825:LYS:HG3	2:N:842:ASP:OD1	2.13	0.48
2:N:830:GLY:O	2:N:845:VAL:HA	2.14	0.48
3:O:318:MET:HB2	3:O:323:LEU:HD22	1.94	0.48
1:A:1242:ILE:HG21	1:A:1567:ASN:ND2	2.27	0.48
1:A:1585:ILE:HD11	1:A:1609:ALA:HA	1.95	0.48
1:A:1624:MET:HG2	1:A:1625:GLY:N	2.28	0.48
3:C:208:GLU:OE1	3:C:210:ASP:HB2	2.12	0.48
3:C:238:PRO:HA	3:C:303:ARG:HA	1.95	0.48
1:M:112:SER:OG	1:M:114:VAL:HG12	2.13	0.48
1:M:501:ASN:HA	1:M:669:THR:HG21	1.96	0.48
1:M:545:GLN:OE1	1:M:592:LYS:HD2	2.12	0.48
1:M:1095:VAL:HG23	1:M:1096:LYS:HD2	1.95	0.48
1:M:1129:PRO:HD2	1:M:1133:TYR:HE1	1.79	0.48
1:M:1284:LYS:HB3	1:M:1296:THR:HB	1.95	0.48
2:N:479:VAL:HG12	2:N:480:HIS:N	2.29	0.48
5:Q:107:ALA:HA	5:Q:108:ASN:HA	1.60	0.48
5:Q:131:GLN:NE2	5:Q:132:GLU:O	2.47	0.48
7:S:99:SER:HA	7:S:115:ARG:HH11	1.75	0.48
8:T:80:VAL:HA	8:T:95:VAL:HA	1.95	0.48
1:A:1284:LYS:HB3	1:A:1296:THR:HB	1.95	0.48
2:B:649:LEU:HD12	2:B:653:GLU:HB2	1.95	0.48
3:C:150:ASN:HB2	3:C:165:VAL:HG13	1.95	0.48
1:M:853:GLN:HA	1:M:856:ASN:HD21	1.78	0.48
1:M:1550:LYS:HA	1:M:1553:TRP:CD1	2.46	0.48
2:N:243:TRP:HD1	2:N:244:ARG:HG2	1.72	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:649:LEU:HD12	2:N:653:GLU:HB2	1.96	0.48
2:N:772:MET:SD	2:N:902:PHE:HB2	2.53	0.48
1:A:107:HIS:O	1:A:338:LYS:HD2	2.11	0.48
1:A:241:GLU:N	1:A:245:LYS:O	2.47	0.48
1:A:1129:PRO:HD2	1:A:1133:TYR:HE1	1.78	0.48
2:B:402:GLN:NE2	2:B:428:LYS:HD3	2.29	0.48
2:B:479:VAL:HG12	2:B:480:HIS:N	2.29	0.48
2:B:742:HIS:CE1	2:B:747:LEU:HB3	2.48	0.48
2:B:801:ARG:HG2	2:B:802:ARG:H	1.79	0.48
4:D:20:ASP:O	4:D:23:SER:OG	2.31	0.48
1:M:1126:ASP:OD2	5:Q:204:ASN:HB2	2.14	0.48
1:M:1151:LYS:NZ	1:M:1152:ASN:HB3	2.28	0.48
1:M:1624:MET:HG2	1:M:1625:GLY:N	2.28	0.48
2:N:107:ARG:HH11	2:N:721:ARG:HH22	1.61	0.48
2:N:349:LEU:O	2:N:353:ILE:HG22	2.12	0.48
1:A:1339:TYR:CE2	1:A:1508:LEU:HD21	2.49	0.48
2:B:191:ASN:HD22	2:B:217:CYS:HA	1.78	0.48
2:B:266:GLU:HA	2:B:269:GLU:OE1	2.14	0.48
11:K:62:PHE:HB3	11:K:80:GLN:HB2	1.96	0.48
1:M:483:ARG:HG3	2:N:1054:ILE:C	2.39	0.48
2:N:999:TYR:CD2	2:N:1006:GLU:HB3	2.49	0.48
2:N:1159:THR:O	2:N:1163:THR:HG23	2.14	0.48
1:A:483:ARG:HG3	2:B:1054:ILE:C	2.38	0.48
1:A:711:LEU:HD23	1:A:746:ILE:HD13	1.95	0.48
1:A:1151:LYS:NZ	1:A:1152:ASN:HB3	2.28	0.48
2:B:123:TRP:HE1	2:B:422:LEU:CG	2.24	0.48
2:B:537:ILE:HB	2:B:538:PRO:HD3	1.95	0.48
2:B:604:LYS:HG3	2:B:605:VAL:HG13	1.96	0.48
3:C:145:LYS:O	3:C:208:GLU:HG2	2.14	0.48
1:M:98:LEU:O	1:M:102:THR:HG23	2.14	0.48
1:M:241:GLU:N	1:M:245:LYS:O	2.47	0.48
1:M:1040:LEU:HA	1:M:1043:LEU:HD23	1.95	0.48
1:M:1339:TYR:CE2	1:M:1508:LEU:HD21	2.49	0.48
2:N:336:LEU:HD22	2:N:338:HIS:HE1	1.79	0.48
2:N:822:TRP:N	2:N:822:TRP:CD1	2.80	0.48
5:Q:111:THR:HG23	5:Q:114:ALA:HB3	1.96	0.48
10:V:23:THR:HA	10:V:26:GLN:HB3	1.96	0.48
1:A:1123:PRO:HG2	5:E:203:TYR:HA	1.94	0.48
2:B:1100:SER:HA	2:B:1113:VAL:HG12	1.96	0.48
5:E:111:THR:HG23	5:E:114:ALA:HB3	1.96	0.48
8:H:80:VAL:HG12	8:H:117:ASP:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:35:PRO:HB2	9:I:38:GLN:HG3	1.95	0.48
1:M:850:LEU:HD13	1:M:929:LEU:HB3	1.95	0.48
2:N:55:LYS:O	2:N:76:SER:HA	2.14	0.48
2:N:266:GLU:HA	2:N:269:GLU:OE1	2.14	0.48
2:N:1060:GLU:OE1	2:N:1060:GLU:N	2.36	0.48
2:N:1082:ASP:OD1	2:N:1082:ASP:N	2.47	0.48
3:O:39:LEU:HD22	11:W:100:ASP:HB3	1.96	0.48
1:A:98:LEU:O	1:A:102:THR:HG23	2.14	0.48
2:B:634:MET:HE3	2:B:651:PRO:HG3	1.94	0.48
2:B:637:PRO:HA	2:B:647:ASP:O	2.14	0.48
2:B:966:SER:OG	2:B:966:SER:O	2.30	0.48
2:B:998:MET:SD	2:B:1013:ILE:HD11	2.54	0.48
2:B:1159:THR:O	2:B:1163:THR:HG23	2.14	0.48
1:M:228:CYS:HB2	1:M:233:SER:H	1.78	0.48
1:M:1242:ILE:HG21	1:M:1567:ASN:ND2	2.27	0.48
2:N:919:VAL:CG2	3:O:78:ILE:HG21	2.44	0.48
2:N:1100:SER:HA	2:N:1113:VAL:HG12	1.96	0.48
3:O:37:TRP:CD1	11:W:97:ASP:HB3	2.49	0.48
3:O:85:ALA:HA	3:O:112:ILE:HD12	1.96	0.48
1:A:125:LEU:HD11	1:A:130:LEU:HD22	1.95	0.47
1:A:640:TYR:CD2	1:A:649:MET:HE1	2.49	0.47
1:A:1069:ASP:OD1	1:A:1070:VAL:HG22	2.14	0.47
1:A:1205:PRO:HA	1:A:1208:GLN:HB2	1.96	0.47
1:A:1299:ILE:O	1:A:1491:THR:HA	2.14	0.47
8:H:37:ASN:O	8:H:104:ILE:HD12	2.14	0.47
10:J:16:ASP:N	10:J:16:ASP:OD1	2.46	0.47
1:M:1041:GLU:CD	2:N:1061:ARG:HH12	2.22	0.47
1:M:1046:GLN:OE1	1:M:1052:ARG:N	2.45	0.47
1:M:1309:TYR:CZ	1:M:1320:ILE:HD11	2.49	0.47
2:N:492:THR:OG1	2:N:493:VAL:N	2.33	0.47
3:O:150:ASN:HB2	3:O:165:VAL:HG13	1.95	0.47
1:A:1588:GLU:O	1:A:1592:VAL:HG23	2.15	0.47
2:B:776:LYS:O	2:B:780:GLU:HG3	2.13	0.47
8:H:74:TYR:HB3	8:H:123:LEU:HB3	1.96	0.47
8:H:80:VAL:HA	8:H:95:VAL:HA	1.95	0.47
1:M:63:CYS:HB3	1:M:66:CYS:SG	2.54	0.47
1:M:767:LYS:HD3	1:M:783:SER:HB3	1.95	0.47
1:A:1095:VAL:HG23	1:A:1096:LYS:HD2	1.95	0.47
1:A:1309:TYR:CZ	1:A:1320:ILE:HD11	2.49	0.47
2:B:75:ILE:HA	2:B:124:SER:O	2.15	0.47
2:B:683:SER:OG	2:B:684:ILE:N	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:825:LYS:HG3	2:B:842:ASP:OD1	2.14	0.47
1:M:640:TYR:CD2	1:M:649:MET:HE1	2.49	0.47
1:M:711:LEU:HD23	1:M:746:ILE:HD13	1.95	0.47
3:O:130:GLU:OE2	3:O:130:GLU:N	2.31	0.47
3:O:130:GLU:HG2	3:O:131:ALA:H	1.78	0.47
8:T:30:VAL:HB	8:T:37:ASN:HD22	1.80	0.47
1:A:118:LEU:HB2	1:A:182:ARG:NH1	2.29	0.47
1:A:407:ASP:O	1:A:411:GLU:N	2.48	0.47
1:A:1247:MET:SD	1:A:1547:VAL:HA	2.54	0.47
3:C:115:ASP:OD2	3:C:118:MET:N	2.48	0.47
3:C:130:GLU:HG2	3:C:131:ALA:H	1.78	0.47
1:M:1041:GLU:OE2	2:N:1061:ARG:NH1	2.48	0.47
1:M:1069:ASP:OD1	1:M:1070:VAL:HG22	2.14	0.47
1:M:1588:GLU:O	1:M:1592:VAL:HG23	2.15	0.47
2:N:996:GLU:N	2:N:1011:ILE:O	2.47	0.47
2:B:137:VAL:HA	2:B:431:ASN:O	2.15	0.47
2:B:336:LEU:HD22	2:B:338:HIS:HE1	1.79	0.47
2:B:420:LYS:O	2:B:423:THR:OG1	2.24	0.47
2:B:561:VAL:HG12	2:B:569:GLY:O	2.14	0.47
2:B:1130:ASP:OD1	2:B:1130:ASP:N	2.47	0.47
3:C:82:PRO:HB2	3:C:217:LEU:HD22	1.96	0.47
3:C:91:ILE:HD11	12:L:58:VAL:HB	1.97	0.47
3:C:155:THR:HG1	3:C:156:ASP:H	1.61	0.47
7:G:138:THR:HG22	7:G:142:ASN:O	2.14	0.47
1:M:1299:ILE:O	1:M:1491:THR:HA	2.14	0.47
2:N:503:PHE:HE1	2:N:636:ARG:HB3	1.78	0.47
2:N:998:MET:SD	2:N:1013:ILE:HD11	2.54	0.47
2:N:1162:LEU:HG	2:N:1167:ILE:O	2.14	0.47
7:S:138:THR:HG22	7:S:142:ASN:O	2.14	0.47
1:A:219:TYR:OH	1:A:347:TYR:OH	2.28	0.47
1:A:686:ILE:HB	1:A:687:GLN:OE1	2.15	0.47
1:A:1038:LYS:HG2	1:A:1638:PHE:HD2	1.74	0.47
1:A:1042:GLY:HA3	1:A:1053:ASP:OD2	2.14	0.47
2:B:55:LYS:O	2:B:76:SER:HA	2.14	0.47
1:M:496:PRO:HD2	2:N:766:TYR:CZ	2.49	0.47
3:O:85:ALA:HB3	3:O:226:PHE:CE1	2.49	0.47
8:T:17:ASP:OD1	8:T:17:ASP:N	2.47	0.47
1:A:228:CYS:CB	1:A:231:CYS:HB3	2.43	0.47
1:A:850:LEU:HD13	1:A:929:LEU:HB3	1.95	0.47
1:A:972:LEU:HA	1:A:972:LEU:HD23	1.61	0.47
1:A:1125:LEU:HD23	1:A:1136:SER:OG	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1189:ASP:OD2	6:F:76:THR:HB	2.15	0.47
1:A:1206:SER:OG	1:A:1207:THR:N	2.47	0.47
1:A:1223:ASN:OD1	1:A:1224:VAL:N	2.46	0.47
2:B:37:ASN:OD1	2:B:147:ASN:HB2	2.15	0.47
2:B:55:LYS:HB3	2:B:400:ARG:HD2	1.97	0.47
2:B:219:ARG:HH11	2:B:223:SER:HB2	1.80	0.47
2:B:355:LYS:HG3	2:B:622:TYR:CD2	2.49	0.47
2:B:383:LEU:O	2:B:387:ILE:HG12	2.15	0.47
2:B:386:GLN:NE2	2:B:452:LEU:HD22	2.30	0.47
2:B:999:TYR:CD2	2:B:1006:GLU:HB3	2.49	0.47
3:C:51:THR:OG1	3:C:59:VAL:HG23	2.13	0.47
3:C:85:ALA:HA	3:C:112:ILE:HD12	1.96	0.47
5:E:151:LEU:HB2	5:E:190:VAL:HG13	1.97	0.47
7:G:54:ILE:HA	7:G:76:VAL:HG12	1.96	0.47
8:H:72:ALA:HB2	8:H:122:LEU:HB3	1.97	0.47
1:M:84:ILE:HD11	1:M:401:ILE:HG21	1.96	0.47
1:M:114:VAL:HG22	1:M:182:ARG:NH1	2.29	0.47
1:M:407:ASP:O	1:M:411:GLU:N	2.48	0.47
1:M:880:SER:OG	1:M:881:THR:N	2.48	0.47
1:M:1062:HIS:NE2	1:M:1125:LEU:O	2.47	0.47
1:M:1125:LEU:HD23	1:M:1136:SER:OG	2.15	0.47
1:M:1579:GLU:OE2	5:Q:193:ILE:HD12	2.15	0.47
2:N:355:LYS:HG3	2:N:622:TYR:CD2	2.49	0.47
2:N:402:GLN:NE2	2:N:428:LYS:HD3	2.29	0.47
2:N:433:ILE:O	2:N:436:LYS:N	2.44	0.47
2:N:561:VAL:HG12	2:N:569:GLY:O	2.14	0.47
2:N:637:PRO:HA	2:N:647:ASP:O	2.14	0.47
2:N:693:ASP:OD2	2:N:969:PHE:N	2.36	0.47
2:N:1130:ASP:OD1	2:N:1130:ASP:N	2.47	0.47
2:N:1147:THR:HG22	2:N:1148:LEU:H	1.80	0.47
3:O:82:PRO:HB2	3:O:217:LEU:HD22	1.96	0.47
3:O:93:ASN:O	3:O:210:ASP:N	2.48	0.47
4:P:20:ASP:O	4:P:23:SER:OG	2.31	0.47
5:Q:116:LYS:HG3	5:Q:117:ILE:N	2.29	0.47
7:S:54:ILE:HA	7:S:76:VAL:HG12	1.96	0.47
8:T:25:SER:HB3	8:T:44:SER:OG	2.15	0.47
8:T:80:VAL:HG12	8:T:117:ASP:O	2.13	0.47
10:V:7:CYS:HB3	10:V:14:ILE:HD13	1.97	0.47
11:W:62:PHE:HB3	11:W:80:GLN:HB2	1.96	0.47
1:A:66:CYS:SG	1:A:73:CYS:CB	3.01	0.47
1:A:501:ASN:HA	1:A:669:THR:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:519:VAL:HG21	1:A:569:LEU:HD21	1.96	0.47
1:A:767:LYS:HD3	1:A:783:SER:HB3	1.95	0.47
1:A:1502:LYS:C	1:A:1503:LEU:HD12	2.39	0.47
2:B:352:MET:HB2	2:B:352:MET:HE3	1.74	0.47
2:B:1082:ASP:N	2:B:1082:ASP:OD1	2.47	0.47
2:B:1162:LEU:HG	2:B:1167:ILE:O	2.14	0.47
3:C:101:GLU:O	3:C:104:SER:OG	2.31	0.47
7:G:82:SER:O	7:G:82:SER:OG	2.30	0.47
8:H:25:SER:HB3	8:H:44:SER:OG	2.15	0.47
1:M:3:ILE:HG22	7:S:68:PRO:HD3	1.96	0.47
1:M:610:THR:HG21	2:N:1060:GLU:HG3	1.96	0.47
1:M:1231:LEU:HA	1:M:1234:ILE:HG22	1.97	0.47
1:M:1589:VAL:HG13	1:M:1605:LEU:HD23	1.96	0.47
1:M:1674:THR:HA	1:M:1677:PHE:CZ	2.50	0.47
2:N:37:ASN:OD1	2:N:147:ASN:HB2	2.15	0.47
2:N:801:ARG:HG2	2:N:802:ARG:H	1.79	0.47
2:N:1088:VAL:HG12	2:N:1149:ILE:HD11	1.97	0.47
3:O:266:GLU:N	3:O:274:GLN:O	2.41	0.47
1:A:63:CYS:HB3	1:A:66:CYS:SG	2.54	0.47
1:A:237:ASN:OD1	1:A:238:PHE:N	2.46	0.47
1:A:472:GLU:HA	1:A:477:LYS:NZ	2.29	0.47
1:A:808:LEU:O	1:A:812:VAL:HG23	2.15	0.47
1:A:844:ARG:HD2	2:B:995:ASN:ND2	2.30	0.47
1:A:901:LYS:HG2	9:I:59:LEU:HD11	1.95	0.47
2:B:509:THR:HG21	2:B:516:GLY:H	1.78	0.47
2:B:672:THR:HG23	2:B:673:HIS:ND1	2.27	0.47
2:B:772:MET:HG2	2:B:911:ILE:N	2.30	0.47
2:B:919:VAL:HG21	3:C:75:ARG:HD3	1.97	0.47
2:B:996:GLU:N	2:B:1011:ILE:O	2.47	0.47
5:E:116:LYS:HG3	5:E:117:ILE:N	2.29	0.47
5:E:117:ILE:HD12	5:E:117:ILE:HA	1.82	0.47
10:J:7:CYS:HB3	10:J:14:ILE:HD13	1.97	0.47
11:K:55:MET:HE2	11:K:63:CYS:HB3	1.97	0.47
1:M:219:TYR:OH	1:M:347:TYR:OH	2.28	0.47
1:M:472:GLU:HA	1:M:477:LYS:NZ	2.29	0.47
1:M:512:LYS:HD3	2:N:1031:VAL:HG11	1.96	0.47
3:O:76:ILE:HG22	3:O:80:GLU:HB2	1.96	0.47
8:T:37:ASN:O	8:T:104:ILE:HD12	2.14	0.47
8:T:74:TYR:HB3	8:T:123:LEU:HB3	1.96	0.47
11:W:55:MET:HE2	11:W:63:CYS:HB3	1.97	0.47
1:A:114:VAL:HG22	1:A:182:ARG:NH1	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:472:GLU:HA	1:A:477:LYS:HZ1	1.80	0.47
1:A:1040:LEU:HA	1:A:1043:LEU:HD23	1.96	0.47
2:B:107:ARG:HH11	2:B:721:ARG:HH22	1.62	0.47
3:C:129:GLN:OE1	3:C:129:GLN:N	2.48	0.47
7:G:84:LYS:HA	7:G:84:LYS:HD2	1.71	0.47
7:G:95:LEU:HG	7:G:102:GLY:HA3	1.97	0.47
1:M:364:ASN:N	1:M:364:ASN:OD1	2.48	0.47
1:M:675:VAL:HG12	1:M:682:LEU:HD22	1.97	0.47
1:M:1205:PRO:HA	1:M:1208:GLN:HB2	1.96	0.47
1:M:1502:LYS:C	1:M:1503:LEU:HD12	2.39	0.47
2:N:1:MET:O	2:N:963:ALA:HB3	2.15	0.47
2:N:86:LYS:HD3	2:N:148:ARG:HD2	1.97	0.47
2:N:185:LEU:HB2	2:N:378:LEU:CD2	2.44	0.47
3:O:342:LEU:N	11:W:22:ILE:HD11	2.30	0.47
7:S:95:LEU:HG	7:S:102:GLY:HA3	1.97	0.47
1:A:84:ILE:HD11	1:A:401:ILE:HG21	1.96	0.46
1:A:1110:TYR:CZ	1:A:1127:LYS:HE2	2.50	0.46
1:A:1269:LYS:HD2	1:A:1520:GLU:HG3	1.97	0.46
1:A:1282:THR:HG22	9:I:45:GLU:OE1	2.15	0.46
2:B:41:ASN:HD22	2:B:147:ASN:ND2	2.13	0.46
8:H:8:ASP:HA	8:H:58:GLN:HG2	1.97	0.46
1:M:1042:GLY:HA3	1:M:1053:ASP:OD2	2.14	0.46
1:M:1087:LYS:HA	1:M:1090:ILE:HG22	1.97	0.46
2:N:197:ILE:HD13	2:N:366:ALA:HB2	1.97	0.46
2:N:604:LYS:HG3	2:N:605:VAL:HG13	1.96	0.46
8:T:72:ALA:HB2	8:T:122:LEU:HB3	1.97	0.46
10:V:31:GLU:OE1	10:V:31:GLU:N	2.33	0.46
1:A:1151:LYS:HZ3	1:A:1152:ASN:HB3	1.80	0.46
1:A:1633:PHE:HB2	1:A:1662:SER:HB2	1.98	0.46
2:B:197:ILE:HD13	2:B:366:ALA:HB2	1.97	0.46
2:B:610:GLU:HG2	2:B:633:ARG:NH2	2.30	0.46
2:B:807:VAL:HG23	2:B:850:GLU:HB2	1.96	0.46
3:C:74:ARG:O	3:C:78:ILE:HG22	2.15	0.46
3:C:266:GLU:N	3:C:274:GLN:O	2.41	0.46
11:K:25:LEU:HB2	11:K:36:THR:OG1	2.16	0.46
1:M:121:CYS:HB3	1:M:186:VAL:CG2	2.44	0.46
1:M:519:VAL:HG21	1:M:569:LEU:HD21	1.96	0.46
1:M:1110:TYR:CZ	1:M:1127:LYS:HE2	2.50	0.46
2:N:137:VAL:HA	2:N:431:ASN:O	2.15	0.46
2:N:690:PRO:HG3	2:N:905:ARG:NH2	2.31	0.46
2:N:693:ASP:OD1	2:N:693:ASP:N	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:115:ASP:OD2	3:O:118:MET:N	2.48	0.46
3:O:129:GLN:OE1	3:O:129:GLN:N	2.48	0.46
3:O:218:GLY:HA3	3:O:226:PHE:CE2	2.51	0.46
1:A:241:GLU:HB2	1:A:245:LYS:HB2	1.98	0.46
1:A:1087:LYS:HA	1:A:1090:ILE:HG22	1.97	0.46
1:A:1231:LEU:HA	1:A:1234:ILE:HG22	1.97	0.46
2:B:1:MET:O	2:B:963:ALA:HB3	2.15	0.46
2:B:86:LYS:HD3	2:B:148:ARG:HD2	1.97	0.46
2:B:311:PHE:O	2:B:315:LEU:HD23	2.16	0.46
2:B:774:LEU:O	2:B:915:LYS:HA	2.16	0.46
2:B:1087:TRP:CD1	2:B:1113:VAL:HG21	2.51	0.46
3:C:218:GLY:HA3	3:C:226:PHE:CE2	2.50	0.46
8:H:30:VAL:HB	8:H:37:ASN:HD22	1.80	0.46
1:M:118:LEU:HB2	1:M:182:ARG:NH1	2.29	0.46
1:M:1068:LEU:HA	1:M:1188:VAL:HG22	1.98	0.46
1:M:1541:LYS:HE3	1:M:1541:LYS:HB2	1.70	0.46
2:N:95:SER:O	2:N:95:SER:OG	2.32	0.46
2:N:383:LEU:O	2:N:387:ILE:HG12	2.15	0.46
2:N:537:ILE:HB	2:N:538:PRO:HD3	1.95	0.46
2:N:774:LEU:O	2:N:915:LYS:HA	2.16	0.46
2:N:807:VAL:HG23	2:N:850:GLU:HB2	1.96	0.46
2:N:972:SER:OG	2:N:974:GLN:HG2	2.16	0.46
1:A:57:TYR:N	1:A:61:SER:OG	2.49	0.46
1:A:734:ILE:HG22	8:H:76:MET:HG2	1.97	0.46
2:B:78:ARG:HH11	2:B:130:ARG:HE	1.64	0.46
2:B:185:LEU:HB2	2:B:378:LEU:CD2	2.44	0.46
2:B:972:SER:OG	2:B:974:GLN:HG2	2.16	0.46
5:E:22:VAL:HG11	5:E:29:VAL:HB	1.96	0.46
10:J:23:THR:HA	10:J:26:GLN:HB3	1.96	0.46
1:M:115:LYS:HE3	1:M:115:LYS:HB2	1.60	0.46
2:N:41:ASN:HD22	2:N:147:ASN:ND2	2.13	0.46
5:Q:22:VAL:HG11	5:Q:29:VAL:HB	1.96	0.46
5:Q:106:TYR:CZ	5:Q:131:GLN:HB3	2.50	0.46
1:A:1062:HIS:NE2	1:A:1125:LEU:O	2.47	0.46
2:B:116:ARG:NH2	7:S:128:ASP:O	2.46	0.46
2:B:827:ASP:HA	2:B:833:PHE:CE1	2.51	0.46
2:B:1147:THR:HG22	2:B:1148:LEU:H	1.80	0.46
4:D:27:ASN:O	4:D:31:GLN:NE2	2.41	0.46
1:M:85:PRO:O	1:M:325:SER:OG	2.27	0.46
1:M:241:GLU:HB2	1:M:245:LYS:HB2	1.98	0.46
1:M:252:SER:O	1:M:256:LEU:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:843:CYS:SG	1:M:938:MET:HB2	2.56	0.46
1:M:1140:LYS:HB3	5:Q:201:GLY:H	1.80	0.46
1:M:1206:SER:OG	1:M:1207:THR:N	2.47	0.46
2:N:75:ILE:HA	2:N:124:SER:O	2.15	0.46
2:N:728:ARG:NH2	3:O:99:GLN:HE22	2.14	0.46
2:N:1169:MET:SD	2:N:1169:MET:N	2.81	0.46
5:Q:62:LYS:HA	5:Q:71:THR:HG1	1.80	0.46
5:Q:151:LEU:HB2	5:Q:190:VAL:HG13	1.97	0.46
11:W:25:LEU:HB2	11:W:36:THR:OG1	2.16	0.46
1:A:77:PHE:HE1	1:A:369:PRO:HD3	1.79	0.46
1:A:181:ILE:O	1:A:184:GLU:HG2	2.16	0.46
1:A:558:THR:HG22	1:A:561:GLN:CD	2.40	0.46
1:A:1068:LEU:HA	1:A:1188:VAL:HG22	1.98	0.46
1:A:1193:SER:O	1:A:1193:SER:OG	2.34	0.46
1:A:1674:THR:HA	1:A:1677:PHE:CZ	2.50	0.46
2:B:873:LEU:HD23	2:B:873:LEU:HA	1.76	0.46
5:E:96:ASP:OD2	5:E:97:HIS:N	2.49	0.46
5:E:106:TYR:CZ	5:E:131:GLN:HB3	2.50	0.46
8:H:108:HIS:O	8:H:112:TYR:HB2	2.15	0.46
1:M:106:CYS:SG	1:M:230:ASN:HB2	2.56	0.46
1:M:485:ASN:HB3	2:N:1033:THR:O	2.15	0.46
1:M:686:ILE:HB	1:M:687:GLN:OE1	2.15	0.46
2:N:219:ARG:HH11	2:N:223:SER:HB2	1.80	0.46
2:N:311:PHE:O	2:N:315:LEU:HD23	2.15	0.46
2:N:386:GLN:NE2	2:N:452:LEU:HD22	2.30	0.46
2:N:772:MET:HG2	2:N:911:ILE:N	2.30	0.46
1:A:746:ILE:O	1:A:749:SER:OG	2.22	0.46
1:A:1679:ILE:O	7:G:63:VAL:HG12	2.15	0.46
2:B:48:ALA:HB1	2:B:389:LYS:HG3	1.98	0.46
2:B:144:VAL:HG21	2:B:172:TYR:CE2	2.51	0.46
3:C:76:ILE:HG22	3:C:80:GLU:HB2	1.96	0.46
1:M:57:TYR:N	1:M:61:SER:OG	2.49	0.46
1:M:475:PHE:HA	1:M:479:MET:CB	2.46	0.46
1:M:613:LYS:HB2	2:N:1067:HIS:CE1	2.50	0.46
2:N:99:ARG:CZ	12:X:47:ARG:HH12	2.29	0.46
2:N:135:ARG:HA	2:N:135:ARG:HD2	1.73	0.46
2:N:144:VAL:HG21	2:N:172:TYR:CE2	2.51	0.46
2:N:420:LYS:O	2:N:423:THR:OG1	2.24	0.46
2:N:706:MET:HB3	2:N:706:MET:HE3	1.85	0.46
2:N:987:LYS:HD3	2:N:987:LYS:HA	1.68	0.46
1:A:106:CYS:SG	1:A:231:CYS:CB	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:843:CYS:SG	1:A:938:MET:HB2	2.56	0.46
2:B:690:PRO:HG3	2:B:905:ARG:NH2	2.31	0.46
8:H:16:VAL:HG13	8:H:27:ILE:HG22	1.98	0.46
8:H:23:ARG:HB3	8:H:24:VAL:H	1.62	0.46
12:L:57:MET:HG2	1:M:561:GLN:HA	1.97	0.46
1:M:808:LEU:O	1:M:812:VAL:HG23	2.15	0.46
1:M:861:LEU:HD13	1:M:920:ILE:HG22	1.98	0.46
1:M:1247:MET:SD	1:M:1547:VAL:HA	2.55	0.46
2:N:778:ALA:O	2:N:783:PHE:HB2	2.16	0.46
2:N:827:ASP:HA	2:N:833:PHE:CE1	2.51	0.46
2:N:882:GLU:O	2:N:884:GLN:HG2	2.16	0.46
2:N:1087:TRP:CD1	2:N:1113:VAL:HG21	2.51	0.46
3:O:334:LYS:HD2	11:W:42:GLU:OE2	2.15	0.46
5:Q:96:ASP:OD2	5:Q:97:HIS:N	2.49	0.46
7:S:81:PHE:O	7:S:83:PRO:HD3	2.16	0.46
7:S:90:GLU:HB3	7:S:151:GLU:CD	2.41	0.46
8:T:8:ASP:HA	8:T:58:GLN:HG2	1.97	0.46
1:A:106:CYS:SG	1:A:230:ASN:HB2	2.56	0.46
1:A:475:PHE:HA	1:A:479:MET:CB	2.46	0.46
1:A:675:VAL:HG12	1:A:682:LEU:HD22	1.98	0.46
1:A:1306:ARG:NH2	1:A:1317:GLN:HG2	2.20	0.46
2:B:195:ALA:HB1	2:B:359:LEU:HD22	1.97	0.46
2:B:916:TRP:CD1	2:B:917:PRO:HD2	2.51	0.46
7:G:81:PHE:O	7:G:83:PRO:HD3	2.16	0.46
8:H:17:ASP:N	8:H:17:ASP:OD1	2.46	0.46
1:M:27:ILE:HG21	2:N:1096:ILE:HG23	1.96	0.46
1:M:736:ARG:NH2	8:T:68:LEU:O	2.49	0.46
1:M:767:LYS:HA	1:M:783:SER:HB2	1.98	0.46
1:M:868:PHE:O	1:M:871:GLU:HB2	2.16	0.46
2:N:822:TRP:O	2:N:826:LEU:N	2.45	0.46
2:N:844:ILE:N	2:N:858:GLU:O	2.44	0.46
2:N:916:TRP:CD1	2:N:917:PRO:HD2	2.51	0.46
1:A:2:ASN:ND2	1:A:545:GLN:HE22	2.13	0.46
1:A:513:LEU:HD21	1:A:653:PHE:CG	2.51	0.46
1:A:767:LYS:HA	1:A:783:SER:HB2	1.97	0.46
1:A:868:PHE:O	1:A:871:GLU:HB2	2.16	0.46
1:A:952:ASN:CG	2:B:943:MET:HE1	2.41	0.46
1:A:1262:ALA:O	1:A:1266:GLU:HG2	2.16	0.46
1:A:1589:VAL:HG13	1:A:1605:LEU:HD23	1.96	0.46
2:B:186:ILE:HG13	2:B:479:VAL:HG11	1.98	0.46
2:B:876:ASN:ND2	2:B:884:GLN:HB2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:882:GLU:O	2:B:884:GLN:HG2	2.16	0.46
3:C:253:LYS:HB2	3:C:253:LYS:HE2	1.81	0.46
6:F:121:PRO:O	6:F:122:LEU:HB2	2.16	0.46
7:G:93:ILE:HD12	7:G:96:VAL:HG21	1.98	0.46
1:M:2:ASN:ND2	1:M:545:GLN:HE22	2.13	0.46
1:M:657:THR:HG22	6:R:89:LEU:HD13	1.98	0.46
1:M:1013:MET:HE2	1:M:1013:MET:HB3	1.76	0.46
1:M:1193:SER:O	1:M:1193:SER:OG	2.34	0.46
1:M:1262:ALA:O	1:M:1266:GLU:HG2	2.16	0.46
2:N:27:LYS:HE2	2:N:27:LYS:HB3	1.60	0.46
2:N:663:PRO:HA	2:N:666:ILE:HD11	1.98	0.46
2:N:851:SER:OG	2:N:852:THR:N	2.49	0.46
2:N:1151:LEU:HD13	2:N:1155:PHE:HD2	1.81	0.46
3:O:253:LYS:HE2	3:O:253:LYS:HB2	1.80	0.46
8:T:108:HIS:O	8:T:112:TYR:HB2	2.16	0.46
1:A:538:TRP:CE2	1:A:539:PRO:HB3	2.51	0.45
1:A:880:SER:OG	1:A:881:THR:N	2.48	0.45
1:A:968:ARG:NH1	1:A:969:ARG:O	2.49	0.45
1:A:1202:ILE:C	1:A:1205:PRO:HD2	2.42	0.45
2:B:116:ARG:HD3	7:S:131:GLU:CD	2.40	0.45
7:G:85:LYS:HA	7:G:154:VAL:HB	1.98	0.45
7:G:90:GLU:HB3	7:G:151:GLU:CD	2.41	0.45
7:G:99:SER:OG	2:N:93:GLU:OE2	2.31	0.45
10:J:3:ILE:HA	10:J:4:PRO:HD3	1.86	0.45
1:M:558:THR:HG22	1:M:561:GLN:CD	2.41	0.45
1:M:1066:ASP:OD1	1:M:1183:TYR:OH	2.29	0.45
2:N:55:LYS:HB3	2:N:400:ARG:HD2	1.97	0.45
3:O:144:ASN:HB3	3:O:210:ASP:OD1	2.16	0.45
1:A:44:PRO:HB3	1:A:50:TYR:O	2.16	0.45
1:A:115:LYS:HB2	1:A:115:LYS:HE3	1.61	0.45
1:A:1142:GLN:HA	1:A:1145:VAL:HG12	1.99	0.45
1:A:1155:LYS:HD2	1:A:1155:LYS:HA	1.77	0.45
5:E:69:LYS:HA	5:E:70:GLY:HA2	1.58	0.45
1:M:1:MET:HB2	2:N:1079:ASN:HB3	1.97	0.45
1:M:237:ASN:OD1	1:M:238:PHE:N	2.46	0.45
2:N:78:ARG:HH11	2:N:130:ARG:HE	1.64	0.45
2:N:876:ASN:ND2	2:N:884:GLN:HB2	2.31	0.45
1:A:1113:LYS:HB3	1:A:1121:TYR:CE1	2.51	0.45
1:M:576:LEU:HB3	1:M:579:SER:HA	1.99	0.45
1:M:1202:ILE:C	1:M:1205:PRO:HD2	2.42	0.45
1:M:1633:PHE:HB2	1:M:1662:SER:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:590:TYR:CD1	2:N:594:LEU:HD23	2.51	0.45
2:N:829:ASP:OD2	12:X:20:MET:HG3	2.17	0.45
2:N:931:ASP:OD1	10:V:9:SER:HA	2.16	0.45
3:O:74:ARG:O	3:O:78:ILE:HG22	2.15	0.45
5:Q:118:ILE:HG22	5:Q:127:ILE:HD13	1.98	0.45
7:S:98:PRO:HD2	7:S:132:GLU:OE1	2.16	0.45
8:T:19:GLN:OE1	8:T:19:GLN:N	2.50	0.45
1:A:687:GLN:HG2	1:A:688:ASP:N	2.31	0.45
1:A:762:LEU:HD11	1:A:811:SER:OG	2.17	0.45
1:A:802:GLY:O	1:A:804:SER:N	2.49	0.45
1:A:846:ASP:HB3	2:B:993:HIS:CG	2.52	0.45
1:A:861:LEU:HD13	1:A:920:ILE:HG22	1.98	0.45
1:A:1046:GLN:OE1	1:A:1052:ARG:N	2.45	0.45
1:A:1505:MET:O	1:A:1509:VAL:HG22	2.17	0.45
2:B:185:LEU:H	2:B:378:LEU:HG	1.82	0.45
2:B:348:LEU:HA	2:B:567:ILE:HD11	1.98	0.45
2:B:851:SER:OG	2:B:852:THR:N	2.49	0.45
3:C:115:ASP:OD2	3:C:118:MET:HG2	2.16	0.45
8:H:107:SER:C	8:H:109:ARG:H	2.24	0.45
1:M:114:VAL:HB	1:M:179:MET:HE2	1.99	0.45
1:M:979:LEU:HB3	1:M:982:PHE:HD2	1.81	0.45
1:M:1158:ALA:HB3	1:M:1166:ASP:OD2	2.16	0.45
1:M:1231:LEU:HA	1:M:1231:LEU:HD12	1.71	0.45
2:N:143:MET:HB2	2:N:173:PHE:CE1	2.52	0.45
2:N:195:ALA:HB1	2:N:359:LEU:HD22	1.97	0.45
3:O:113:SER:OG	3:O:192:ARG:O	2.33	0.45
5:Q:7:ASN:ND2	5:Q:54:ARG:HH22	2.08	0.45
6:R:121:PRO:O	6:R:122:LEU:HB2	2.16	0.45
1:A:401:ILE:HD12	1:A:434:PHE:HD1	1.82	0.45
1:A:1158:ALA:HB3	1:A:1166:ASP:OD2	2.16	0.45
2:B:166:SER:HB3	2:B:167:GLU:OE1	2.17	0.45
2:B:800:ARG:HD3	2:B:805:PRO:C	2.42	0.45
2:B:1090:ARG:HE	2:B:1090:ARG:HB2	1.53	0.45
2:B:1151:LEU:HD13	2:B:1155:PHE:HD2	1.81	0.45
1:M:1269:LYS:HD2	1:M:1520:GLU:HG3	1.97	0.45
2:N:985:LEU:CG	2:N:990:TYR:HB2	2.47	0.45
3:O:155:THR:HG1	3:O:156:ASP:H	1.60	0.45
3:O:290:LEU:HD21	3:O:301:LEU:HD13	1.98	0.45
8:T:16:VAL:HG22	8:T:27:ILE:HG22	1.99	0.45
10:V:51:THR:O	10:V:51:THR:OG1	2.32	0.45
12:X:41:CYS:N	12:X:46:HIS:O	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:888:LEU:HA	1:A:891:ASN:HD22	1.82	0.45
1:A:906:ASP:OD1	1:A:907:ALA:N	2.49	0.45
1:A:1163:SER:HA	1:A:1166:ASP:CG	2.42	0.45
2:B:822:TRP:O	2:B:826:LEU:N	2.45	0.45
5:E:103:ILE:HA	5:E:128:GLU:O	2.16	0.45
7:G:48:VAL:HG13	7:G:78:VAL:HG23	1.98	0.45
7:G:125:ILE:O	7:G:125:ILE:HG13	2.16	0.45
8:H:19:GLN:N	8:H:19:GLN:OE1	2.50	0.45
1:M:181:ILE:O	1:M:184:GLU:HG2	2.16	0.45
1:M:774:TYR:CZ	1:M:943:VAL:HG21	2.52	0.45
1:M:968:ARG:NH1	1:M:969:ARG:O	2.49	0.45
1:M:1113:LYS:HB3	1:M:1121:TYR:CE1	2.51	0.45
1:M:1140:LYS:CB	5:Q:201:GLY:H	2.30	0.45
1:M:1591:SER:O	1:M:1594:GLY:N	2.49	0.45
2:N:610:GLU:HG2	2:N:633:ARG:NH2	2.30	0.45
2:N:982:GLY:HA3	2:N:992:TYR:CE1	2.52	0.45
3:O:69:ILE:HG22	3:O:73:PHE:CE2	2.52	0.45
7:S:85:LYS:HA	7:S:154:VAL:HB	1.98	0.45
1:A:499:GLU:HG3	1:A:501:ASN:H	1.81	0.45
1:A:1283:GLU:HB2	9:I:44:VAL:O	2.17	0.45
1:A:1591:SER:O	1:A:1594:GLY:N	2.49	0.45
2:B:27:LYS:HE2	2:B:27:LYS:HB3	1.60	0.45
2:B:982:GLY:HA3	2:B:992:TYR:CE1	2.52	0.45
6:F:96:PRO:HG3	7:G:23:ARG:HD3	1.97	0.45
1:M:513:LEU:HD21	1:M:653:PHE:CG	2.51	0.45
1:M:606:ASN:HD22	1:M:616:MET:HG3	1.81	0.45
1:M:687:GLN:HG2	1:M:688:ASP:N	2.31	0.45
1:M:906:ASP:OD1	1:M:907:ALA:N	2.49	0.45
1:M:1151:LYS:HZ3	1:M:1152:ASN:HB3	1.81	0.45
2:N:113:TYR:O	2:N:141:PRO:HA	2.17	0.45
2:N:213:LEU:HD23	2:N:214:SER:N	2.32	0.45
2:N:800:ARG:HD3	2:N:805:PRO:C	2.42	0.45
5:Q:8:ILE:HD11	5:Q:42:LYS:HG2	1.99	0.45
2:B:137:VAL:HG22	2:B:433:ILE:HG12	1.99	0.45
2:B:274:LYS:HD2	2:B:554:HIS:NE2	2.32	0.45
2:B:663:PRO:HA	2:B:666:ILE:HD11	1.98	0.45
10:J:51:THR:O	10:J:51:THR:OG1	2.32	0.45
1:M:44:PRO:HB3	1:M:50:TYR:O	2.17	0.45
1:M:538:TRP:CE2	1:M:539:PRO:HB3	2.51	0.45
1:M:762:LEU:HD11	1:M:811:SER:OG	2.17	0.45
1:M:927:ASP:HA	1:M:932:LYS:NZ	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:1004:ALA:N	1:M:1007:GLU:OE1	2.27	0.45
1:M:1060:GLN:HE21	1:M:1610:ASP:CG	2.23	0.45
2:N:137:VAL:HG22	2:N:433:ILE:HG12	1.99	0.45
3:O:94:ASN:O	12:X:53:ARG:HD3	2.17	0.45
9:U:24:TRP:CZ2	9:U:35:PRO:HA	2.52	0.45
1:A:1231:LEU:HA	1:A:1231:LEU:HD12	1.71	0.45
1:A:1483:ASP:HB3	1:A:1488:GLU:H	1.82	0.45
2:B:1088:VAL:HG12	2:B:1149:ILE:HD11	1.97	0.45
3:C:304:VAL:HG12	3:C:306:ASP:H	1.81	0.45
8:H:85:GLU:HG2	8:H:91:VAL:HG12	1.99	0.45
1:M:132:ASN:O	1:M:136:MET:HG2	2.17	0.45
1:M:237:ASN:O	1:M:248:GLU:HB3	2.17	0.45
2:N:48:ALA:HB1	2:N:389:LYS:HG3	1.98	0.45
3:O:147:CYS:O	3:O:205:PRO:HA	2.17	0.45
8:T:85:GLU:HG2	8:T:91:VAL:HG12	1.99	0.45
1:A:120:PHE:HB2	1:A:342:VAL:HG22	1.99	0.45
1:A:576:LEU:HG	1:A:578:SER:H	1.81	0.45
1:A:1325:SER:O	1:A:1329:LEU:HB2	2.17	0.45
1:A:1506:VAL:HG13	1:A:1507:SER:H	1.82	0.45
3:C:93:ASN:O	3:C:210:ASP:N	2.48	0.45
3:C:144:ASN:HB3	3:C:210:ASP:OD1	2.16	0.45
3:C:147:CYS:O	3:C:205:PRO:HA	2.17	0.45
5:E:7:ASN:ND2	5:E:54:ARG:HH22	2.08	0.45
5:E:118:ILE:HG22	5:E:127:ILE:HD13	1.99	0.45
7:G:88:CYS:O	7:G:89:LEU:HD22	2.17	0.45
7:G:96:VAL:HG12	7:G:124:PHE:CE1	2.39	0.45
9:I:24:TRP:CZ2	9:I:35:PRO:HA	2.52	0.45
12:L:31:ASN:ND2	12:L:42:ARG:H	2.08	0.45
1:M:503:ILE:HG13	1:M:631:ARG:O	2.17	0.45
1:M:978:SER:HB2	1:M:991:SER:OG	2.17	0.45
1:M:1280:ARG:O	1:M:1299:ILE:HD12	2.17	0.45
1:M:1505:MET:O	1:M:1509:VAL:HG22	2.17	0.45
3:O:57:THR:HA	3:O:313:GLU:OE1	2.17	0.45
7:S:88:CYS:O	7:S:89:LEU:HD22	2.17	0.45
1:A:114:VAL:HB	1:A:179:MET:HE2	1.99	0.44
1:A:774:TYR:CZ	1:A:943:VAL:HG21	2.52	0.44
1:A:978:SER:HB2	1:A:991:SER:OG	2.17	0.44
1:A:1280:ARG:O	1:A:1299:ILE:HD12	2.17	0.44
1:A:1504:LEU:O	1:A:1508:LEU:HG	2.18	0.44
4:D:17:LEU:HD13	7:G:8:LYS:N	2.32	0.44
6:F:117:GLN:HB2	6:F:119:LYS:HG3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:126:ARG:O	6:F:133:TYR:HA	2.17	0.44
8:H:43:ASN:CG	8:H:46:ILE:HG22	2.42	0.44
1:M:499:GLU:HG3	1:M:501:ASN:H	1.81	0.44
1:M:726:ARG:NH2	11:W:61:GLU:OE1	2.50	0.44
1:M:1483:ASP:HB3	1:M:1488:GLU:H	1.82	0.44
1:M:1530:LYS:HD2	1:M:1531:PRO:HD2	1.98	0.44
1:M:1585:ILE:HG13	1:M:1586:VAL:N	2.32	0.44
2:N:186:ILE:HG13	2:N:479:VAL:HG11	1.98	0.44
2:N:388:LEU:O	2:N:392:ILE:HG12	2.17	0.44
2:N:610:GLU:HB2	2:N:653:GLU:OE2	2.17	0.44
3:O:179:GLN:HB2	3:O:182:GLN:CD	2.42	0.44
3:O:304:VAL:HG12	3:O:306:ASP:H	1.81	0.44
7:S:48:VAL:HG13	7:S:78:VAL:HG23	1.98	0.44
1:A:29:VAL:HG11	1:A:65:THR:OG1	2.18	0.44
1:A:68:LEU:HD23	1:A:68:LEU:HA	1.78	0.44
1:A:606:ASN:HD22	1:A:616:MET:HG3	1.81	0.44
1:A:1138:SER:HB3	1:A:1141:PHE:CB	2.47	0.44
1:A:1147:GLU:O	1:A:1151:LYS:HG2	2.17	0.44
1:A:1560:SER:O	1:A:1560:SER:OG	2.31	0.44
2:B:125:VAL:O	2:B:126:ASN:ND2	2.50	0.44
2:B:346:PHE:HA	2:B:349:LEU:HD12	2.00	0.44
2:B:733:GLN:HB2	10:J:51:THR:O	2.18	0.44
2:B:828:ALA:HB3	12:L:20:MET:HE2	1.99	0.44
3:C:48:VAL:HG11	11:K:109:PHE:HD1	1.82	0.44
3:C:179:GLN:HB2	3:C:182:GLN:CD	2.42	0.44
7:G:98:PRO:HD2	7:G:132:GLU:OE1	2.16	0.44
1:M:848:LEU:HA	1:M:848:LEU:HD23	1.71	0.44
1:M:1006:GLN:NE2	2:N:661:CYS:SG	2.64	0.44
1:M:1506:VAL:HG13	1:M:1507:SER:H	1.82	0.44
2:N:185:LEU:H	2:N:378:LEU:HG	1.82	0.44
8:T:16:VAL:HG13	8:T:27:ILE:HG22	1.98	0.44
1:A:18:ILE:HD13	1:A:359:MET:HA	1.99	0.44
1:A:503:ILE:HG13	1:A:631:ARG:O	2.17	0.44
1:A:927:ASP:HA	1:A:932:LYS:NZ	2.32	0.44
1:A:979:LEU:HB3	1:A:982:PHE:HD2	1.81	0.44
1:A:1267:VAL:HG12	1:A:1555:PHE:CZ	2.51	0.44
3:C:57:THR:HA	3:C:313:GLU:OE1	2.17	0.44
3:C:65:ILE:HG13	3:C:66:ASP:N	2.32	0.44
1:M:802:GLY:O	1:M:804:SER:N	2.48	0.44
1:M:888:LEU:HA	1:M:891:ASN:HD22	1.82	0.44
2:N:125:VAL:O	2:N:126:ASN:ND2	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:65:ILE:HG13	3:O:66:ASP:N	2.32	0.44
3:O:235:ARG:HH11	3:O:309:LEU:HD23	1.82	0.44
5:Q:194:VAL:HG13	5:Q:204:ASN:OD1	2.17	0.44
6:R:120:ILE:HA	6:R:121:PRO:HD3	1.90	0.44
1:A:334:ARG:HD3	1:A:334:ARG:HA	1.87	0.44
1:A:364:ASN:OD1	1:A:364:ASN:N	2.48	0.44
1:A:701:THR:HG23	1:A:743:GLY:H	1.83	0.44
1:A:739:ILE:HD12	1:A:741:TRP:HH2	1.83	0.44
2:B:49:VAL:O	2:B:52:ILE:HB	2.17	0.44
2:B:706:MET:HE3	2:B:706:MET:HB3	1.85	0.44
2:B:778:ALA:O	2:B:783:PHE:HB2	2.16	0.44
2:B:951:SER:OG	2:B:1014:GLY:HA3	2.17	0.44
7:G:121:ASP:HB2	7:G:139:ASN:HB3	2.00	0.44
8:H:16:VAL:HG22	8:H:27:ILE:HG22	1.99	0.44
1:M:29:VAL:HG11	1:M:65:THR:OG1	2.18	0.44
1:M:605:LEU:HA	1:M:605:LEU:HD23	1.74	0.44
1:M:842:THR:O	1:M:937:HIS:ND1	2.50	0.44
2:N:71:PHE:HE2	2:N:74:LYS:HB2	1.83	0.44
2:N:274:LYS:HD2	2:N:554:HIS:NE2	2.32	0.44
2:N:812:PHE:CE1	2:N:822:TRP:HE3	2.35	0.44
3:O:338:VAL:HG13	11:W:22:ILE:HD13	2.00	0.44
5:Q:103:ILE:HA	5:Q:128:GLU:O	2.17	0.44
7:S:84:LYS:HA	7:S:84:LYS:HD2	1.71	0.44
7:S:125:ILE:O	7:S:125:ILE:HG13	2.16	0.44
8:T:70:GLU:HG3	8:T:71:ALA:H	1.82	0.44
8:T:107:SER:C	8:T:109:ARG:H	2.25	0.44
1:A:58:LEU:HD23	1:A:58:LEU:HA	1.79	0.44
1:A:178:LEU:HD21	1:A:182:ARG:NH2	2.33	0.44
1:A:500:THR:HG22	1:A:826:SER:OG	2.18	0.44
1:A:548:ASP:OD2	1:A:550:THR:HG23	2.18	0.44
1:A:576:LEU:HB3	1:A:579:SER:HA	1.99	0.44
1:A:1256:SER:O	1:A:1260:ALA:N	2.38	0.44
2:B:329:PHE:O	2:B:333:LYS:HG2	2.17	0.44
2:B:480:HIS:CE1	2:B:482:GLY:H	2.36	0.44
2:B:610:GLU:HB2	2:B:653:GLU:OE2	2.17	0.44
3:C:72:ALA:O	3:C:76:ILE:HG12	2.17	0.44
8:H:109:ARG:C	8:H:111:LEU:N	2.75	0.44
1:M:120:PHE:HB2	1:M:342:VAL:HG22	1.99	0.44
1:M:769:LYS:N	1:M:797:ASP:OD2	2.48	0.44
1:M:1066:ASP:O	1:M:1067:SER:C	2.60	0.44
1:M:1123:PRO:HG2	5:Q:203:TYR:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:1498:ILE:CD1	9:U:22:ALA:HB2	2.47	0.44
1:M:1520:GLU:OE1	1:M:1523:GLY:N	2.40	0.44
2:N:99:ARG:NH1	12:X:47:ARG:HH12	2.15	0.44
3:O:115:ASP:OD2	3:O:118:MET:HG2	2.16	0.44
6:R:126:ARG:O	6:R:133:TYR:HA	2.17	0.44
7:S:121:ASP:HB2	7:S:139:ASN:HB3	1.99	0.44
11:W:96:ASP:HA	11:W:99:ILE:HD12	2.00	0.44
1:A:111:LEU:CD1	1:A:222:ILE:HG22	2.48	0.44
1:A:479:MET:HE2	1:A:1665:VAL:HA	1.99	0.44
1:A:842:THR:O	1:A:937:HIS:ND1	2.51	0.44
1:A:1530:LYS:HD2	1:A:1531:PRO:HD2	1.98	0.44
2:B:1032:ARG:NE	2:B:1044:PRO:HB3	2.32	0.44
2:B:1090:ARG:HH21	2:B:1147:THR:HG1	1.52	0.44
7:G:61:ALA:CB	7:G:72:ILE:HB	2.47	0.44
1:M:1147:GLU:O	1:M:1151:LYS:HG2	2.17	0.44
3:O:42:PHE:CZ	11:W:101:LEU:HG	2.53	0.44
8:T:109:ARG:C	8:T:111:LEU:N	2.75	0.44
11:W:29:SER:OG	11:W:33:THR:N	2.51	0.44
1:A:1:MET:CB	2:B:1079:ASN:HB3	2.47	0.44
1:A:24:VAL:O	1:A:28:SER:OG	2.25	0.44
1:A:237:ASN:O	1:A:248:GLU:HB3	2.17	0.44
1:A:247:PHE:CE2	1:A:323:MET:HB2	2.53	0.44
1:A:252:SER:O	1:A:256:LEU:N	2.48	0.44
1:A:829:SER:OG	1:A:830:ARG:N	2.51	0.44
1:A:1070:VAL:HA	1:A:1073:GLN:HG3	2.00	0.44
2:B:54:GLU:CB	2:B:78:ARG:HB3	2.44	0.44
2:B:143:MET:HB2	2:B:173:PHE:CE1	2.52	0.44
2:B:505:CYS:SG	2:B:506:PRO:HD2	2.58	0.44
3:C:69:ILE:HG21	11:K:101:LEU:HD21	1.98	0.44
3:C:204:ARG:NE	10:J:60:LEU:HB3	2.32	0.44
5:E:175:LEU:HD21	5:E:187:ARG:HG2	2.00	0.44
5:E:194:VAL:HG13	5:E:204:ASN:OD1	2.16	0.44
11:K:96:ASP:HA	11:K:99:ILE:HD12	2.00	0.44
1:M:401:ILE:HD12	1:M:434:PHE:HD1	1.82	0.44
1:M:476:ARG:NH1	1:M:1638:PHE:HA	2.33	0.44
1:M:879:LEU:HD23	1:M:883:SER:HB3	1.99	0.44
1:M:1052:ARG:HG2	1:M:1058:ILE:HD13	1.99	0.44
2:N:49:VAL:O	2:N:52:ILE:HB	2.18	0.44
2:N:236:VAL:HG12	2:N:237:THR:N	2.32	0.44
2:N:329:PHE:O	2:N:333:LYS:HG2	2.17	0.44
2:N:346:PHE:HA	2:N:349:LEU:HD12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:348:LEU:HA	2:N:567:ILE:HD11	1.99	0.44
1:A:1041:GLU:OE2	2:B:1061:ARG:NH1	2.50	0.44
1:A:1279:VAL:HG23	9:I:53:PHE:CE2	2.53	0.44
2:B:388:LEU:O	2:B:392:ILE:HG12	2.17	0.44
2:B:812:PHE:CE1	2:B:822:TRP:HE3	2.35	0.44
2:B:985:LEU:CG	2:B:990:TYR:HB2	2.47	0.44
1:M:114:VAL:HG21	1:M:178:LEU:HD23	2.00	0.44
1:M:479:MET:HE2	1:M:1665:VAL:HA	1.99	0.44
1:M:800:SER:O	1:M:808:LEU:N	2.48	0.44
1:M:1037:MET:HE2	2:N:1062:ASP:OD2	2.16	0.44
1:M:1142:GLN:HA	1:M:1145:VAL:HG12	1.99	0.44
1:M:1163:SER:HA	1:M:1166:ASP:CG	2.42	0.44
1:M:1267:VAL:HG12	1:M:1555:PHE:CZ	2.51	0.44
2:N:166:SER:HB3	2:N:167:GLU:OE1	2.17	0.44
2:N:254:MET:HE3	2:N:303:THR:HB	2.00	0.44
2:N:836:ILE:HD13	12:X:56:ARG:NE	2.32	0.44
2:N:844:ILE:HD11	2:N:860:TYR:HA	2.00	0.44
2:N:895:SER:O	2:N:897:ILE:HG23	2.18	0.44
6:R:117:GLN:HB2	6:R:119:LYS:HG3	1.98	0.44
7:S:119:PRO:HD3	7:S:170:LEU:C	2.43	0.44
1:A:121:CYS:HB3	1:A:186:VAL:CG2	2.44	0.44
1:A:132:ASN:O	1:A:136:MET:HG2	2.17	0.44
1:A:736:ARG:HD3	8:H:75:ILE:CD1	2.48	0.44
1:A:997:SER:HG	1:A:1003:ILE:HG22	1.83	0.44
1:A:1066:ASP:O	1:A:1067:SER:C	2.60	0.44
2:B:113:TYR:O	2:B:141:PRO:HA	2.17	0.44
2:B:213:LEU:HD23	2:B:214:SER:N	2.32	0.44
2:B:235:GLY:CA	2:B:284:ARG:HH11	2.26	0.44
2:B:254:MET:HE3	2:B:303:THR:HB	2.00	0.44
2:B:590:TYR:CD1	2:B:594:LEU:HD23	2.51	0.44
7:G:37:ILE:HA	7:G:48:VAL:HB	1.99	0.44
7:G:97:SER:HB2	2:N:93:GLU:OE1	2.17	0.44
10:J:40:LEU:HD13	10:J:46:ARG:HA	2.00	0.44
1:M:247:PHE:CE2	1:M:323:MET:HB2	2.53	0.44
2:N:240:ARG:NE	2:N:242:HIS:HE1	2.15	0.44
2:N:339:LEU:HD23	2:N:339:LEU:HA	1.83	0.44
5:Q:4:GLU:OE2	5:Q:5:GLU:HB2	2.18	0.44
7:S:93:ILE:HD12	7:S:96:VAL:HG21	1.98	0.44
8:T:80:VAL:HG13	8:T:116:LEU:HA	2.00	0.44
1:A:769:LYS:N	1:A:797:ASP:OD2	2.48	0.43
1:A:1249:LEU:HD12	1:A:1542:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1659:ASN:OD1	1:A:1659:ASN:N	2.49	0.43
1:A:1672:PHE:CZ	2:B:1065:ILE:HG22	2.53	0.43
2:B:28:ALA:O	2:B:477:ARG:HD3	2.18	0.43
2:B:772:MET:HG2	2:B:911:ILE:H	1.83	0.43
2:B:837:LYS:HA	2:B:867:PHE:HD1	1.83	0.43
2:B:1061:ARG:O	2:B:1065:ILE:HG12	2.18	0.43
2:B:1077:LEU:HA	2:B:1077:LEU:HD23	1.78	0.43
3:C:69:ILE:HG22	3:C:73:PHE:CE2	2.52	0.43
3:C:107:ILE:C	3:C:109:LEU:N	2.75	0.43
3:C:290:LEU:HD21	3:C:301:LEU:HD13	1.98	0.43
3:C:321:ASP:O	3:C:325:ILE:HG13	2.18	0.43
5:E:4:GLU:OE2	5:E:5:GLU:HB2	2.18	0.43
5:E:107:ALA:HA	5:E:108:ASN:HA	1.60	0.43
8:H:70:GLU:HG3	8:H:71:ALA:H	1.82	0.43
1:M:111:LEU:CD1	1:M:222:ILE:HG22	2.48	0.43
1:M:500:THR:HG22	1:M:826:SER:OG	2.18	0.43
1:M:1105:GLU:H	1:M:1105:GLU:CD	2.26	0.43
1:M:1276:VAL:HG22	1:M:1277:ARG:O	2.18	0.43
2:N:99:ARG:NH2	12:X:46:HIS:HA	2.30	0.43
2:N:145:ARG:HH21	2:N:168:GLU:HB3	1.83	0.43
2:N:819:ARG:NH1	2:N:820:ARG:HA	2.33	0.43
2:N:837:LYS:HA	2:N:867:PHE:HD1	1.83	0.43
7:S:92:LYS:HA	7:S:92:LYS:HD3	1.80	0.43
1:A:104:LEU:HD12	1:A:236:PRO:HG2	2.00	0.43
1:A:682:LEU:HD23	1:A:683:ARG:H	1.82	0.43
1:A:1585:ILE:HG13	1:A:1586:VAL:N	2.32	0.43
2:B:94:ARG:HG3	2:B:878:VAL:HG22	2.00	0.43
2:B:537:ILE:O	2:B:541:LEU:HG	2.18	0.43
2:B:844:ILE:HD11	2:B:860:TYR:HA	2.00	0.43
2:B:895:SER:O	2:B:897:ILE:HG23	2.18	0.43
2:B:1021:LEU:HD23	2:B:1023:HIS:CE1	2.54	0.43
3:C:235:ARG:HH11	3:C:309:LEU:HD23	1.82	0.43
3:C:260:LYS:HD3	3:C:260:LYS:HA	1.69	0.43
7:G:119:PRO:HD3	7:G:170:LEU:C	2.43	0.43
7:G:125:ILE:HG12	7:G:135:ARG:HB2	2.00	0.43
12:L:34:GLN:HB2	2:N:1107:VAL:HG11	2.00	0.43
1:M:576:LEU:HG	1:M:578:SER:H	1.81	0.43
1:M:1070:VAL:HA	1:M:1073:GLN:NE2	2.32	0.43
1:M:1140:LYS:H	5:Q:201:GLY:CA	2.31	0.43
2:N:757:VAL:HG21	10:V:9:SER:HB3	2.00	0.43
2:N:877:ASP:OD1	2:N:881:SER:OG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:101:GLU:O	3:O:104:SER:OG	2.31	0.43
3:O:339:LYS:HZ2	11:W:92:ARG:HG3	1.83	0.43
4:P:19:LYS:HE2	4:P:19:LYS:HB2	1.86	0.43
5:Q:175:LEU:HD21	5:Q:187:ARG:HG2	2.00	0.43
7:S:61:ALA:CB	7:S:72:ILE:HB	2.47	0.43
8:T:43:ASN:CG	8:T:46:ILE:HG22	2.42	0.43
8:T:71:ALA:HB1	8:T:124:ARG:HH21	1.83	0.43
8:T:72:ALA:CB	8:T:122:LEU:HB3	2.48	0.43
1:A:34:ASN:OD1	1:A:34:ASN:N	2.45	0.43
1:A:327:GLU:HG3	1:A:328:VAL:H	1.83	0.43
1:A:495:ASP:N	1:A:632:MET:O	2.51	0.43
1:A:1004:ALA:N	1:A:1007:GLU:OE1	2.27	0.43
2:B:71:PHE:HE2	2:B:74:LYS:HB2	1.82	0.43
2:B:190:ARG:HG3	2:B:376:GLU:CD	2.44	0.43
2:B:236:VAL:HG12	2:B:237:THR:N	2.32	0.43
2:B:540:LEU:HD21	2:B:586:MET:SD	2.59	0.43
3:C:90:TYR:CE1	1:M:560:GLU:HG2	2.47	0.43
5:E:8:ILE:HD11	5:E:42:LYS:HG2	1.99	0.43
6:F:109:GLN:CB	6:F:112:MET:HE2	2.49	0.43
6:F:109:GLN:O	6:F:112:MET:HB2	2.19	0.43
8:H:80:VAL:HG13	8:H:116:LEU:HA	2.00	0.43
1:M:401:ILE:HD12	1:M:434:PHE:CD1	2.53	0.43
1:M:700:ASP:O	8:T:23:ARG:NH1	2.52	0.43
1:M:839:ARG:O	2:N:1007:MET:HB3	2.19	0.43
1:M:1325:SER:O	1:M:1329:LEU:HB2	2.17	0.43
1:M:1582:ARG:NH2	5:Q:195:ARG:HD3	2.33	0.43
2:N:90:SER:HB3	2:N:878:VAL:HG23	2.00	0.43
2:N:251:PRO:HG2	2:N:254:MET:HB2	2.01	0.43
2:N:379:LEU:HD12	2:N:382:PHE:CE2	2.53	0.43
2:N:592:VAL:HB	2:N:645:GLU:HG2	2.00	0.43
2:N:728:ARG:NH2	3:O:99:GLN:NE2	2.66	0.43
2:N:951:SER:OG	2:N:1014:GLY:HA3	2.17	0.43
2:N:1061:ARG:O	2:N:1065:ILE:HG12	2.18	0.43
7:S:37:ILE:HA	7:S:48:VAL:HB	1.99	0.43
1:A:21:VAL:HG23	1:A:364:ASN:OD1	2.19	0.43
1:A:879:LEU:HD23	1:A:883:SER:HB3	1.99	0.43
1:A:951:VAL:O	1:A:955:GLN:HG3	2.18	0.43
1:A:1009:TYR:OH	2:B:500:ALA:HB3	2.18	0.43
1:A:1276:VAL:HG22	1:A:1277:ARG:O	2.18	0.43
2:B:240:ARG:NE	2:B:242:HIS:HE1	2.16	0.43
2:B:733:GLN:OE1	10:J:51:THR:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:987:LYS:HD3	2:B:987:LYS:HA	1.68	0.43
3:C:170:TYR:HA	3:C:199:VAL:HA	1.99	0.43
3:C:231:THR:HG21	10:J:42:ARG:CZ	2.48	0.43
8:H:71:ALA:HB1	8:H:124:ARG:HH21	1.83	0.43
1:M:66:CYS:SG	1:M:73:CYS:CB	3.01	0.43
1:M:90:LEU:HD23	1:M:90:LEU:HA	1.86	0.43
1:M:327:GLU:HG3	1:M:328:VAL:H	1.83	0.43
1:M:951:VAL:O	1:M:955:GLN:HG3	2.18	0.43
1:M:1050:THR:O	1:M:1050:THR:OG1	2.36	0.43
1:M:1530:LYS:HB3	1:M:1543:ILE:HD13	2.01	0.43
2:N:181:LEU:HD12	2:N:182:ILE:H	1.84	0.43
2:N:288:MET:HE3	2:N:288:MET:HB3	1.90	0.43
2:N:754:THR:OG1	2:N:755:ASN:N	2.50	0.43
2:N:772:MET:HG2	2:N:911:ILE:H	1.83	0.43
2:N:875:GLY:HA2	12:X:39:ILE:CG2	2.48	0.43
2:N:1021:LEU:HD23	2:N:1023:HIS:CE1	2.54	0.43
3:O:46:LEU:HD11	11:W:105:VAL:HG22	2.01	0.43
6:R:109:GLN:CB	6:R:112:MET:HE2	2.49	0.43
1:A:19:TYR:CE2	2:B:1168:LYS:HD2	2.53	0.43
1:A:82:LEU:HB2	1:A:84:ILE:CD1	2.48	0.43
1:A:358:ASP:HA	1:A:361:PHE:CE1	2.53	0.43
1:A:476:ARG:NH1	1:A:1638:PHE:HA	2.33	0.43
1:A:1041:GLU:HG2	1:A:1659:ASN:HB2	2.01	0.43
1:A:1052:ARG:HG2	1:A:1058:ILE:HD13	2.00	0.43
2:B:700:ASN:O	2:B:703:GLN:HB3	2.18	0.43
2:B:754:THR:OG1	2:B:755:ASN:N	2.50	0.43
3:C:257:CYS:SG	3:C:288:GLU:HG3	2.59	0.43
3:C:328:ILE:HG21	11:K:106:THR:HG22	1.99	0.43
5:E:57:LEU:HB2	5:E:76:PHE:HB2	2.00	0.43
1:M:358:ASP:HA	1:M:361:PHE:CE1	2.53	0.43
1:M:578:SER:HB2	1:M:584:SER:HB2	2.00	0.43
1:M:736:ARG:HA	1:M:737:PRO:C	2.44	0.43
1:M:829:SER:OG	1:M:830:ARG:N	2.51	0.43
2:N:480:HIS:CE1	2:N:482:GLY:H	2.36	0.43
3:O:78:ILE:HG23	3:O:79:ALA:H	1.84	0.43
1:A:401:ILE:HD12	1:A:434:PHE:CD1	2.53	0.43
1:A:1110:TYR:OH	1:A:1127:LYS:HE2	2.18	0.43
1:A:1189:ASP:OD1	6:F:77:LYS:HB3	2.17	0.43
1:A:1246:THR:H	1:A:1566:THR:CB	2.24	0.43
1:A:1320:ILE:O	1:A:1324:PHE:HB3	2.18	0.43
2:B:181:LEU:HD12	2:B:182:ILE:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:193:PRO:HB3	2:B:352:MET:HE2	2.00	0.43
3:C:70:ALA:HB1	3:C:310:PHE:HZ	1.83	0.43
3:C:267:GLU:O	3:C:267:GLU:HG2	2.19	0.43
8:H:72:ALA:CB	8:H:122:LEU:HB3	2.48	0.43
10:J:24:LEU:HD13	10:J:34:ALA:HB1	2.00	0.43
2:N:74:LYS:H	2:N:126:ASN:ND2	2.16	0.43
2:N:778:ALA:CB	10:V:8:PHE:HB3	2.45	0.43
3:O:89:VAL:C	12:X:59:GLN:HE22	2.26	0.43
3:O:170:TYR:HA	3:O:199:VAL:HA	1.99	0.43
5:Q:57:LEU:HB2	5:Q:76:PHE:HB2	2.00	0.43
8:T:11:PHE:HA	8:T:31:SER:HB2	2.00	0.43
1:A:119:PHE:CD2	1:A:218:PHE:HB2	2.54	0.43
2:B:74:LYS:H	2:B:126:ASN:ND2	2.17	0.43
2:B:90:SER:HB3	2:B:878:VAL:HG23	2.00	0.43
2:B:227:ASN:OD1	2:B:227:ASN:N	2.52	0.43
2:B:819:ARG:NH1	2:B:820:ARG:HA	2.33	0.43
3:C:78:ILE:HG23	3:C:79:ALA:H	1.84	0.43
3:C:265:LEU:HD23	3:C:265:LEU:HA	1.75	0.43
1:M:595:ARG:NH2	1:M:596:HIS:O	2.52	0.43
1:M:670:ASP:OD1	1:M:818:PRO:HB2	2.19	0.43
1:M:1110:TYR:OH	1:M:1127:LYS:HE2	2.18	0.43
1:M:1249:LEU:HD12	1:M:1542:VAL:HG13	2.00	0.43
2:N:829:ASP:OD2	12:X:22:TYR:OH	2.37	0.43
3:O:107:ILE:C	3:O:109:LEU:N	2.75	0.43
1:A:27:ILE:HG21	2:B:1096:ILE:HG23	1.99	0.43
1:A:470:LYS:C	1:A:472:GLU:N	2.74	0.43
1:A:618:ALA:C	1:A:619:HIS:HD2	2.27	0.43
1:A:1066:ASP:OD1	1:A:1067:SER:N	2.52	0.43
1:A:1103:ASP:OD2	1:A:1106:THR:OG1	2.25	0.43
2:B:402:GLN:HG3	2:B:425:VAL:HG23	2.01	0.43
2:B:684:ILE:H	2:B:684:ILE:HG13	1.69	0.43
3:C:43:LYS:HE2	11:K:108:LYS:HE2	1.99	0.43
1:M:18:ILE:HD13	1:M:359:MET:HA	1.99	0.43
1:M:30:LYS:HE2	1:M:51:ASP:OD1	2.19	0.43
1:M:682:LEU:HD23	1:M:683:ARG:H	1.82	0.43
1:M:701:THR:HG23	1:M:743:GLY:H	1.83	0.43
1:M:1001:THR:HA	2:N:976:THR:HG23	2.01	0.43
1:M:1019:LEU:O	1:M:1022:THR:OG1	2.26	0.43
1:M:1504:LEU:O	1:M:1508:LEU:HG	2.18	0.43
2:N:94:ARG:HG3	2:N:878:VAL:HG22	2.00	0.43
2:N:235:GLY:CA	2:N:284:ARG:HH11	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:589:GLU:O	2:N:593:LYS:HG3	2.19	0.43
2:N:795:ASP:HA	2:N:884:GLN:O	2.19	0.43
10:V:22:LEU:HA	10:V:22:LEU:HD12	1.76	0.43
1:A:891:ASN:O	1:A:895:VAL:HG23	2.19	0.43
1:A:1045:VAL:HG12	1:A:1190:PRO:HA	2.01	0.43
1:A:1070:VAL:HA	1:A:1073:GLN:NE2	2.32	0.43
1:A:1083:ALA:HB2	1:A:1175:PHE:CE1	2.54	0.43
1:A:1624:MET:SD	1:A:1624:MET:N	2.91	0.43
2:B:145:ARG:HH21	2:B:168:GLU:HB3	1.83	0.43
2:B:197:ILE:HD13	2:B:366:ALA:CB	2.49	0.43
2:B:251:PRO:HG2	2:B:254:MET:HB2	2.01	0.43
2:B:379:LEU:HD12	2:B:382:PHE:CE2	2.53	0.43
2:B:901:LYS:C	2:B:1021:LEU:HD13	2.44	0.43
3:C:318:MET:HB2	3:C:323:LEU:CD2	2.49	0.43
5:E:40:GLN:O	5:E:44:MET:HG2	2.19	0.43
5:E:82:VAL:HB	5:E:86:GLU:HB2	2.01	0.43
9:I:7:LEU:HD23	9:I:7:LEU:HA	1.81	0.43
1:M:178:LEU:HD21	1:M:182:ARG:NH2	2.33	0.43
1:M:1229:PRO:O	1:M:1233:GLU:HG2	2.19	0.43
2:N:181:LEU:HD12	2:N:182:ILE:N	2.34	0.43
2:N:643:THR:HG23	2:N:645:GLU:H	1.84	0.43
3:O:40:ASP:O	3:O:44:LYS:HG2	2.19	0.43
3:O:72:ALA:O	3:O:76:ILE:HG12	2.17	0.43
3:O:257:CYS:SG	3:O:288:GLU:HG3	2.59	0.43
1:A:873:ALA:O	1:A:877:VAL:HG23	2.18	0.43
2:B:868:VAL:HG13	2:B:888:VAL:HG23	2.01	0.43
2:B:928:MET:HE3	10:J:42:ARG:HD3	2.01	0.43
2:B:1138:LYS:H	2:B:1138:LYS:HG3	1.69	0.43
3:C:89:VAL:C	12:L:59:GLN:HE22	2.27	0.43
3:C:138:THR:HG22	3:C:216:ILE:HG22	2.01	0.43
5:E:59:PHE:C	5:E:74:ILE:HG12	2.44	0.43
5:E:186:LYS:O	5:E:189:GLU:HG2	2.19	0.43
11:K:86:THR:OG1	11:K:87:ALA:N	2.52	0.43
1:M:475:PHE:HA	1:M:475:PHE:HD1	1.72	0.43
1:M:1083:ALA:HB2	1:M:1175:PHE:CE1	2.54	0.43
2:N:505:CYS:SG	2:N:506:PRO:HD2	2.58	0.43
2:N:868:VAL:HG13	2:N:888:VAL:HG23	2.01	0.43
3:O:321:ASP:O	3:O:325:ILE:HG13	2.18	0.43
3:O:332:LYS:HB2	3:O:332:LYS:HE3	1.74	0.43
5:Q:59:PHE:C	5:Q:74:ILE:HG12	2.44	0.43
1:A:27:ILE:O	2:B:1116:ARG:NE	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:595:ARG:NH2	1:A:596:HIS:O	2.52	0.42
1:A:670:ASP:OD1	1:A:818:PRO:HB2	2.19	0.42
1:A:1060:GLN:HE21	1:A:1610:ASP:CG	2.23	0.42
2:B:854:GLN:HG3	2:B:856:PHE:CE2	2.54	0.42
2:B:1059:MET:HE3	2:B:1059:MET:HB2	1.81	0.42
3:C:77:LEU:HD13	3:C:327:SER:OG	2.19	0.42
3:C:335:CYS:HB3	11:K:99:ILE:CG1	2.49	0.42
8:H:11:PHE:HA	8:H:31:SER:CB	2.49	0.42
12:L:37:GLU:HG2	12:L:38:VAL:O	2.19	0.42
1:M:69:ASP:CG	1:M:71:ARG:H	2.27	0.42
1:M:95:MET:HE3	1:M:95:MET:HB3	1.78	0.42
1:M:104:LEU:HD12	1:M:236:PRO:HG2	2.00	0.42
1:M:548:ASP:OD2	1:M:550:THR:HG23	2.18	0.42
1:M:603:LEU:HD22	1:M:621:ALA:HB2	2.00	0.42
1:M:618:ALA:C	1:M:619:HIS:HD2	2.27	0.42
1:M:873:ALA:O	1:M:877:VAL:HG23	2.18	0.42
1:M:1115:LEU:HD23	1:M:1115:LEU:HA	1.90	0.42
1:M:1246:THR:H	1:M:1566:THR:CB	2.24	0.42
1:M:1320:ILE:O	1:M:1324:PHE:HB3	2.18	0.42
2:N:28:ALA:O	2:N:477:ARG:HD3	2.18	0.42
2:N:190:ARG:HG3	2:N:376:GLU:CD	2.44	0.42
2:N:402:GLN:HG3	2:N:425:VAL:HG23	2.01	0.42
2:N:540:LEU:HD21	2:N:586:MET:SD	2.59	0.42
2:N:781:ARG:NH1	10:V:8:PHE:O	2.51	0.42
3:O:70:ALA:HB1	3:O:310:PHE:HZ	1.83	0.42
3:O:90:TYR:HA	12:X:59:GLN:OE1	2.19	0.42
7:S:98:PRO:O	7:S:115:ARG:NH1	2.53	0.42
1:A:578:SER:HB2	1:A:584:SER:HB2	2.00	0.42
1:A:736:ARG:HA	1:A:737:PRO:C	2.44	0.42
2:B:95:SER:O	2:B:95:SER:OG	2.32	0.42
2:B:508:HIS:CE1	2:B:520:HIS:CG	3.08	0.42
2:B:589:GLU:O	2:B:593:LYS:HG3	2.19	0.42
3:C:291:ARG:HE	3:C:291:ARG:HB3	1.65	0.42
3:C:332:LYS:HE3	3:C:332:LYS:HB2	1.74	0.42
5:E:4:GLU:N	5:E:6:LYS:HE2	2.34	0.42
10:J:47:ARG:H	10:J:47:ARG:HG3	1.70	0.42
12:L:20:MET:HB3	12:L:22:TYR:CZ	2.55	0.42
1:M:372:PHE:CE1	2:N:1157:TYR:HA	2.55	0.42
1:M:1070:VAL:HA	1:M:1073:GLN:HG3	2.00	0.42
1:M:1156:LEU:HA	1:M:1170:LEU:HD13	2.01	0.42
1:M:1560:SER:O	1:M:1560:SER:OG	2.31	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:1673:GLY:HA2	6:R:78:TYR:CD1	2.54	0.42
2:N:642:SER:OG	2:N:643:THR:N	2.53	0.42
2:N:700:ASN:O	2:N:703:GLN:HB3	2.19	0.42
2:N:1114:ARG:HG3	2:N:1132:TRP:NE1	2.34	0.42
3:O:89:VAL:H	12:X:59:GLN:NE2	2.17	0.42
3:O:267:GLU:HG2	3:O:267:GLU:O	2.19	0.42
5:Q:85:LYS:HA	5:Q:85:LYS:HD3	1.92	0.42
5:Q:147:LYS:HB3	5:Q:194:VAL:HB	2.01	0.42
6:R:109:GLN:O	6:R:112:MET:HB2	2.19	0.42
10:V:24:LEU:HD13	10:V:34:ALA:HB1	2.00	0.42
1:A:212:LYS:HE3	1:A:1627:GLU:OE2	2.19	0.42
2:B:192:HIS:HD2	2:B:193:PRO:HD2	1.84	0.42
2:B:642:SER:OG	2:B:643:THR:N	2.52	0.42
2:B:643:THR:HG23	2:B:645:GLU:H	1.84	0.42
2:B:840:ASP:HA	2:B:860:TYR:HD2	1.84	0.42
3:C:86:PHE:CD1	3:C:112:ILE:HD11	2.54	0.42
3:C:113:SER:O	3:C:191:ILE:HG23	2.19	0.42
6:F:120:ILE:HA	6:F:121:PRO:HD3	1.90	0.42
7:G:13:LEU:O	7:G:73:TRP:HA	2.20	0.42
7:G:98:PRO:O	7:G:115:ARG:NH1	2.53	0.42
1:M:119:PHE:CD2	1:M:218:PHE:HB2	2.54	0.42
1:M:212:LYS:HE3	1:M:1627:GLU:OE2	2.19	0.42
1:M:1605:LEU:H	1:M:1605:LEU:HD12	1.85	0.42
2:N:195:ALA:HB3	2:N:367:ASP:H	1.85	0.42
2:N:227:ASN:OD1	2:N:227:ASN:N	2.52	0.42
2:N:537:ILE:O	2:N:541:LEU:HG	2.18	0.42
2:N:901:LYS:C	2:N:1021:LEU:HD13	2.44	0.42
3:O:113:SER:HB3	3:O:194:VAL:HB	2.01	0.42
3:O:265:LEU:HD23	3:O:265:LEU:HA	1.75	0.42
3:O:318:MET:HB2	3:O:323:LEU:CD2	2.49	0.42
1:A:30:LYS:HE2	1:A:51:ASP:OD1	2.19	0.42
1:A:114:VAL:HG21	1:A:178:LEU:HD23	2.00	0.42
1:A:421:GLU:O	1:A:425:ARG:HG2	2.20	0.42
2:B:101:VAL:HG23	2:B:101:VAL:O	2.20	0.42
2:B:463:VAL:O	2:B:465:GLU:N	2.53	0.42
2:B:592:VAL:HB	2:B:645:GLU:HG2	2.00	0.42
2:B:1114:ARG:HG3	2:B:1132:TRP:NE1	2.34	0.42
7:G:78:VAL:HG22	7:G:79:LEU:H	1.84	0.42
8:H:71:ALA:HB1	8:H:124:ARG:HE	1.84	0.42
1:M:21:VAL:HG23	1:M:364:ASN:OD1	2.19	0.42
1:M:367:VAL:HA	1:M:368:PRO:HD3	1.86	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:543:HIS:HE1	1:M:551:LEU:HD11	1.84	0.42
1:M:1066:ASP:OD1	1:M:1067:SER:N	2.52	0.42
1:M:1607:LEU:HD12	1:M:1607:LEU:HA	1.80	0.42
2:N:590:TYR:HA	2:N:593:LYS:HD2	2.01	0.42
2:N:1034:THR:HG22	2:N:1035:GLY:N	2.34	0.42
4:P:46:VAL:HG23	4:P:47:LEU:H	1.84	0.42
5:Q:4:GLU:N	5:Q:6:LYS:HE2	2.34	0.42
7:S:78:VAL:HG22	7:S:79:LEU:H	1.84	0.42
7:S:88:CYS:HA	7:S:152:PHE:O	2.19	0.42
7:S:124:PHE:HB2	7:S:136:TRP:HE3	1.83	0.42
7:S:125:ILE:HG12	7:S:135:ARG:HB2	2.00	0.42
1:A:543:HIS:HE1	1:A:551:LEU:HD11	1.84	0.42
1:A:578:SER:HB3	1:A:581:TYR:O	2.19	0.42
1:A:603:LEU:HD22	1:A:621:ALA:HB2	2.00	0.42
1:A:1229:PRO:O	1:A:1233:GLU:HG2	2.19	0.42
1:A:1605:LEU:H	1:A:1605:LEU:HD12	1.85	0.42
2:B:365:CYS:HB2	2:B:619:ASN:O	2.19	0.42
2:B:609:LEU:HD12	2:B:629:SER:HB3	2.02	0.42
2:B:811:GLY:N	2:B:846:ALA:O	2.31	0.42
3:C:218:GLY:HA3	3:C:226:PHE:CZ	2.54	0.42
4:D:46:VAL:HG23	4:D:47:LEU:H	1.84	0.42
11:K:52:TYR:CE1	11:K:56:LYS:HE3	2.55	0.42
12:L:41:CYS:N	12:L:46:HIS:O	2.39	0.42
1:M:15:LYS:NZ	1:M:1652:GLY:O	2.52	0.42
1:M:58:LEU:HD23	1:M:58:LEU:HA	1.79	0.42
1:M:599:ASN:HD22	1:M:622:ARG:HA	1.84	0.42
1:M:847:ASP:OD2	1:M:936:ASN:ND2	2.53	0.42
2:N:78:ARG:NH1	2:N:130:ARG:HE	2.17	0.42
2:N:101:VAL:HG23	2:N:101:VAL:O	2.20	0.42
2:N:197:ILE:HD13	2:N:366:ALA:CB	2.49	0.42
2:N:595:ARG:NH2	2:N:645:GLU:OE2	2.53	0.42
3:O:86:PHE:CD1	3:O:112:ILE:HD11	2.54	0.42
3:O:218:GLY:HA3	3:O:226:PHE:CZ	2.54	0.42
7:S:77:ASP:OD1	7:S:77:ASP:N	2.51	0.42
8:T:11:PHE:HA	8:T:31:SER:CB	2.49	0.42
8:T:71:ALA:HB1	8:T:124:ARG:HE	1.84	0.42
1:A:695:TRP:CZ2	1:A:937:HIS:HD2	2.37	0.42
1:A:959:LEU:HA	1:A:997:SER:O	2.19	0.42
2:B:96:SER:O	7:S:95:LEU:HD22	2.19	0.42
2:B:116:ARG:NE	7:S:131:GLU:HB2	2.35	0.42
2:B:181:LEU:HD12	2:B:182:ILE:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:821:GLU:HB2	2:B:822:TRP:HD1	1.85	0.42
2:B:834:ILE:HD11	2:B:871:VAL:HG22	2.02	0.42
8:H:11:PHE:HA	8:H:31:SER:HB2	2.00	0.42
1:M:578:SER:HB3	1:M:581:TYR:O	2.19	0.42
1:M:695:TRP:CZ2	1:M:937:HIS:HD2	2.37	0.42
1:M:739:ILE:HD12	1:M:741:TRP:HH2	1.83	0.42
1:M:1259:ARG:NH2	1:M:1557:ASN:HD21	2.17	0.42
2:N:192:HIS:HD2	2:N:193:PRO:HD2	1.84	0.42
2:N:609:LEU:HD12	2:N:629:SER:HB3	2.02	0.42
3:O:261:GLY:O	3:O:278:ALA:HB3	2.20	0.42
4:P:56:TYR:CE1	7:S:106:LEU:HA	2.55	0.42
1:A:37:LEU:HD11	1:A:50:TYR:CD2	2.55	0.42
1:A:88:HIS:CD2	1:A:362:LEU:HD11	2.55	0.42
1:A:610:THR:O	2:B:1059:MET:HG2	2.19	0.42
1:A:924:CYS:O	1:A:928:GLY:N	2.40	0.42
1:A:1001:THR:HG23	2:B:976:THR:HG23	2.01	0.42
1:A:1530:LYS:HB3	1:A:1543:ILE:HD13	2.01	0.42
1:A:1657:LEU:HD11	1:A:1663:ARG:HD3	2.01	0.42
2:B:348:LEU:HD13	2:B:567:ILE:HG13	2.02	0.42
2:B:872:ARG:HB2	2:B:887:HIS:HB3	2.02	0.42
3:C:125:PRO:HB2	3:C:129:GLN:CB	2.50	0.42
3:C:130:GLU:H	3:C:130:GLU:CD	2.19	0.42
1:M:421:GLU:O	1:M:425:ARG:HG2	2.20	0.42
1:M:610:THR:O	2:N:1059:MET:HG2	2.19	0.42
1:M:891:ASN:O	1:M:895:VAL:HG23	2.19	0.42
1:M:901:LYS:HE2	9:U:62:SER:HB2	2.01	0.42
2:N:419:ARG:O	2:N:423:THR:HG23	2.20	0.42
2:N:873:LEU:HD23	2:N:873:LEU:HA	1.76	0.42
3:O:186:PHE:HB3	3:O:189:ASN:O	2.20	0.42
5:Q:40:GLN:O	5:Q:44:MET:HG2	2.19	0.42
9:U:7:LEU:HA	9:U:7:LEU:HD23	1.81	0.42
10:V:40:LEU:HD13	10:V:46:ARG:HA	2.00	0.42
1:A:599:ASN:HD22	1:A:622:ARG:HA	1.84	0.42
1:A:1256:SER:H	1:A:1259:ARG:HB3	1.84	0.42
1:A:1336:ILE:HD11	1:A:1505:MET:HE1	2.01	0.42
1:A:1582:ARG:O	1:A:1586:VAL:HG23	2.20	0.42
3:C:40:ASP:O	3:C:44:LYS:HG2	2.19	0.42
3:C:81:ILE:HD11	3:C:228:PRO:HG3	2.02	0.42
3:C:113:SER:HB3	3:C:194:VAL:HB	2.02	0.42
7:G:88:CYS:HA	7:G:152:PHE:O	2.19	0.42
8:H:59:ILE:HG13	8:H:59:ILE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:2:ASN:HD21	1:M:545:GLN:HE22	1.67	0.42
1:M:543:HIS:HA	1:M:554:LEU:HD12	2.02	0.42
2:N:365:CYS:HB2	2:N:619:ASN:O	2.19	0.42
2:N:834:ILE:HD11	2:N:871:VAL:HG22	2.02	0.42
3:O:53:LEU:HD23	3:O:54:ASP:N	2.35	0.42
11:W:44:HIS:CD2	11:W:44:HIS:H	2.38	0.42
1:A:630:ILE:HG21	1:A:651:MET:HE1	2.02	0.42
1:A:774:TYR:HD1	1:A:933:PHE:CD1	2.38	0.42
1:A:847:ASP:OD2	1:A:936:ASN:ND2	2.53	0.42
1:A:1156:LEU:HA	1:A:1170:LEU:HD13	2.01	0.42
2:B:151:LEU:HA	2:B:154:LEU:HD12	2.02	0.42
2:B:595:ARG:NH2	2:B:645:GLU:OE2	2.53	0.42
2:B:1162:LEU:HD12	2:B:1162:LEU:HA	1.83	0.42
3:C:147:CYS:HB3	3:C:204:ARG:O	2.18	0.42
3:C:157:GLU:O	3:C:159:ASP:N	2.50	0.42
3:C:160:PRO:HG3	3:C:204:ARG:NH1	2.35	0.42
5:E:147:LYS:HB3	5:E:194:VAL:HB	2.01	0.42
8:H:67:ASP:OD1	8:H:71:ALA:HB3	2.20	0.42
8:H:114:LEU:HD13	8:H:114:LEU:HA	1.86	0.42
12:L:41:CYS:HB3	12:L:45:GLY:H	1.85	0.42
1:M:397:SER:O	1:M:401:ILE:HG12	2.20	0.42
1:M:733:ALA:O	8:T:77:TYR:N	2.53	0.42
1:M:1038:LYS:NZ	1:M:1629:ASN:HD22	2.17	0.42
1:M:1045:VAL:HG12	1:M:1190:PRO:HA	2.01	0.42
1:M:1624:MET:SD	1:M:1624:MET:N	2.91	0.42
1:M:1679:ILE:HA	6:R:124:VAL:HA	2.01	0.42
2:N:279:THR:HG21	9:U:46:THR:HA	2.01	0.42
2:N:734:THR:O	10:V:51:THR:OG1	2.38	0.42
2:N:840:ASP:HA	2:N:860:TYR:HD2	1.84	0.42
2:N:854:GLN:HG3	2:N:856:PHE:CE2	2.54	0.42
3:O:78:ILE:HG23	3:O:79:ALA:N	2.35	0.42
3:O:138:THR:HG22	3:O:216:ILE:HG22	2.01	0.42
8:T:24:VAL:HG13	8:T:42:ILE:O	2.20	0.42
1:A:1:MET:HE2	1:A:1:MET:HA	2.02	0.42
1:A:69:ASP:CG	1:A:71:ARG:H	2.27	0.42
1:A:511:THR:HA	1:A:596:HIS:CE1	2.55	0.42
1:A:543:HIS:CE1	1:A:551:LEU:HD11	2.55	0.42
1:A:893:GLU:HG2	2:B:618:HIS:CE1	2.55	0.42
2:B:419:ARG:O	2:B:423:THR:HG23	2.20	0.42
2:B:781:ARG:HB3	10:J:8:PHE:HD1	1.85	0.42
2:B:795:ASP:HA	2:B:884:GLN:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:78:ILE:HG23	3:C:79:ALA:N	2.35	0.42
3:C:179:GLN:HB2	3:C:182:GLN:NE2	2.35	0.42
3:C:203:LEU:HD22	3:C:207:GLN:HG3	2.02	0.42
3:C:334:LYS:HB3	11:K:46:LEU:HD12	2.01	0.42
5:E:71:THR:HG1	5:E:72:ILE:H	1.68	0.42
11:K:44:HIS:CD2	11:K:44:HIS:H	2.38	0.42
1:M:37:LEU:HD11	1:M:50:TYR:CD2	2.55	0.42
1:M:68:LEU:HA	1:M:68:LEU:HD23	1.78	0.42
1:M:77:PHE:CE2	2:N:1096:ILE:HG12	2.55	0.42
1:M:82:LEU:HB2	1:M:84:ILE:CD1	2.48	0.42
1:M:495:ASP:N	1:M:632:MET:O	2.52	0.42
1:M:531:VAL:HG21	1:M:569:LEU:CD1	2.50	0.42
1:M:674:LEU:HD22	1:M:679:GLY:O	2.20	0.42
1:M:759:ARG:CZ	1:M:1092:LYS:HB2	2.50	0.42
1:M:885:ILE:HG22	1:M:889:ASN:ND2	2.35	0.42
1:M:962:GLN:OE1	1:M:994:PHE:HB2	2.20	0.42
2:N:39:LEU:HA	2:N:39:LEU:HD12	1.75	0.42
2:N:180:LYS:HD3	2:N:180:LYS:HA	1.68	0.42
2:N:564:ASP:HA	2:N:628:PHE:CD1	2.55	0.42
2:N:1032:ARG:NH1	2:N:1035:GLY:HA3	2.35	0.42
2:N:1059:MET:HE3	2:N:1059:MET:HB2	1.81	0.42
3:O:179:GLN:HB2	3:O:182:GLN:NE2	2.35	0.42
8:T:59:ILE:O	8:T:59:ILE:HG13	2.20	0.42
1:A:390:LEU:HB3	1:A:444:LEU:HD13	2.02	0.41
1:A:489:ARG:NH2	1:A:648:GLU:OE2	2.53	0.41
1:A:495:ASP:OD1	1:A:497:ASN:N	2.53	0.41
1:A:1105:GLU:H	1:A:1105:GLU:CD	2.26	0.41
1:A:1631:SER:O	1:A:1631:SER:OG	2.36	0.41
2:B:91:SER:OG	7:S:131:GLU:HB3	2.20	0.41
2:B:367:ASP:O	2:B:369:PRO:HD3	2.20	0.41
2:B:402:GLN:HE21	2:B:428:LYS:HD3	1.84	0.41
3:C:237:LEU:HD11	3:C:281:ARG:HG2	2.02	0.41
4:D:17:LEU:HD23	4:D:17:LEU:N	2.35	0.41
5:E:54:ARG:CB	5:E:78:LYS:HD3	2.50	0.41
1:M:88:HIS:CD2	1:M:362:LEU:HD11	2.54	0.41
1:M:489:ARG:NH2	1:M:648:GLU:OE2	2.53	0.41
1:M:959:LEU:HA	1:M:997:SER:O	2.19	0.41
1:M:1041:GLU:HG2	1:M:1659:ASN:HB2	2.01	0.41
1:M:1138:SER:HB3	1:M:1141:PHE:CB	2.47	0.41
1:M:1662:SER:O	1:M:1666:VAL:HG22	2.20	0.41
2:N:508:HIS:CE1	2:N:520:HIS:CG	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:510:PRO:O	2:N:515:CYS:HA	2.20	0.41
2:N:678:PRO:O	2:N:681:VAL:HG12	2.20	0.41
2:N:821:GLU:HB2	2:N:822:TRP:HD1	1.85	0.41
2:N:1165:MET:O	2:N:1167:ILE:HD12	2.20	0.41
3:O:147:CYS:HB3	3:O:204:ARG:O	2.19	0.41
5:Q:186:LYS:O	5:Q:189:GLU:HG2	2.19	0.41
7:S:13:LEU:O	7:S:73:TRP:HA	2.20	0.41
11:W:52:TYR:CE1	11:W:56:LYS:HE3	2.55	0.41
1:A:96:TYR:CD1	1:A:240:LYS:HB3	2.55	0.41
1:A:571:THR:HG23	1:A:573:GLN:HG2	2.03	0.41
1:A:613:LYS:CG	1:A:614:PRO:HD3	2.50	0.41
1:A:674:LEU:HD22	1:A:679:GLY:O	2.20	0.41
1:A:697:THR:O	1:A:744:LYS:HE2	2.21	0.41
1:A:763:ASN:OD1	1:A:763:ASN:N	2.54	0.41
1:A:1037:MET:HE2	2:B:1062:ASP:OD2	2.20	0.41
2:B:180:LYS:HZ3	2:B:463:VAL:HB	1.85	0.41
2:B:190:ARG:HB2	2:B:630:ASN:ND2	2.35	0.41
2:B:237:THR:OG1	2:B:252:SER:OG	2.13	0.41
7:G:44:ILE:HD12	7:G:44:ILE:HA	1.93	0.41
1:M:495:ASP:OD1	1:M:497:ASN:N	2.53	0.41
1:M:1549:LEU:HD11	1:M:1565:TYR:CE2	2.55	0.41
1:M:1582:ARG:O	1:M:1586:VAL:HG23	2.20	0.41
2:N:24:ASP:OD2	2:N:25:LEU:N	2.53	0.41
2:N:348:LEU:HD13	2:N:567:ILE:HG13	2.02	0.41
2:N:463:VAL:O	2:N:465:GLU:N	2.53	0.41
2:N:1032:ARG:NE	2:N:1044:PRO:HB3	2.32	0.41
7:S:98:PRO:HD3	7:S:124:PHE:CD2	2.55	0.41
11:W:28:HIS:HB3	11:W:35:VAL:HG23	2.02	0.41
12:X:20:MET:HB3	12:X:22:TYR:CZ	2.55	0.41
12:X:41:CYS:HB3	12:X:45:GLY:H	1.85	0.41
1:A:2:ASN:HD21	1:A:545:GLN:HE22	1.66	0.41
1:A:531:VAL:HG21	1:A:569:LEU:CD1	2.50	0.41
1:A:717:LYS:NZ	11:K:67:ILE:O	2.46	0.41
1:A:1124:VAL:HG22	1:A:1128:TYR:HB2	2.02	0.41
1:A:1572:ILE:HG13	1:A:1576:TYR:HD2	1.85	0.41
2:B:74:LYS:HB3	2:B:126:ASN:HB3	2.03	0.41
2:B:192:HIS:HB2	2:B:628:PHE:CZ	2.55	0.41
2:B:274:LYS:O	2:B:275:ASP:C	2.63	0.41
2:B:507:VAL:HA	2:B:701:MET:HE2	2.02	0.41
2:B:510:PRO:O	2:B:515:CYS:HA	2.20	0.41
2:B:590:TYR:OH	2:B:601:GLU:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1165:MET:O	2:B:1167:ILE:HD12	2.20	0.41
7:G:85:LYS:HD3	7:G:155:ASP:O	2.21	0.41
7:G:98:PRO:HD3	7:G:124:PHE:CD2	2.56	0.41
7:G:119:PRO:HB2	7:G:121:ASP:OD1	2.19	0.41
11:K:29:SER:OG	11:K:33:THR:N	2.50	0.41
1:M:511:THR:HA	1:M:596:HIS:CE1	2.55	0.41
1:M:685:LEU:HD13	1:M:689:HIS:HB3	2.03	0.41
1:M:1251:LEU:HD13	1:M:1251:LEU:HA	1.87	0.41
1:M:1336:ILE:O	1:M:1340:LEU:HD23	2.20	0.41
2:N:123:TRP:HE1	2:N:422:LEU:CG	2.24	0.41
2:N:190:ARG:HB2	2:N:630:ASN:ND2	2.35	0.41
2:N:197:ILE:HD11	2:N:359:LEU:HD21	2.01	0.41
2:N:354:ARG:NH1	2:N:358:ALA:HB2	2.34	0.41
3:O:50:ILE:CD1	11:W:113:LEU:HB3	2.48	0.41
5:Q:23:HIS:HE1	5:Q:34:LEU:HD11	1.85	0.41
8:T:15:SER:HB3	8:T:28:THR:CG2	2.50	0.41
1:A:1005:PRO:HG3	2:B:969:PHE:CG	2.56	0.41
1:A:1259:ARG:NH2	1:A:1557:ASN:HD21	2.17	0.41
1:A:1549:LEU:HD11	1:A:1565:TYR:CE2	2.55	0.41
2:B:56:CYS:SG	2:B:76:SER:HB2	2.60	0.41
2:B:78:ARG:NH1	2:B:130:ARG:HE	2.17	0.41
2:B:188:PRO:HA	2:B:374:HIS:O	2.20	0.41
2:B:271:ILE:HG13	2:B:272:VAL:HG13	2.03	0.41
2:B:609:LEU:HG	2:B:628:PHE:O	2.20	0.41
2:B:1032:ARG:NH1	2:B:1035:GLY:HA3	2.35	0.41
1:M:1:MET:HA	1:M:1:MET:HE2	2.02	0.41
1:M:527:MET:O	1:M:531:VAL:HG23	2.21	0.41
1:M:613:LYS:CG	1:M:614:PRO:HD3	2.50	0.41
2:N:56:CYS:SG	2:N:76:SER:HB2	2.60	0.41
2:N:117:LEU:HD22	2:N:140:ILE:HG21	2.03	0.41
2:N:193:PRO:HB3	2:N:352:MET:HE2	2.00	0.41
2:N:262:THR:HG22	2:N:266:GLU:HB2	2.01	0.41
2:N:590:TYR:OH	2:N:601:GLU:N	2.53	0.41
2:N:734:THR:OG1	10:V:51:THR:OG1	2.19	0.41
2:N:908:GLN:NE2	2:N:938:ALA:HB1	2.36	0.41
2:N:985:LEU:HD12	2:N:985:LEU:HA	1.83	0.41
3:O:160:PRO:HG3	3:O:204:ARG:NH1	2.35	0.41
7:S:8:LYS:HE2	7:S:8:LYS:HB2	1.76	0.41
7:S:53:ASN:HB3	7:S:55:ARG:NH1	2.35	0.41
8:T:3:GLU:HG3	8:T:5:VAL:HG23	2.02	0.41
12:X:37:GLU:HG2	12:X:38:VAL:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:MET:HE3	1:A:95:MET:HB3	1.78	0.41
1:A:759:ARG:CZ	1:A:1092:LYS:HB2	2.50	0.41
2:B:29:VAL:C	2:B:31:PRO:HD2	2.46	0.41
2:B:167:GLU:OE1	2:B:167:GLU:N	2.53	0.41
2:B:630:ASN:OD1	2:B:633:ARG:HD3	2.21	0.41
3:C:163:LEU:HG	3:C:164:TYR:CE1	2.56	0.41
5:E:62:LYS:HA	5:E:71:THR:HG1	1.84	0.41
8:H:15:SER:HB3	8:H:28:THR:CG2	2.50	0.41
8:H:24:VAL:HG13	8:H:42:ILE:O	2.20	0.41
10:J:33:GLU:O	10:J:36:ASP:HB2	2.20	0.41
1:M:106:CYS:SG	1:M:231:CYS:CB	3.03	0.41
1:M:849:ARG:HH12	2:N:993:HIS:CE1	2.38	0.41
1:M:972:LEU:HD23	1:M:972:LEU:HA	1.61	0.41
1:M:1659:ASN:OD1	1:M:1659:ASN:N	2.49	0.41
2:N:1104:MET:HG3	2:N:1105:ASN:N	2.35	0.41
3:O:77:LEU:HD13	3:O:327:SER:OG	2.19	0.41
3:O:81:ILE:HD11	3:O:228:PRO:HG3	2.02	0.41
3:O:260:LYS:HA	3:O:260:LYS:HD3	1.69	0.41
5:Q:82:VAL:HB	5:Q:86:GLU:HB2	2.01	0.41
7:S:127:PRO:HG2	7:S:133:GLN:O	2.21	0.41
8:T:107:SER:OG	8:T:109:ARG:NH1	2.53	0.41
1:A:77:PHE:CD2	2:B:1096:ILE:HG12	2.55	0.41
1:A:246:ILE:O	1:A:247:PHE:CG	2.74	0.41
1:A:333:ARG:HH11	1:A:361:PHE:HZ	1.68	0.41
1:A:397:SER:O	1:A:401:ILE:HG12	2.20	0.41
1:A:685:LEU:HD12	1:A:801:PHE:CD2	2.56	0.41
1:A:688:ASP:HA	2:B:937:HIS:CE1	2.55	0.41
1:A:1261:SER:HB2	1:A:1265:LYS:HE3	2.03	0.41
1:A:1583:ASN:OD1	1:A:1583:ASN:N	2.54	0.41
2:B:424:ARG:O	2:B:428:LYS:HG3	2.20	0.41
2:B:664:LYS:HE3	2:B:664:LYS:HB2	1.87	0.41
2:B:697:SER:OG	2:B:698:PRO:HD3	2.21	0.41
3:C:53:LEU:HD23	3:C:54:ASP:N	2.35	0.41
3:C:109:LEU:CD2	3:C:225:LYS:HB3	2.51	0.41
3:C:186:PHE:HB3	3:C:189:ASN:O	2.20	0.41
3:C:248:GLY:O	3:C:252:VAL:HG23	2.21	0.41
5:E:193:ILE:O	5:E:204:ASN:HA	2.21	0.41
8:H:107:SER:OG	8:H:109:ARG:NH1	2.53	0.41
11:K:28:HIS:HB3	11:K:35:VAL:HG23	2.02	0.41
1:M:246:ILE:O	1:M:247:PHE:CG	2.74	0.41
1:M:1657:LEU:HD11	1:M:1663:ARG:HD3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:29:VAL:C	2:N:31:PRO:HD2	2.46	0.41
2:N:179:GLU:CB	2:N:464:ALA:HB3	2.48	0.41
2:N:271:ILE:HG13	2:N:272:VAL:HG13	2.03	0.41
2:N:527:ILE:HD13	2:N:634:MET:HA	2.02	0.41
2:N:535:SER:O	2:N:538:PRO:HD2	2.21	0.41
2:N:961:GLY:HA2	10:V:50:LEU:HD11	2.02	0.41
3:O:109:LEU:CD2	3:O:225:LYS:HB3	2.51	0.41
3:O:125:PRO:HB2	3:O:129:GLN:CB	2.50	0.41
3:O:144:ASN:OD1	3:O:144:ASN:N	2.54	0.41
5:Q:54:ARG:CB	5:Q:78:LYS:HD3	2.50	0.41
1:A:346:LEU:HD12	1:A:346:LEU:HA	1.73	0.41
1:A:1226:LEU:HD11	1:A:1595:VAL:HG11	2.02	0.41
2:B:197:ILE:HD11	2:B:359:LEU:HD21	2.01	0.41
2:B:262:THR:HG22	2:B:266:GLU:HB2	2.01	0.41
2:B:590:TYR:HA	2:B:593:LYS:HD2	2.01	0.41
3:C:94:ASN:O	12:L:53:ARG:NH1	2.54	0.41
7:G:135:ARG:NE	7:G:135:ARG:HA	2.36	0.41
1:M:77:PHE:HE1	1:M:369:PRO:HD3	1.79	0.41
1:M:475:PHE:CE2	1:M:1636:MET:HB3	2.55	0.41
1:M:492:ILE:HD11	1:M:649:MET:HB2	2.02	0.41
1:M:506:PRO:HB3	1:M:627:GLU:O	2.21	0.41
1:M:774:TYR:HD1	1:M:933:PHE:CD1	2.38	0.41
1:M:1256:SER:H	1:M:1259:ARG:HB3	1.84	0.41
1:M:1261:SER:HB2	1:M:1265:LYS:HE3	2.03	0.41
1:M:1274:GLU:HB3	1:M:1313:TYR:OH	2.21	0.41
2:N:151:LEU:HA	2:N:154:LEU:HD12	2.01	0.41
2:N:192:HIS:HB2	2:N:628:PHE:CZ	2.56	0.41
2:N:313:VAL:HG13	2:N:314:VAL:H	1.85	0.41
2:N:367:ASP:O	2:N:369:PRO:HD3	2.20	0.41
2:N:402:GLN:HE21	2:N:428:LYS:HD3	1.84	0.41
2:N:420:LYS:HB3	2:N:420:LYS:HE2	1.70	0.41
2:N:684:ILE:H	2:N:684:ILE:HG13	1.69	0.41
2:N:779:HIS:CD2	2:N:896:PRO:HB2	2.56	0.41
3:O:248:GLY:O	3:O:252:VAL:HG23	2.21	0.41
3:O:289:CYS:SG	3:O:290:LEU:N	2.94	0.41
1:A:15:LYS:NZ	1:A:1652:GLY:O	2.52	0.41
1:A:595:ARG:HG3	1:A:596:HIS:O	2.21	0.41
1:A:1203:GLY:O	1:A:1206:SER:OG	2.23	0.41
1:A:1662:SER:O	1:A:1666:VAL:HG22	2.20	0.41
2:B:195:ALA:HB3	2:B:367:ASP:H	1.85	0.41
2:B:354:ARG:NH1	2:B:358:ALA:HB2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:808:HIS:HB3	2:B:847:TYR:CD2	2.56	0.41
3:C:289:CYS:SG	3:C:290:LEU:N	2.94	0.41
10:J:30:THR:HG21	10:J:37:LYS:NZ	2.36	0.41
11:K:32:LEU:HD12	11:K:32:LEU:HA	1.94	0.41
1:M:96:TYR:CD1	1:M:240:LYS:HB3	2.55	0.41
1:M:338:LYS:HE2	1:M:338:LYS:HB2	1.82	0.41
2:N:109:ARG:HA	2:N:874:LEU:HD23	2.03	0.41
2:N:307:LEU:HD12	2:N:307:LEU:HA	1.95	0.41
2:N:808:HIS:HB3	2:N:847:TYR:CD2	2.56	0.41
3:O:31:PHE:CD2	11:W:58:PRO:HB3	2.56	0.41
3:O:113:SER:O	3:O:191:ILE:HG23	2.20	0.41
10:V:30:THR:HG21	10:V:37:LYS:NZ	2.36	0.41
10:V:33:GLU:O	10:V:36:ASP:HB2	2.20	0.41
11:W:41:LYS:N	11:W:73:ALA:O	2.54	0.41
1:A:85:PRO:O	1:A:325:SER:OG	2.27	0.41
1:A:513:LEU:HD22	1:A:597:VAL:CG1	2.51	0.41
1:A:824:LEU:HA	1:A:827:VAL:HG12	2.02	0.41
1:A:919:SER:OG	1:A:920:ILE:N	2.54	0.41
1:A:962:GLN:OE1	1:A:994:PHE:HB2	2.20	0.41
1:A:998:ARG:NH2	1:A:1001:THR:OG1	2.54	0.41
1:A:1086:TYR:CD1	1:A:1178:LEU:HD13	2.56	0.41
1:A:1274:GLU:HB3	1:A:1313:TYR:OH	2.21	0.41
1:A:1336:ILE:O	1:A:1340:LEU:HD23	2.20	0.41
2:B:24:ASP:OD2	2:B:25:LEU:N	2.53	0.41
2:B:89:LEU:O	2:B:90:SER:C	2.64	0.41
2:B:271:ILE:O	2:B:354:ARG:HD3	2.21	0.41
2:B:313:VAL:HG13	2:B:314:VAL:H	1.85	0.41
2:B:432:ASP:O	2:B:436:LYS:NZ	2.53	0.41
2:B:527:ILE:HD13	2:B:634:MET:HA	2.02	0.41
2:B:564:ASP:HA	2:B:628:PHE:CD1	2.55	0.41
2:B:678:PRO:O	2:B:681:VAL:HG12	2.20	0.41
2:B:844:ILE:N	2:B:858:GLU:O	2.44	0.41
2:B:922:PRO:HB2	2:B:998:MET:HE2	2.03	0.41
2:B:1034:THR:HG22	2:B:1035:GLY:N	2.34	0.41
3:C:261:GLY:O	3:C:278:ALA:HB3	2.20	0.41
4:D:14:SER:HA	7:G:9:GLN:HB3	2.03	0.41
5:E:75:GLU:HG3	5:E:104:LEU:HD23	2.03	0.41
7:G:53:ASN:HB3	7:G:55:ARG:NH1	2.35	0.41
10:J:22:LEU:HD12	10:J:22:LEU:HA	1.76	0.41
11:K:95:LEU:O	11:K:99:ILE:HG13	2.20	0.41
1:M:474:LEU:HA	1:M:474:LEU:HD13	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:543:HIS:CE1	1:M:551:LEU:HD11	2.55	0.41
1:M:571:THR:HG23	1:M:573:GLN:HG2	2.02	0.41
1:M:998:ARG:NH2	1:M:1001:THR:OG1	2.54	0.41
1:M:1124:VAL:HG22	1:M:1128:TYR:HB2	2.03	0.41
1:M:1169:LEU:O	1:M:1170:LEU:HG	2.21	0.41
1:M:1258:LYS:HE3	1:M:1258:LYS:HB3	1.88	0.41
1:M:1336:ILE:HD11	1:M:1505:MET:HE1	2.01	0.41
1:M:1624:MET:HG2	1:M:1625:GLY:H	1.85	0.41
2:N:44:LEU:HD12	2:N:44:LEU:HA	1.89	0.41
2:N:188:PRO:HA	2:N:374:HIS:O	2.20	0.41
2:N:290:ARG:HA	2:N:290:ARG:HD2	1.85	0.41
2:N:424:ARG:O	2:N:428:LYS:HG3	2.20	0.41
2:N:493:VAL:C	2:N:495:LYS:N	2.79	0.41
2:N:630:ASN:OD1	2:N:633:ARG:HD3	2.21	0.41
2:N:637:PRO:HB2	2:N:646:LEU:HD11	2.03	0.41
2:N:741:LEU:HD23	2:N:741:LEU:HA	1.81	0.41
2:N:781:ARG:HD3	10:V:7:CYS:O	2.21	0.41
2:N:845:VAL:HG11	2:N:886:ILE:HD12	2.02	0.41
3:O:109:LEU:HD23	3:O:109:LEU:HA	1.71	0.41
3:O:203:LEU:HA	3:O:207:GLN:NE2	2.36	0.41
3:O:230:ALA:O	10:V:11:GLY:HA3	2.21	0.41
4:P:17:LEU:N	4:P:17:LEU:HD23	2.35	0.41
4:P:27:ASN:O	4:P:31:GLN:NE2	2.41	0.41
5:Q:69:LYS:HA	5:Q:70:GLY:HA2	1.58	0.41
5:Q:111:THR:HA	5:Q:112:PRO:HD3	1.97	0.41
5:Q:128:GLU:HG3	5:Q:129:THR:OG1	2.21	0.41
5:Q:193:ILE:O	5:Q:204:ASN:HA	2.21	0.41
7:S:56:PHE:HA	7:S:74:VAL:HA	2.03	0.41
7:S:70:SER:HG	7:S:71:PHE:H	1.67	0.41
10:V:40:LEU:HA	10:V:40:LEU:HD23	1.85	0.41
11:W:40:GLN:HG3	11:W:41:LYS:CG	2.41	0.41
11:W:44:HIS:O	11:W:45:THR:C	2.64	0.41
11:W:95:LEU:O	11:W:99:ILE:HG13	2.20	0.41
12:X:25:ALA:HB3	12:X:46:HIS:ND1	2.36	0.41
1:A:3:ILE:HG21	6:F:89:LEU:HD11	2.03	0.41
1:A:204:THR:HG22	1:A:205:THR:H	1.86	0.41
1:A:527:MET:O	1:A:531:VAL:HG23	2.21	0.41
1:A:603:LEU:HD23	1:A:603:LEU:H	1.86	0.41
1:A:671:SER:O	1:A:672:GLN:NE2	2.54	0.41
1:A:762:LEU:HD22	1:A:786:PHE:CZ	2.56	0.41
2:B:56:CYS:HA	2:B:75:ILE:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:422:LEU:HA	2:B:425:VAL:HG12	2.03	0.41
2:B:535:SER:O	2:B:538:PRO:HD2	2.21	0.41
2:B:640:HIS:HA	2:B:673:HIS:CD2	2.56	0.41
3:C:91:ILE:HG12	12:L:58:VAL:O	2.21	0.41
6:F:66:LYS:HG3	6:F:69:ARG:NH2	2.36	0.41
7:G:70:SER:HG	7:G:71:PHE:H	1.67	0.41
8:H:30:VAL:HG12	8:H:38:LEU:H	1.86	0.41
8:H:62:ASN:HB2	8:H:64:ASN:OD1	2.21	0.41
1:M:37:LEU:CD1	1:M:49:LEU:HB3	2.51	0.41
1:M:820:ILE:HD13	1:M:820:ILE:HA	1.86	0.41
1:M:919:SER:OG	1:M:920:ILE:N	2.54	0.41
1:M:1226:LEU:HD11	1:M:1595:VAL:HG11	2.02	0.41
1:M:1572:ILE:HG13	1:M:1576:TYR:HD2	1.85	0.41
2:N:74:LYS:HB3	2:N:126:ASN:HB3	2.03	0.41
2:N:167:GLU:OE1	2:N:167:GLU:N	2.53	0.41
2:N:640:HIS:HA	2:N:673:HIS:CD2	2.56	0.41
3:O:42:PHE:CE2	11:W:101:LEU:HG	2.56	0.41
4:P:27:ASN:O	4:P:31:GLN:HG2	2.21	0.41
5:Q:87:MET:HE1	5:Q:110:MET:SD	2.61	0.41
5:Q:87:MET:HG2	5:Q:118:ILE:HG12	2.02	0.41
5:Q:105:ILE:HG23	5:Q:132:GLU:N	2.37	0.41
6:R:66:LYS:HG3	6:R:69:ARG:NH2	2.36	0.41
1:A:37:LEU:CD1	1:A:49:LEU:HB3	2.51	0.40
1:A:204:THR:HG22	1:A:205:THR:N	2.36	0.40
1:A:471:LYS:HA	1:A:471:LYS:HD2	1.95	0.40
1:A:511:THR:HA	1:A:596:HIS:NE2	2.36	0.40
1:A:543:HIS:HA	1:A:554:LEU:HD12	2.02	0.40
1:A:1050:THR:O	1:A:1050:THR:OG1	2.36	0.40
1:A:1125:LEU:HD11	1:A:1138:SER:HA	2.03	0.40
1:A:1624:MET:HG2	1:A:1625:GLY:H	1.85	0.40
2:B:562:GLN:OE1	2:B:567:ILE:HG12	2.21	0.40
1:M:603:LEU:H	1:M:603:LEU:HD23	1.86	0.40
1:M:630:ILE:HG21	1:M:651:MET:HE1	2.02	0.40
1:M:979:LEU:HB3	1:M:982:PHE:CD2	2.56	0.40
1:M:1582:ARG:CZ	5:Q:195:ARG:HD3	2.51	0.40
2:N:471:ARG:HG3	2:N:475:HIS:NE2	2.37	0.40
3:O:163:LEU:HG	3:O:164:TYR:CE1	2.56	0.40
3:O:237:LEU:HD11	3:O:281:ARG:HG2	2.02	0.40
3:O:271:GLY:O	3:O:272:LYS:HD2	2.21	0.40
5:Q:173:ILE:HG13	5:Q:207:ARG:HB3	2.03	0.40
7:S:85:LYS:HD3	7:S:155:ASP:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:T:67:ASP:OD1	8:T:71:ALA:HB3	2.20	0.40
1:A:96:TYR:CE1	1:A:240:LYS:HB3	2.56	0.40
1:A:569:LEU:O	1:A:591:LYS:HD2	2.22	0.40
1:A:606:ASN:HB2	1:A:616:MET:HG3	2.03	0.40
1:A:896:TYR:OH	1:A:985:TYR:CD1	2.71	0.40
1:A:979:LEU:HB3	1:A:982:PHE:CD2	2.56	0.40
1:A:1063:TYR:O	1:A:1066:ASP:HA	2.21	0.40
2:B:191:ASN:ND2	2:B:217:CYS:HA	2.36	0.40
2:B:208:TYR:CZ	2:B:238:MET:HG3	2.56	0.40
2:B:560:CYS:HB2	2:B:570:TRP:CZ3	2.56	0.40
2:B:741:LEU:HA	2:B:744:THR:HB	2.04	0.40
2:B:908:GLN:NE2	2:B:938:ALA:HB1	2.36	0.40
2:B:1104:MET:HG3	2:B:1105:ASN:N	2.35	0.40
3:C:76:ILE:HG12	3:C:76:ILE:H	1.42	0.40
5:E:87:MET:HG2	5:E:118:ILE:HG12	2.02	0.40
6:F:107:PRO:HA	6:F:110:ILE:HD12	2.03	0.40
12:L:22:TYR:HE2	12:L:51:LYS:HG3	1.86	0.40
1:M:49:LEU:HD21	1:M:388:ASN:HB3	2.02	0.40
1:M:685:LEU:HD12	1:M:801:PHE:CD2	2.56	0.40
1:M:688:ASP:HA	2:N:937:HIS:CE1	2.56	0.40
1:M:762:LEU:HD22	1:M:786:PHE:CZ	2.56	0.40
1:M:824:LEU:HA	1:M:827:VAL:HG12	2.02	0.40
1:M:1063:TYR:O	1:M:1066:ASP:HA	2.21	0.40
1:M:1579:GLU:CD	5:Q:193:ILE:HD12	2.46	0.40
2:N:356:LEU:O	2:N:360:VAL:HG23	2.22	0.40
2:N:507:VAL:HA	2:N:701:MET:HE2	2.03	0.40
2:N:524:LYS:HB3	2:N:680:ASN:OD1	2.22	0.40
2:N:872:ARG:HB2	2:N:887:HIS:HB3	2.02	0.40
2:N:909:LYS:HB3	2:N:909:LYS:HE2	1.91	0.40
4:P:20:ASP:O	4:P:24:LYS:HD3	2.21	0.40
7:S:119:PRO:HB2	7:S:121:ASP:OD1	2.20	0.40
1:A:49:LEU:HD21	1:A:388:ASN:HB3	2.02	0.40
1:A:506:PRO:HB3	1:A:627:GLU:O	2.21	0.40
1:A:961:GLY:HA2	1:A:994:PHE:CE1	2.56	0.40
2:B:145:ARG:NH2	2:B:168:GLU:HB3	2.37	0.40
2:B:563:LEU:HD12	2:B:563:LEU:HA	1.93	0.40
2:B:779:HIS:CD2	2:B:896:PRO:HB2	2.56	0.40
2:B:1134:ASP:OD1	2:B:1136:SER:OG	2.35	0.40
7:G:97:SER:OG	7:G:132:GLU:HB3	2.21	0.40
7:G:127:PRO:HG2	7:G:133:GLN:O	2.21	0.40
7:G:170:LEU:HD23	7:G:170:LEU:HA	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:72:GLU:H	11:K:72:GLU:HG2	1.47	0.40
1:M:20:ASP:O	1:M:24:VAL:HG23	2.21	0.40
1:M:341:VAL:O	1:M:344:SER:OG	2.30	0.40
1:M:390:LEU:HB3	1:M:444:LEU:HD13	2.02	0.40
1:M:535:PRO:O	1:M:536:HIS:HD2	2.05	0.40
1:M:590:ASN:HD21	6:R:94:ASN:ND2	2.19	0.40
1:M:961:GLY:HA2	1:M:994:PHE:CE1	2.56	0.40
1:M:1583:ASN:OD1	1:M:1583:ASN:N	2.54	0.40
2:N:271:ILE:O	2:N:354:ARG:HD3	2.21	0.40
2:N:432:ASP:O	2:N:436:LYS:NZ	2.53	0.40
2:N:560:CYS:HB2	2:N:570:TRP:CZ3	2.56	0.40
2:N:609:LEU:HG	2:N:628:PHE:O	2.20	0.40
2:N:729:LEU:HD23	2:N:730:GLN:N	2.37	0.40
2:N:783:PHE:O	2:N:784:GLY:C	2.65	0.40
2:N:922:PRO:HB2	2:N:998:MET:HE2	2.03	0.40
5:Q:48:MET:H	5:Q:48:MET:HG2	1.47	0.40
5:Q:118:ILE:HA	5:Q:121:VAL:HG22	2.03	0.40
7:S:82:SER:O	7:S:82:SER:OG	2.30	0.40
7:S:103:LEU:HB2	7:S:111:ALA:HB3	2.03	0.40
8:T:56:SER:OG	8:T:124:ARG:HB3	2.22	0.40
8:T:114:LEU:HA	8:T:114:LEU:HD13	1.86	0.40
1:A:341:VAL:O	1:A:344:SER:OG	2.30	0.40
1:A:492:ILE:HD11	1:A:649:MET:HB2	2.02	0.40
1:A:559:ILE:HG13	1:A:560:GLU:N	2.36	0.40
1:A:912:LYS:HB2	1:A:912:LYS:HE2	1.87	0.40
1:A:939:GLN:O	1:A:943:VAL:HG12	2.21	0.40
2:B:204:ARG:HH22	2:B:230:HIS:CD2	2.40	0.40
2:B:730:GLN:O	10:J:1:MET:N	2.54	0.40
3:C:335:CYS:CB	11:K:99:ILE:HG12	2.52	0.40
5:E:128:GLU:HG3	5:E:129:THR:OG1	2.21	0.40
5:E:173:ILE:HG13	5:E:207:ARG:HB3	2.03	0.40
8:H:3:GLU:HG3	8:H:5:VAL:HG23	2.02	0.40
1:M:204:THR:HG22	1:M:205:THR:H	1.86	0.40
1:M:513:LEU:HD22	1:M:597:VAL:CG1	2.51	0.40
1:M:784:VAL:HA	1:M:794:GLY:HA3	2.04	0.40
1:M:1068:LEU:HG	1:M:1069:ASP:N	2.37	0.40
1:M:1125:LEU:HD11	1:M:1138:SER:HA	2.03	0.40
2:N:56:CYS:HA	2:N:75:ILE:O	2.21	0.40
2:N:208:TYR:CZ	2:N:238:MET:HG3	2.56	0.40
2:N:274:LYS:O	2:N:275:ASP:C	2.63	0.40
2:N:1038:HIS:N	2:N:1043:GLN:O	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:R:121:PRO:HB2	6:R:122:LEU:HD12	2.03	0.40
7:S:103:LEU:HD21	7:S:150:LEU:HB3	2.04	0.40
8:T:62:ASN:HB2	8:T:64:ASN:OD1	2.21	0.40
12:X:22:TYR:HE2	12:X:51:LYS:HG3	1.86	0.40
1:A:20:ASP:O	1:A:24:VAL:HG23	2.21	0.40
1:A:347:TYR:HA	1:A:1651:ARG:HA	2.03	0.40
1:A:471:LYS:NZ	1:A:476:ARG:HD2	2.36	0.40
1:A:483:ARG:HD2	2:B:1046:LYS:NZ	2.37	0.40
1:A:622:ARG:NH1	1:A:624:LEU:HD11	2.37	0.40
1:A:1012:CYS:SG	2:B:506:PRO:HB2	2.61	0.40
1:A:1038:LYS:NZ	1:A:1629:ASN:HD22	2.17	0.40
1:A:1225:THR:H	1:A:1244:THR:HG21	1.87	0.40
1:A:1679:ILE:HD12	6:F:83:ILE:HG12	2.02	0.40
2:B:869:ASP:CG	2:B:891:ARG:HE	2.29	0.40
2:B:923:PHE:HB3	2:B:929:GLN:OE1	2.22	0.40
2:B:985:LEU:HD23	2:B:991:ASN:O	2.21	0.40
2:B:1038:HIS:N	2:B:1043:GLN:O	2.55	0.40
3:C:94:ASN:OD1	3:C:209:ILE:HG12	2.21	0.40
3:C:174:LEU:HD23	3:C:174:LEU:HA	1.80	0.40
3:C:271:GLY:O	3:C:272:LYS:HD2	2.21	0.40
4:D:27:ASN:O	4:D:31:GLN:HG2	2.22	0.40
5:E:23:HIS:HE1	5:E:34:LEU:HD11	1.85	0.40
7:G:103:LEU:HB2	7:G:111:ALA:HB3	2.04	0.40
8:H:30:VAL:HB	8:H:37:ASN:HA	2.04	0.40
1:M:88:HIS:HA	1:M:89:PRO:HD3	1.92	0.40
1:M:124:LYS:O	1:M:127:ASP:HB3	2.22	0.40
1:M:559:ILE:HA	1:M:562:ARG:HG3	2.03	0.40
1:M:595:ARG:HG3	1:M:596:HIS:O	2.21	0.40
1:M:697:THR:O	1:M:744:LYS:HE2	2.21	0.40
1:M:849:ARG:HH12	2:N:993:HIS:HE1	1.67	0.40
2:N:425:VAL:O	2:N:428:LYS:HB2	2.21	0.40
2:N:562:GLN:OE1	2:N:567:ILE:HG12	2.21	0.40
2:N:697:SER:OG	2:N:698:PRO:HD3	2.21	0.40
2:N:951:SER:HB3	2:N:1012:TYR:OH	2.22	0.40
2:N:985:LEU:HD23	2:N:991:ASN:O	2.21	0.40
3:O:157:GLU:O	3:O:159:ASP:N	2.50	0.40
7:S:96:VAL:HG12	7:S:124:PHE:CE1	2.39	0.40
8:T:47:TYR:CE1	8:T:74:TYR:HB2	2.57	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 PDB entries followed by that with respect to all EM entries.

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	1356/1689 (80%)	1213 (90%)	136 (10%)	7 (0%)	24	63
1	M	1356/1689 (80%)	1214 (90%)	135 (10%)	7 (0%)	24	63
2	B	1148/1174 (98%)	1015 (88%)	129 (11%)	4 (0%)	36	71
2	N	1148/1174 (98%)	1015 (88%)	129 (11%)	4 (0%)	36	71
3	C	315/348 (90%)	290 (92%)	25 (8%)	0	100	100
3	O	315/348 (90%)	290 (92%)	25 (8%)	0	100	100
4	D	35/147 (24%)	34 (97%)	1 (3%)	0	100	100
4	P	35/147 (24%)	34 (97%)	1 (3%)	0	100	100
5	E	205/210 (98%)	180 (88%)	25 (12%)	0	100	100
5	Q	205/210 (98%)	179 (87%)	26 (13%)	0	100	100
6	F	80/142 (56%)	75 (94%)	4 (5%)	1 (1%)	9	41
6	R	80/142 (56%)	75 (94%)	4 (5%)	1 (1%)	9	41
7	G	156/173 (90%)	139 (89%)	17 (11%)	0	100	100
7	S	156/173 (90%)	139 (89%)	17 (11%)	0	100	100
8	H	121/125 (97%)	95 (78%)	26 (22%)	0	100	100
8	T	121/125 (97%)	95 (78%)	26 (22%)	0	100	100
9	I	55/119 (46%)	50 (91%)	5 (9%)	0	100	100
9	U	55/119 (46%)	50 (91%)	5 (9%)	0	100	100
10	J	66/71 (93%)	46 (70%)	20 (30%)	0	100	100
10	V	66/71 (93%)	46 (70%)	20 (30%)	0	100	100
11	K	93/125 (74%)	90 (97%)	3 (3%)	0	100	100
11	W	93/125 (74%)	90 (97%)	3 (3%)	0	100	100
12	L	43/63 (68%)	40 (93%)	3 (7%)	0	100	100
12	X	43/63 (68%)	40 (93%)	3 (7%)	0	100	100
All	All	7346/8772 (84%)	6534 (89%)	788 (11%)	24 (0%)	37	71

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1066	ASP
1	M	1066	ASP
1	A	1154	ASP
1	M	1154	ASP
2	B	206	THR
2	N	206	THR
1	A	1043	LEU
2	B	492	THR
2	B	827	ASP
1	M	1043	LEU
2	N	492	THR
2	N	827	ASP
1	A	968	ARG
2	B	493	VAL
1	M	968	ARG
2	N	493	VAL
1	A	85	PRO
1	A	782	GLY
1	M	85	PRO
1	M	782	GLY
1	A	580	PRO
1	M	580	PRO
6	F	121	PRO
6	R	121	PRO

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 PDB entries followed by that with respect to all EM entries.

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	1225/1484 (82%)	1214 (99%)	11 (1%)	70	76
1	M	1225/1484 (82%)	1214 (99%)	11 (1%)	70	76
2	B	1001/1013 (99%)	989 (99%)	12 (1%)	63	73
2	N	1001/1013 (99%)	989 (99%)	12 (1%)	63	73
3	C	281/308 (91%)	271 (96%)	10 (4%)	31	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	O	281/308 (91%)	271 (96%)	10 (4%)	31	52
4	D	37/134 (28%)	36 (97%)	1 (3%)	39	59
4	P	37/134 (28%)	36 (97%)	1 (3%)	39	59
5	E	182/184 (99%)	174 (96%)	8 (4%)	25	47
5	Q	182/184 (99%)	174 (96%)	8 (4%)	25	47
6	F	70/121 (58%)	67 (96%)	3 (4%)	26	48
6	R	70/121 (58%)	67 (96%)	3 (4%)	26	48
7	G	143/154 (93%)	138 (96%)	5 (4%)	32	53
7	S	143/154 (93%)	138 (96%)	5 (4%)	32	53
8	H	112/114 (98%)	110 (98%)	2 (2%)	51	67
8	T	112/114 (98%)	110 (98%)	2 (2%)	51	67
9	I	51/105 (49%)	44 (86%)	7 (14%)	3	15
9	U	51/105 (49%)	44 (86%)	7 (14%)	3	15
10	J	63/66 (96%)	61 (97%)	2 (3%)	34	55
10	V	63/66 (96%)	61 (97%)	2 (3%)	34	55
11	K	86/111 (78%)	84 (98%)	2 (2%)	44	63
11	W	86/111 (78%)	84 (98%)	2 (2%)	44	63
12	L	39/53 (74%)	38 (97%)	1 (3%)	40	60
12	X	39/53 (74%)	38 (97%)	1 (3%)	40	60
All	All	6580/7694 (86%)	6452 (98%)	128 (2%)	49	66

All (128) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	542	SER
1	A	551	LEU
1	A	553	SER
1	A	624	LEU
1	A	881	THR
1	A	1164	LYS
1	A	1249	LEU
1	A	1307	ASP
1	A	1322	SER
1	A	1529	SER

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Mol	Chain	Res	Type
2	B	178	ILE
2	B	237	THR
2	B	252	SER
2	B	262	THR
2	B	267	ILE
2	B	693	ASP
2	B	764	THR
2	B	773	ILE
2	B	864	GLU
2	B	933	ILE
2	B	1069	THR
2	B	1144	THR
3	C	65	ILE
3	C	76	ILE
3	C	110	VAL
3	C	139	VAL
3	C	155	THR
3	C	197	ASP
3	C	231	THR
3	C	330	VAL
3	C	333	SER
3	C	340	SER
4	D	48	SER
5	E	9	VAL
5	E	11	VAL
5	E	48	MET
5	E	117	ILE
5	E	120	THR
5	E	133	SER
5	E	196	ARG
5	E	199	THR
6	F	68	ASP
6	F	86	THR
6	F	123	LEU
7	G	79	LEU
7	G	82	SER
7	G	88	CYS
7	G	143	ILE
7	G	169	THR
8	H	28	THR
8	H	56	SER
9	I	6	SER

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Mol	Chain	Res	Type
9	I	17	LEU
9	I	21	THR
9	I	48	SER
9	I	49	SER
9	I	57	LEU
9	I	62	SER
10	J	19	ASP
10	J	45	CYS
11	K	33	THR
11	K	46	LEU
12	L	19	THR
1	M	1	MET
1	M	542	SER
1	M	551	LEU
1	M	553	SER
1	M	624	LEU
1	M	881	THR
1	M	1164	LYS
1	M	1249	LEU
1	M	1307	ASP
1	M	1322	SER
1	M	1529	SER
2	N	178	ILE
2	N	237	THR
2	N	252	SER
2	N	262	THR
2	N	267	ILE
2	N	693	ASP
2	N	764	THR
2	N	773	ILE
2	N	864	GLU
2	N	933	ILE
2	N	1069	THR
2	N	1144	THR
3	O	65	ILE
3	O	76	ILE
3	O	110	VAL
3	O	139	VAL
3	O	155	THR
3	O	197	ASP
3	O	231	THR
3	O	330	VAL

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Mol	Chain	Res	Type
3	O	333	SER
3	O	340	SER
4	P	48	SER
5	Q	9	VAL
5	Q	11	VAL
5	Q	48	MET
5	Q	117	ILE
5	Q	120	THR
5	Q	133	SER
5	Q	196	ARG
5	Q	199	THR
6	R	68	ASP
6	R	86	THR
6	R	123	LEU
7	S	79	LEU
7	S	82	SER
7	S	88	CYS
7	S	143	ILE
7	S	169	THR
8	T	28	THR
8	T	56	SER
9	U	6	SER
9	U	17	LEU
9	U	21	THR
9	U	48	SER
9	U	49	SER
9	U	57	LEU
9	U	62	SER
10	V	19	ASP
10	V	45	CYS
11	W	33	THR
11	W	46	LEU
12	X	19	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (138) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	117	HIS
1	A	230	ASN
1	A	232	GLN
1	A	257	GLN

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Mol	Chain	Res	Type
1	A	388	ASN
1	A	501	ASN
1	A	533	ASN
1	A	536	HIS
1	A	543	HIS
1	A	545	GLN
1	A	568	GLN
1	A	599	ASN
1	A	619	HIS
1	A	638	ASN
1	A	735	GLN
1	A	856	ASN
1	A	860	GLN
1	A	889	ASN
1	A	891	ASN
1	A	1073	GLN
1	A	1075	HIS
1	A	1345	GLN
1	A	1479	HIS
1	A	1519	HIS
1	A	1557	ASN
1	A	1604	HIS
1	A	1629	ASN
2	B	126	ASN
2	B	147	ASN
2	B	191	ASN
2	B	192	HIS
2	B	230	HIS
2	B	300	GLN
2	B	374	HIS
2	B	386	GLN
2	B	402	GLN
2	B	431	ASN
2	B	621	GLN
2	B	640	HIS
2	B	687	ASN
2	B	733	GLN
2	B	752	ASN
2	B	779	HIS
2	B	908	GLN
2	B	1023	HIS
2	B	1038	HIS

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Mol	Chain	Res	Type
2	B	1043	GLN
3	C	166	ASN
3	C	182	GLN
3	C	207	GLN
3	C	223	HIS
3	C	292	HIS
4	D	51	ASN
5	E	7	ASN
5	E	20	GLN
5	E	68	ASN
5	E	131	GLN
5	E	138	ASN
5	E	169	GLN
7	G	21	HIS
7	G	30	GLN
7	G	100	HIS
7	G	167	GLN
8	H	37	ASN
8	H	118	HIS
10	J	63	ASN
11	K	112	GLN
12	L	31	ASN
1	M	60	ASN
1	M	117	HIS
1	M	230	ASN
1	M	232	GLN
1	M	257	GLN
1	M	388	ASN
1	M	501	ASN
1	M	533	ASN
1	M	536	HIS
1	M	543	HIS
1	M	545	GLN
1	M	568	GLN
1	M	590	ASN
1	M	599	ASN
1	M	619	HIS
1	M	638	ASN
1	M	856	ASN
1	M	860	GLN
1	M	889	ASN
1	M	891	ASN

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Mol	Chain	Res	Type
1	M	1073	GLN
1	M	1075	HIS
1	M	1345	GLN
1	M	1479	HIS
1	M	1557	ASN
1	M	1604	HIS
1	M	1629	ASN
2	N	126	ASN
2	N	147	ASN
2	N	191	ASN
2	N	192	HIS
2	N	230	HIS
2	N	300	GLN
2	N	374	HIS
2	N	386	GLN
2	N	402	GLN
2	N	431	ASN
2	N	578	HIS
2	N	621	GLN
2	N	640	HIS
2	N	687	ASN
2	N	733	GLN
2	N	752	ASN
2	N	779	HIS
2	N	908	GLN
2	N	1023	HIS
2	N	1038	HIS
2	N	1043	GLN
3	O	99	GLN
3	O	166	ASN
3	O	182	GLN
3	O	207	GLN
3	O	223	HIS
3	O	292	HIS
4	P	51	ASN
5	Q	7	ASN
5	Q	20	GLN
5	Q	68	ASN
5	Q	131	GLN
5	Q	138	ASN
7	S	21	HIS
7	S	30	GLN

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Mol	Chain	Res	Type
7	S	100	HIS
7	S	110	ASN
7	S	167	GLN
8	T	37	ASN
8	T	118	HIS
10	V	63	ASN
12	X	31	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 12 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

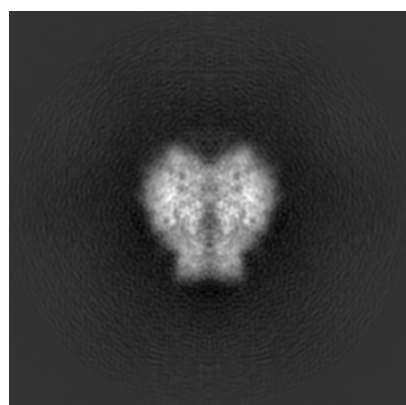
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11841. These allow visual inspection of the internal detail of the map and identification of artifacts.

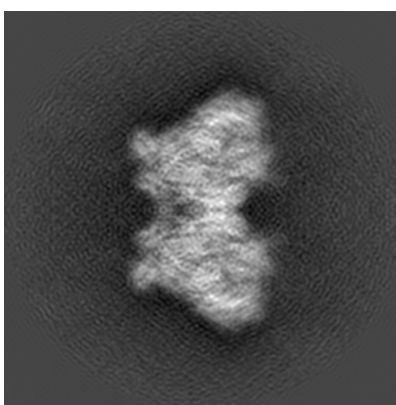
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

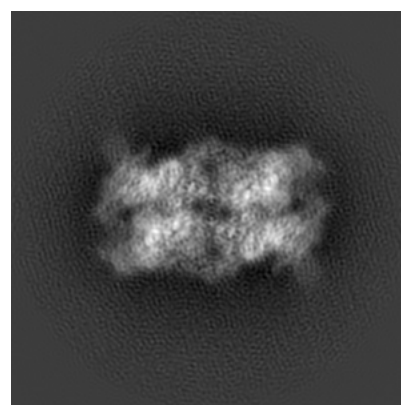
6.1.1 Primary map



X



Y

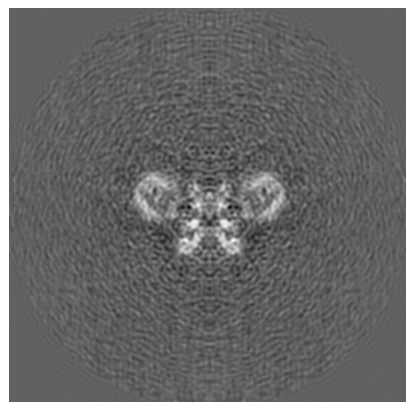


Z

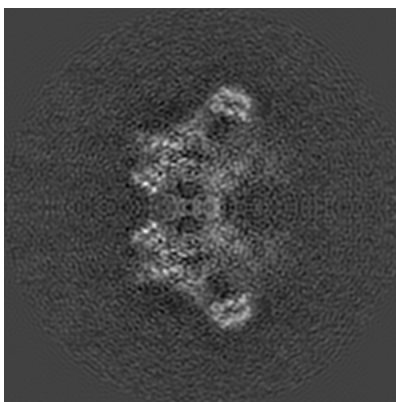
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

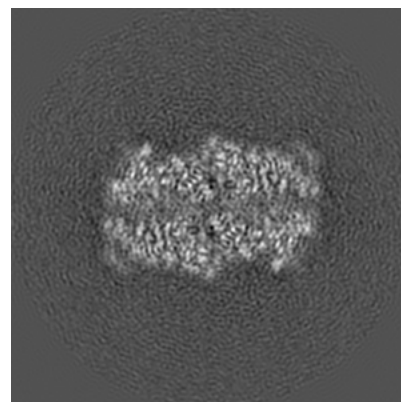
6.2.1 Primary map



X Index: 180



Y Index: 180

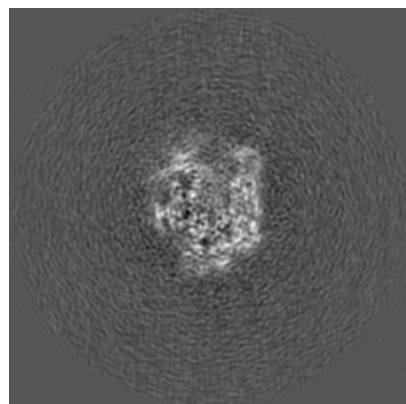


Z Index: 180

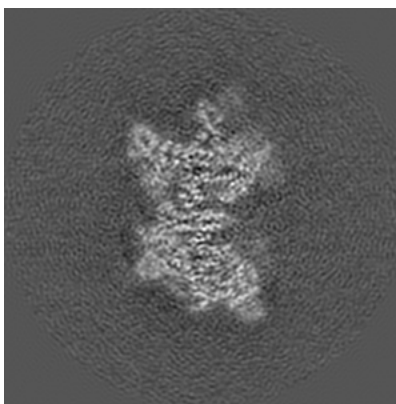
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

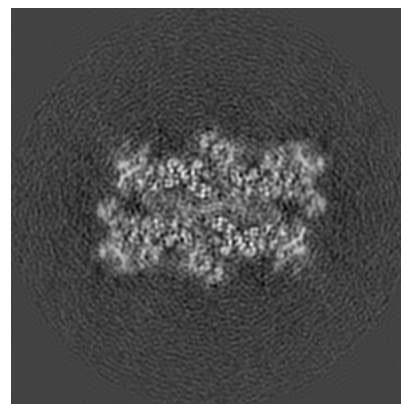
6.3.1 Primary map



X Index: 145



Y Index: 200

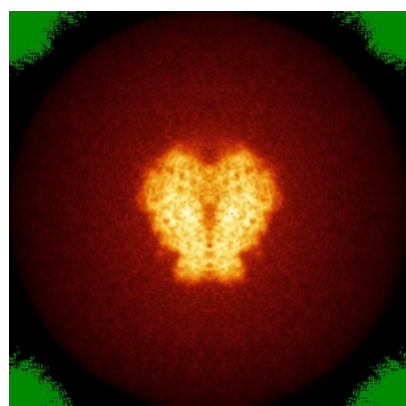


Z Index: 189

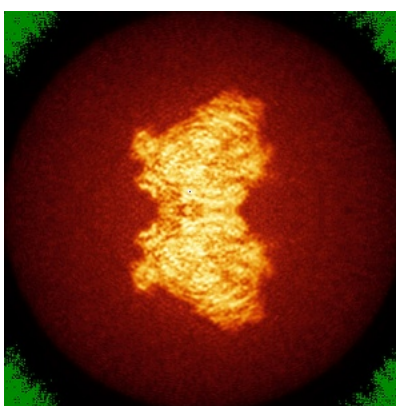
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

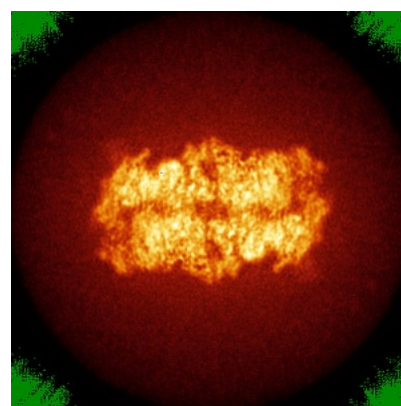
6.4.1 Primary map



X



Y

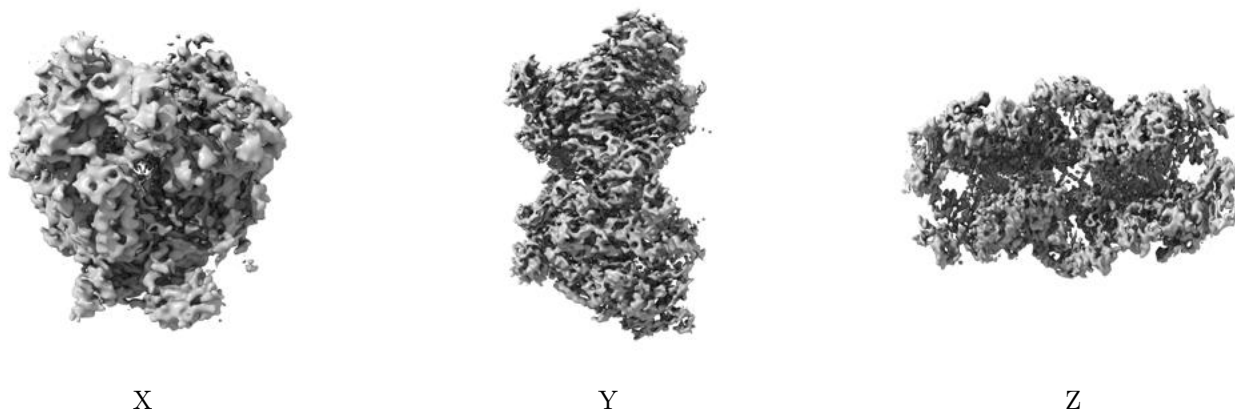


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.033. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

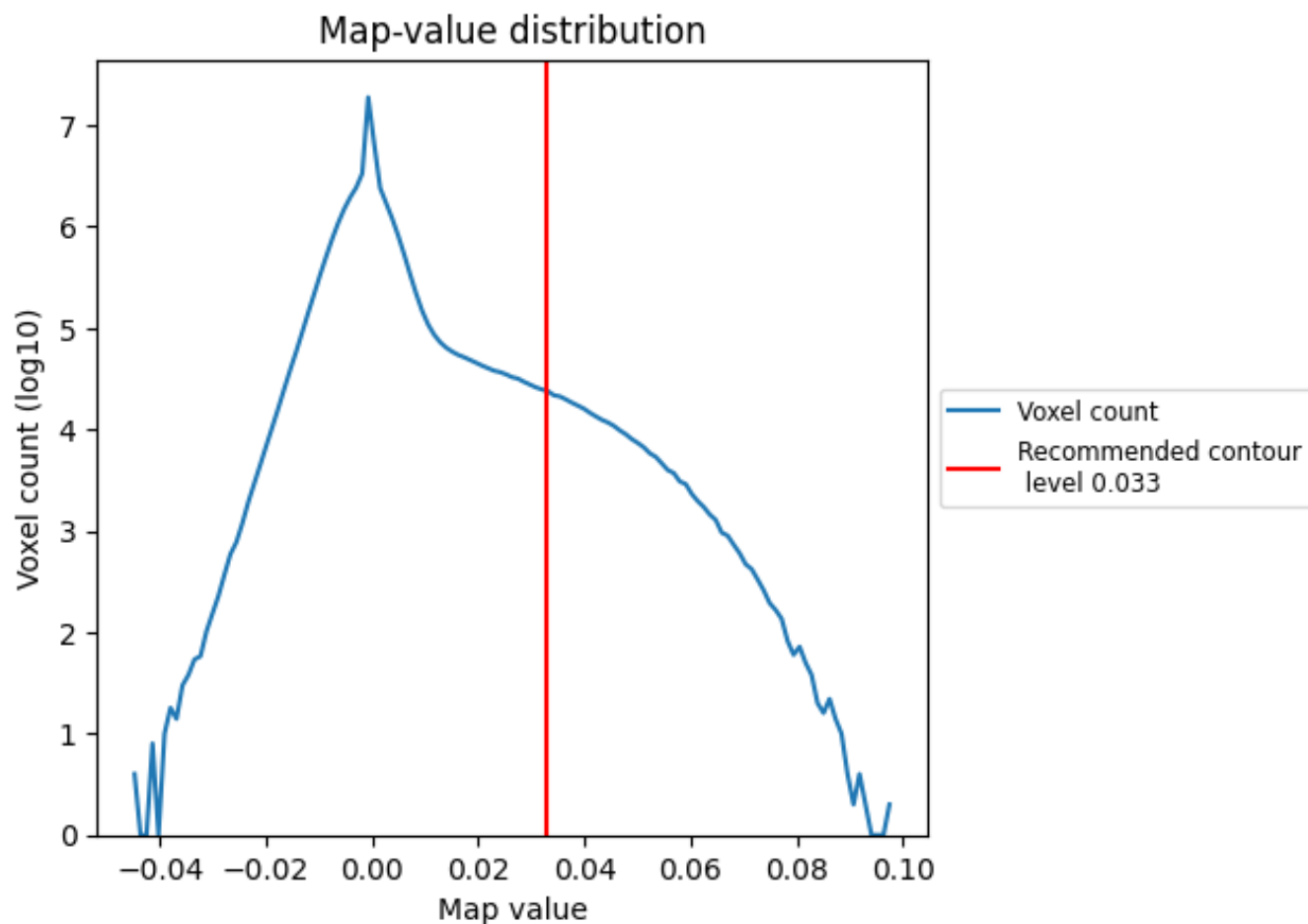
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

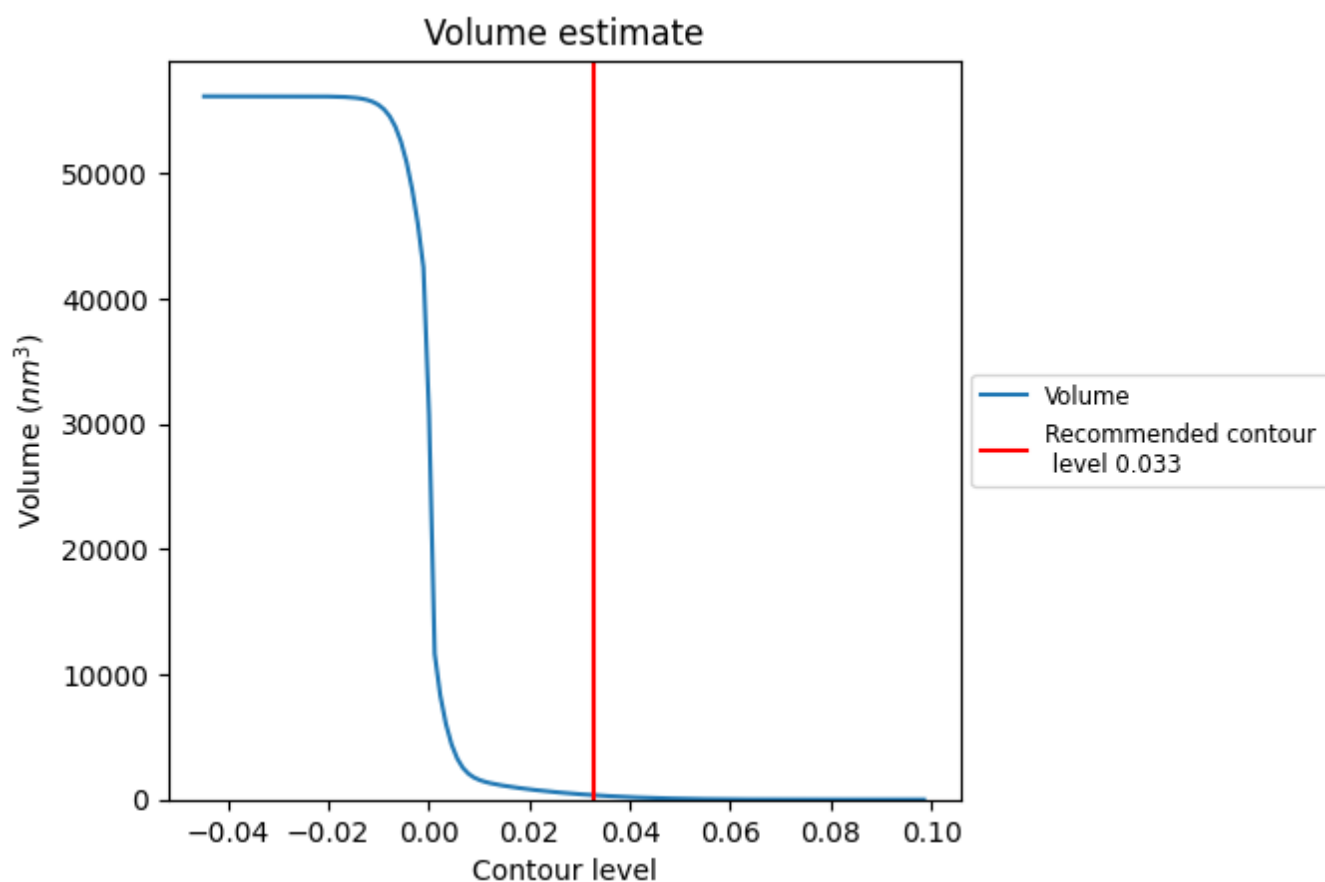
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

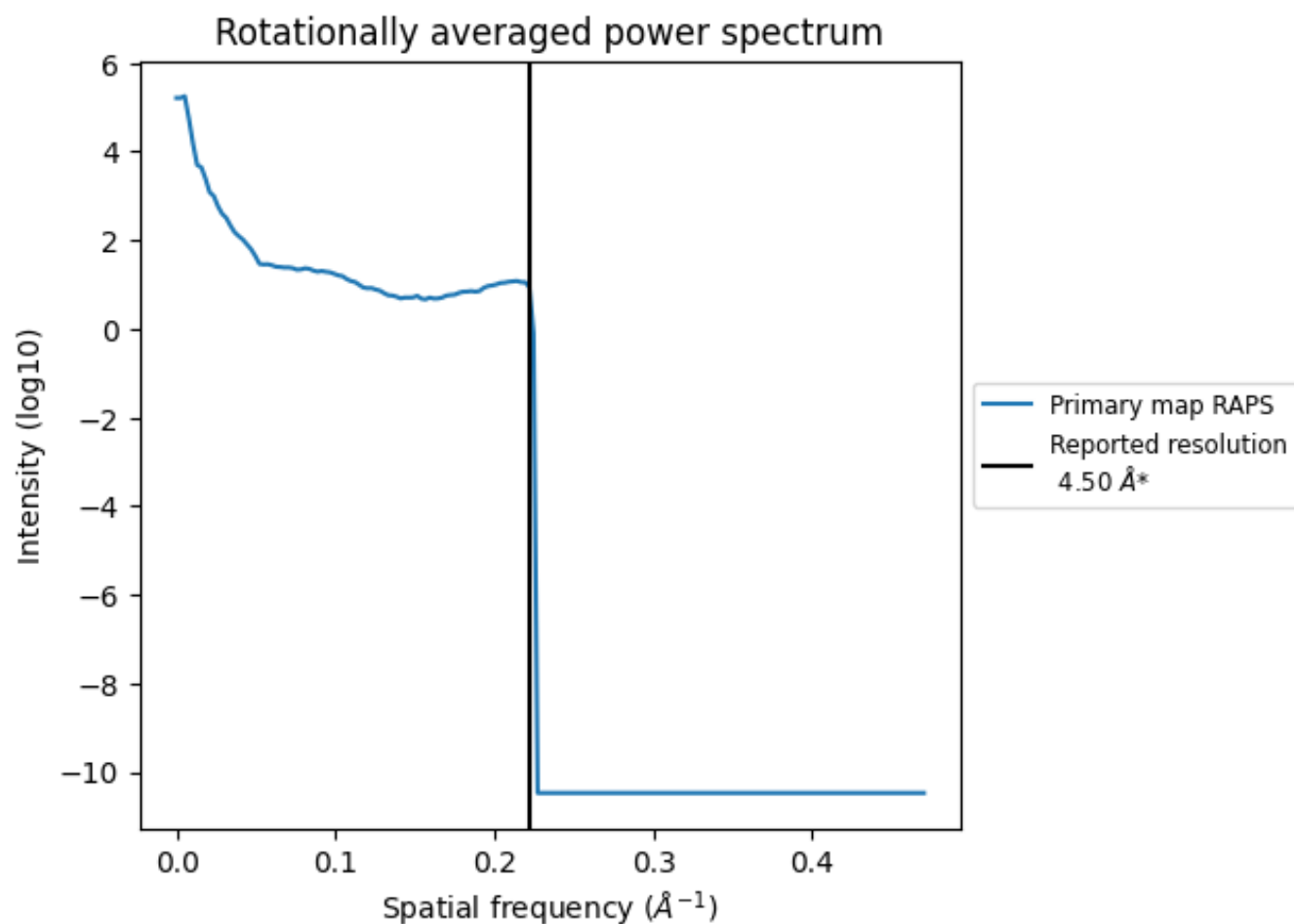
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 347 nm³; this corresponds to an approximate mass of 314 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.222 Å⁻¹

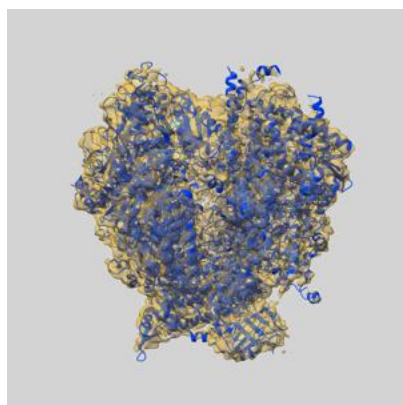
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

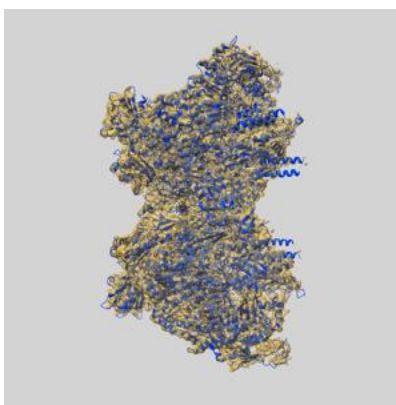
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11841 and PDB model 7AOD. Per-residue inclusion information can be found in section [3](#) on page [7](#).

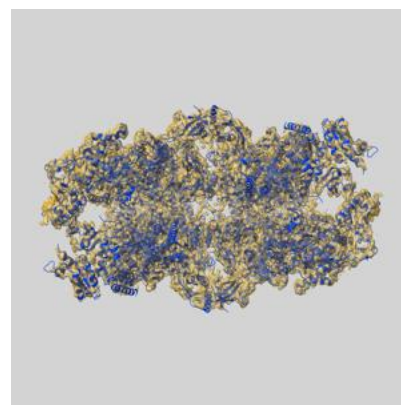
9.1 Map-model overlay [i](#)



X



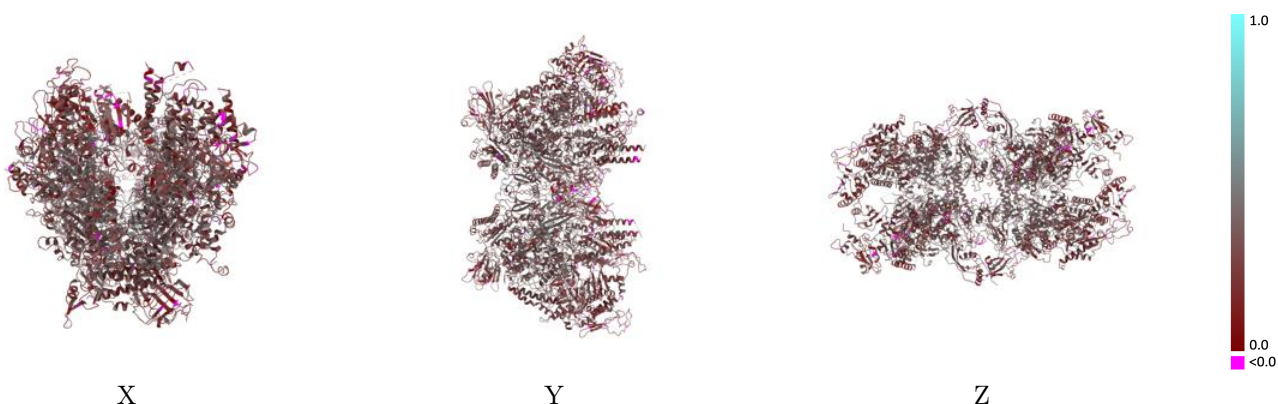
Y



Z

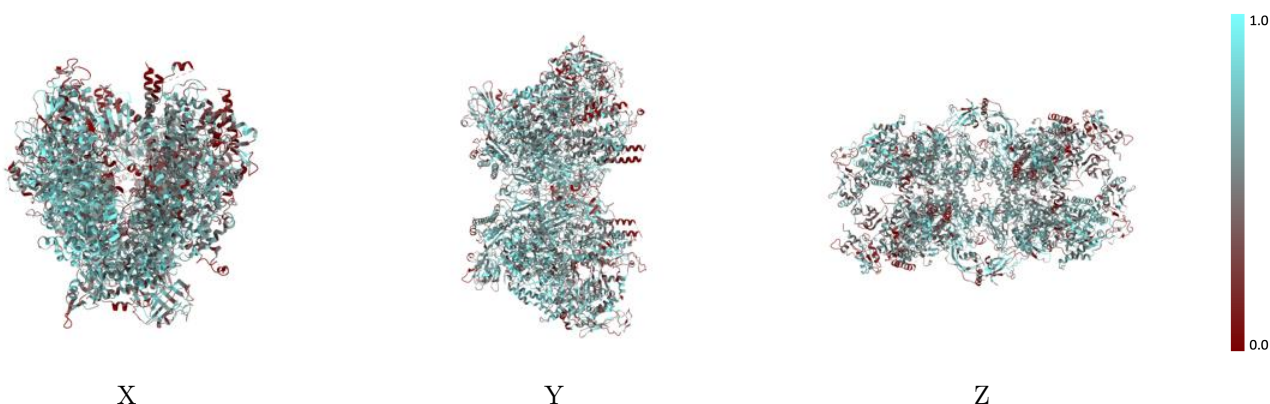
The images above show the 3D surface view of the map at the recommended contour level 0.033 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



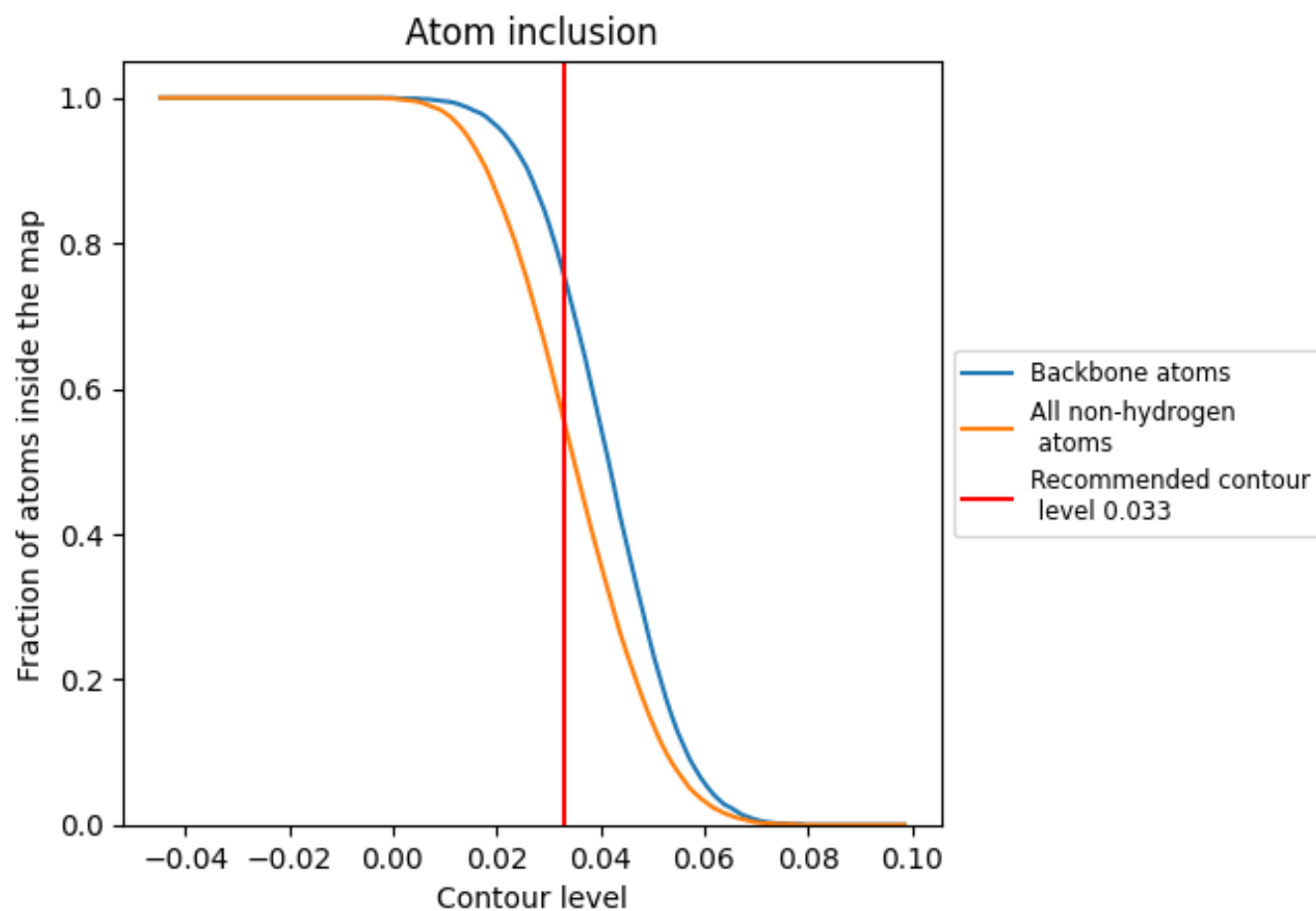
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.033).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 56% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.033) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5550	 0.3090
A	 0.5320	 0.3070
B	 0.5950	 0.3230
C	 0.5730	 0.3120
D	 0.3950	 0.2420
E	 0.4360	 0.2740
F	 0.6220	 0.3460
G	 0.5960	 0.2870
H	 0.5440	 0.2730
I	 0.3300	 0.2280
J	 0.7010	 0.3360
K	 0.6010	 0.2960
L	 0.5440	 0.3340
M	 0.5300	 0.3070
N	 0.5950	 0.3220
O	 0.5750	 0.3190
P	 0.3820	 0.2390
Q	 0.4460	 0.2780
R	 0.6160	 0.3530
S	 0.5990	 0.2910
T	 0.5520	 0.2720
U	 0.3330	 0.2410
V	 0.7070	 0.3460
W	 0.6000	 0.2950
X	 0.5500	 0.3400

