



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 12:17 AM UTC

PDB ID : 6PSW / pdb_00006psw
EMDB ID : EMD-20466
Title : Escherichia coli RNA polymerase promoter unwinding intermediate (TRPo)
with TraR and rpsT P2 promoter
Authors : Chen, J.; Chiu, C.E.; Campbell, E.A.; Darst, S.A.
Deposited on : 2019-07-13
Resolution : 3.70 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

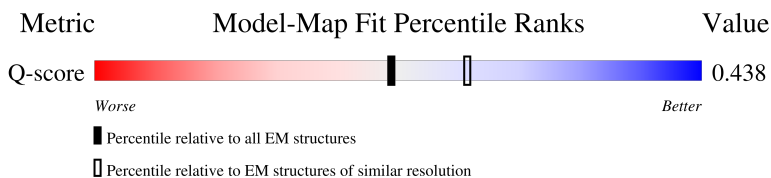
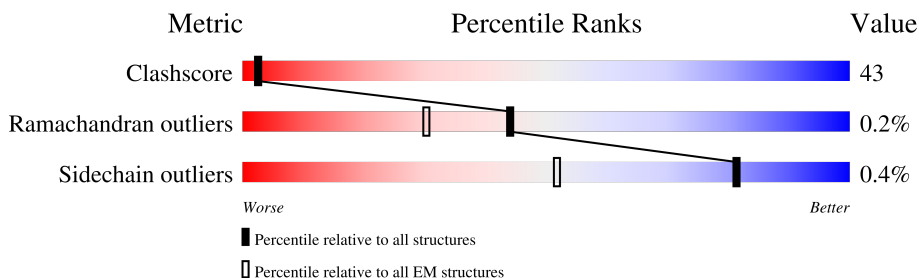
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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.



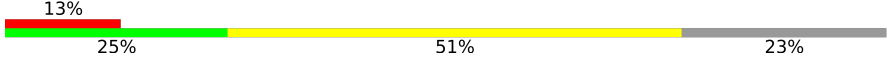
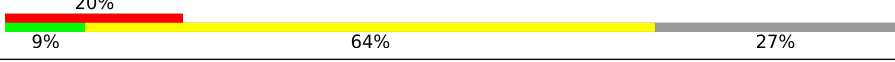
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	G	329	
1	H	329	
1	M	329	
2	I	1342	

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Mol	Chain	Length	Quality of chain
3	J	1430	
4	K	91	
5	L	616	
6	N	72	
7	O	85	
8	P	85	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 32773 atoms, of which 78 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 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	G	229	Total	C	N	O	S	0	0
			1762	1100	313	343	6		
1	H	219	Total	C	N	O	S	0	0
			1678	1048	295	329	6		
1	M	73	Total	C	N	O	S	0	0
			572	362	100	108	2		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	1341	Total	C	N	O	S	0	0
			10571	6633	1839	2056	43		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	1345	Total	C	N	O	S	0	0
			10460	6574	1864	1972	50		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1	VAL	-	expression tag	UNP P0A8T7
J	1408	LEU	-	expression tag	UNP P0A8T7
J	1409	GLU	-	expression tag	UNP P0A8T7
J	1410	LEU	-	expression tag	UNP P0A8T7
J	1411	GLU	-	expression tag	UNP P0A8T7
J	1412	VAL	-	expression tag	UNP P0A8T7
J	1413	LEU	-	expression tag	UNP P0A8T7
J	1414	PHE	-	expression tag	UNP P0A8T7
J	1415	GLN	-	expression tag	UNP P0A8T7
J	1416	GLY	-	expression tag	UNP P0A8T7
J	1417	PRO	-	expression tag	UNP P0A8T7

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1418	SER	-	expression tag	UNP P0A8T7
J	1419	SER	-	expression tag	UNP P0A8T7
J	1420	GLY	-	expression tag	UNP P0A8T7
J	1421	HIS	-	expression tag	UNP P0A8T7
J	1422	HIS	-	expression tag	UNP P0A8T7
J	1423	HIS	-	expression tag	UNP P0A8T7
J	1424	HIS	-	expression tag	UNP P0A8T7
J	1425	HIS	-	expression tag	UNP P0A8T7
J	1426	HIS	-	expression tag	UNP P0A8T7
J	1427	HIS	-	expression tag	UNP P0A8T7
J	1428	HIS	-	expression tag	UNP P0A8T7
J	1429	HIS	-	expression tag	UNP P0A8T7
J	1430	HIS	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	79	Total	C	N	O	S	0	0
			627	382	118	126	1		

- Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	473	Total	C	N	O	S	0	0
			3854	2412	687	732	23		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	-2	SER	-	expression tag	UNP Q0P6L9
L	-1	GLU	-	expression tag	UNP Q0P6L9
L	0	PHE	-	expression tag	UNP Q0P6L9

- Molecule 6 is a protein called Protein TraR.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	72	Total	C	N	O	S	0	0
			571	353	105	108	5		

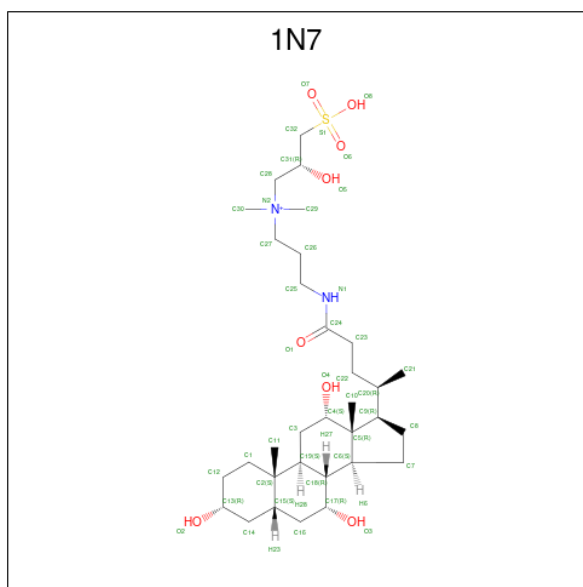
- Molecule 7 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	O	62	Total	C	N	O	P	0	0
			1270	606	237	365	62		

- Molecule 8 is a DNA chain called DNA (85-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	62	Total	C	N	O	P	0	0
			1272	609	222	379	62		

- Molecule 9 is CHAPSO (CCD ID: 1N7) (formula: C₃₂H₅₉N₂O₈S).



Mol	Chain	Residues	Atoms				AltConf
9	I	1	Total	C	H	O	0
			66	24	39	3	
9	J	1	Total	C	H	O	0
			66	24	39	3	

- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
10	J	1	Total	Mg	0
			1	1	

- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn).

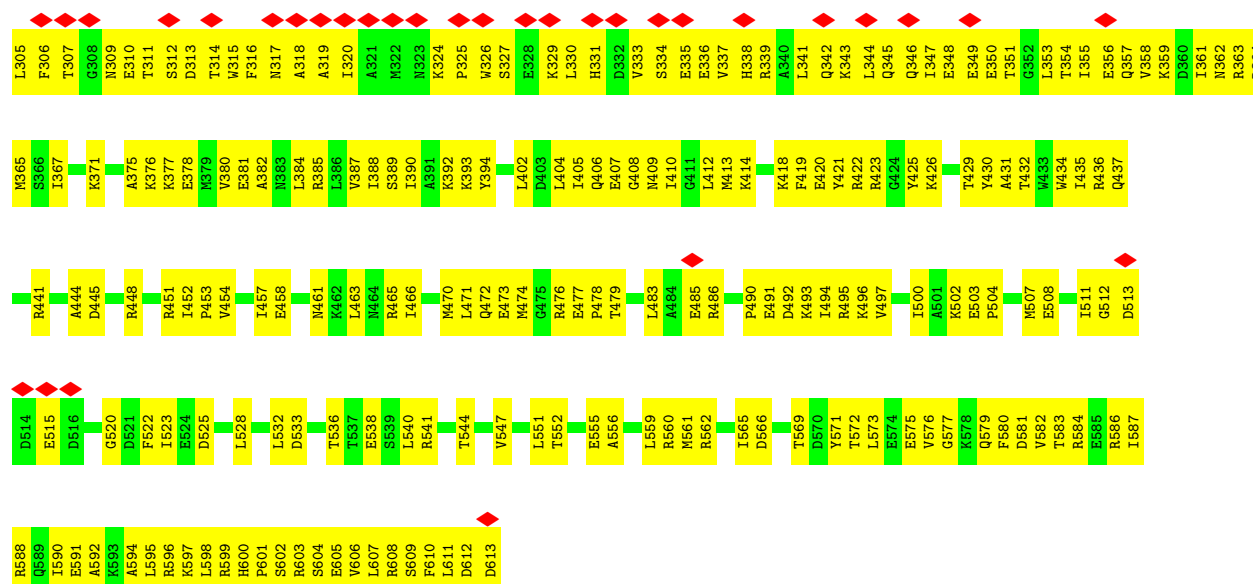
Mol	Chain	Residues	Atoms		AltConf
11	J	2	Total 2	Zn 2	0
11	N	1	Total 1	Zn 1	0

- Molecule 1: DNA-directed RNA polymerase subunit alpha



T1054	K992	L930	T853	G782	E713	D643	T567	P498	P427	V357	R281	M909	E136	E69
G1055	E993	T931	A854	L783	E714	M644	S568	I499	I428	G358	L282	S210	R137	C70
L1056	S994	M932	D855	A784	K715	P647	K570	V501	L429	P359	A287	T212	V138	C72
S1057	Y995	R933	I856	D785	Q716	L857	T573	S502	H430	L363	D288	K213	E142	G73
S1058	K996	T934	L857	T786	S718	K649	V574	Q504	A432	H364	P289	R214	S143	K74
L1059	Y997	H936	V858	K789	F719	K650	G575	Q506	G433	L368	T990	K215	Y144	Y75
V1060	P998	H937	R860	K790	S720	H651	R576	V506	A434	L369	L291	K216	V145	K76
L1061	Y999	GLY	L864	A791	T722	E652	A577	D506	Q435	P369	R292	L217	V146	R77
D1062	Y999	GLY	H865	L796	I722	E653	I578	G509	A436	K371	N294	K218	E148	L78
A1063	Y999	GLY	H866	L797	I723	E654	I579	L510	A437	M372	E295	G149	L147	K79
L1064	Y999	GLY	H867	L798	I724	E655	I580	L511	A438	K373	R296	R220	G150	H80
A1065	Y999	GLY	H868	L799	I725	E656	I581	M513	A439	L374	R297	I221	G151	V83
L1066	Y999	GLY	H869	L800	I726	E657	I582	T514	A440	E375	R298	K222	M151	R84
A1067	Y999	GLY	H870	L801	I727	E658	I583	R515	A441	L376	L299	L223	T152	C85
L1068	Y999	GLY	H871	L802	I728	E659	I584	R516	A442	L377	L299	L224	N153	E86
A1069	Y999	GLY	H872	L803	I729	E660	I585	D517	A443	L378	Q301	V228	L154	K87
G1070	Y999	GLY	H873	L804	I730	E661	I586	C517	A444	L379	E302	Q157	Q157	C88
L1071	Y999	GLY	H874	L805	I731	E662	I587	D518	A445	L380	A303	N232	Q158	Q89
K1072	Y999	GLY	H875	L806	I732	E663	I588	C519	A446	L381	V303	K233	I159	V92
D1073	Y999	GLY	H876	L807	I733	E664	I589	D520	A447	L382	D304	N234	L160	T93
L1074	Y999	GLY	H877	L808	I734	E665	I590	G521	A448	L383	A305	K235	T161	T94
R1075	Y999	GLY	H878	L809	I735	E666	I591	G522	A449	L384	L306	W236	E162	T95
L1076	Y999	GLY	H879	L810	I736	E667	I592	G523	A450	L385	L307	W237	E163	K96
A1077	Y999	GLY	H880	L811	I737	E668	I593	G524	A451	L386	L308	I238	Q164	V97
L1078	Y999	GLY	H881	L812	I738	E669	I594	G525	A452	L387	D309	P243	Y165	R98
K1079	Y999	GLY	H882	L813	I739	E670	I595	G526	A453	L388	L310	P244	K166	R99
L1080	Y999	GLY	H883	L814	I740	E671	I596	G527	A454	L389	L311	P245	Y166	V99
V1081	Y999	GLY	H884	L815	I741	E672	I597	G528	A455	L390	L312	P246	Y167	K96
L1082	Y999	GLY	H885	L816	I742	E673	I598	G529	A456	L391	L313	P247	Y168	V97
A1083	Y999	GLY	H886	L817	I743	E674	I599	G530	A457	L392	L314	P248	Y169	R98
Q1084	Y999	GLY	H887	L818	I744	E675	I600	G531	A458	L393	L315	P249	Y170	E100
G1085	Y999	GLY	H888	L819	I745	E676	I601	G532	A459	L394	L316	P250	Y171	R101
L1086	Y999	GLY	H889	L820	I746	E677	I602	G533	A460	L395	L317	P251	Y172	M102
N1087	Y999	GLY	H890	L821	I747	E678	I603	G534	A461	L396	L318	P252	Y173	G103
V1088	Y999	GLY	H891	L822	I748	E679	I604	G535	A462	L397	L319	P253	Y174	H104
L1089	Y999	GLY	H892	L823	I749	E680	I605	G536	A463	L398	L320	P254	Y175	I105
P1091	Y999	GLY	H893	L824	I750	E681	I606	G537	A464	L399	L321	P255	Y176	E106
G1092	Y999	GLY	H894	L825	I751	E682	I607	G538	A465	L400	L322	P256	Y177	L107
T1093	Y999	GLY	H895	L826	I752	E683	I608	G539	A466	L401	L323	P257	Y178	A108
D1094	Y999	GLY	H896	L827	I753	E684	I609	G540	A467	L402	L324	P258	Y179	T111
M1095	Y999	GLY	H897	L828	I754	E685	I610	G541	A468	L403	L325	P259	Y180	I114
P1096	Y999	GLY	H898	L829	I755	E686	I611	G542	A469	L404	L326	P260	Y181	W115
A1097	Y999	GLY	H899	L830	I756	E687	I612	G543	A470	L405	L327	P261	Y182	F116
Q1098	Y999	GLY	H900	L831	I757	E688	I613	G544	A471	L406	L328	P262	Y183	L117
Y1099	Y999	GLY	H901	L832	I758	E689	I614	G545	A472	L407	L329	P263	Y184	S122
F1100	Y999	GLY	H902	L833	I759	E690	I615	G546	A473	L408	L330	P264	Y185	R123
L1101	Y999	GLY	H903	L834	I760	E691	I616	G547	A474	L409	L331	P265	Y186	I124
P1102	Y999	GLY	H904	L835	I761	E692	I617	G548	A475	L410	L332	P266	Y187	G125
A1103	Y999	GLY	H905	L836	I762	E693	I618	G549	A476	L411	L333	P267	Y188	L126
K1104	Y999	GLY	H906	L837	I763	E694	I619	G550	A477	L412	L334	P268	Y189	L127
L1105	Y999	GLY	H907	L838	I764	E695	I620	G551	A478	L413	L335	P269	Y190	Q200
A1106	Y999	GLY	H908	L839	I765	E696	I621	G552	A479	L414	L336	P270	Y191	L201
T1107	Y999	GLY	H909	L840	I766	E697	I622	G553	A480	L415	L337	P271	Y192	D129
Q1108	Y999	GLY	H910	L841	I767	E698	I623	G554	A481	L416	L338	P272	Y193	L128
L1109	Y999	GLY	H911	L842	I768	E699	I624	G555	A482	L417	L339	P273	Y194	L129
D1110	Y999	GLY	H912	L843	I769	E700	I625	G556	A483	L418	L340	P274	Y195	M130
E1111	Y999	GLY	H913	L844	I770	E701	I626	G557	A484	L419	L341	P275	Y196	P131
G1112	Y999	GLY	H914	L845	I771	E702	I627	G558	A485	L420	L342	P276	Y197	R132
V1113	Y999	GLY	H915	L846	I772	E703	I628	G559	A486	L421	L343	P277	Y198	E203
			H916	L847	I773	E704	I629	G560	A487	L422	L344	P278	Y199	R133
			H917	L848	I774	E705	I630	G561	A488	L423	L345	P279	Y200	L134
			H918	L849	I775	E706	I631	G562	A489	L424	L346	P280	Y201	R135
			H919	L850	I776	E707	I632	G563	A490	L425	L347	P281	Y202	E204
			H920	L851	I777	E708	I633	G564	A491	L426	L348	P282	Y203	R136
			H921	L852	I778	E709	I634	G565	A492	L427	L349	P283	Y204	L137
			H922	L853	I779	E710	I635	G566	A493	L428	L350	P284	Y205	E205
			H923	L854	I780	E711	I636	G567	A494	L429	L351	P285	Y206	R137
			H924	L855	I781	E712	I637	G568	A495	L430	L352	P286	Y207	L138
			H925	L856	I782	E713	I638	G569	A496	L431	L353	P287	Y208	E206
			H926	L857	I783	E714	I639	G570	A497	L432	L354	P288	Y209	R138
			H927	L858	I784	E715	I640	G571	A498	L433	L355	P289	Y210	L139
			H928	L859	I785	E716	I641	G572	A499	L434	L356	P290	Y211	E207
			H929	L860	I786	E717	I642	G573	A500	L435	L357	P291	Y212	R139
			H930	L861	I787	E718	I643	G574	A501	L436	L358	P292	Y213	L140
			H931	L862	I788	E719	I644	G575	A502	L437	L359	P293	Y214	E208
			H932	L863	I789	E720	I645	G576	A503	L438	L360	P294	Y215	R140
			H933	L864	I790	E721	I646	G577	A504	L439	L361	P295	Y216	L141
			H934	L865	I791	E722	I647	G578	A505	L440	L362	P296	Y217	E209
			H935	L866	I792	E723	I648	G579	A506	L441	L363	P297	Y218	R141
			H936	L867	I793	E724	I649	G580	A507	L442	L364	P298	Y219	L142
			H937	L868	I794	E725	I650	G581	A508	L443	L365	P299	Y220	E210
			H938	L869	I795	E726	I651	G582	A509	L444	L366	P300	Y221	R142
			H939	L870	I796	E727	I652	G583	A510	L445	L367	P301	Y222	L143
			H940	L871	I797	E728	I653	G584	A511	L446	L368	P302	Y223	E211
			H941	L872	I798	E729	I654	G585	A512	L447	L369	P303	Y224	R143
			H942	L873	I799	E730	I655	G586	A513	L448	L370	P304	Y225	L144
			H943	L874	I800	E731	I656	G587	A514	L449	L371	P305	Y226	E212
			H944	L875	I801	E732	I657	G588	A515	L450	L372	P306	Y227	R144
			H945	L876	I802	E733	I658	G589	A516	L451	L373	P307	Y228	L145
			H946	L877	I803	E734	I659	G590	A517	L452	L374	P308	Y229	E213
			H947	L878	I804	E735	I660	G591	A518	L453	L375	P309	Y230	R145
			H948	L879	I805	E736	I661	G592	A519	L454	L376	P310	Y231	L146
			H949	L880	I806	E737	I662	G593	A520	L455	L377	P311	Y232	E214
			H950	L881	I807	E738	I663	G594	A521	L456	L378	P312	Y233	R146
			H951	L882	I808	E739	I664	G595	A522	L457	L379	P313	Y234	L147
			H952	L883	I809	E740	I665	G596	A523	L458	L380	P314	Y235	E215
			H953	L884	I810	E741	I666	G597	A524	L459	L381	P315	Y236	R147
			H954	L885	I811	E742	I667	G598	A525	L460	L382	P316	Y237	L148
			H955	L886	I812	E743	I668	G599	A526	L461	L383	P317	Y238	E216
			H956	L887	I813	E744	I669	G600	A527	L462	L384	P318	Y239	R148
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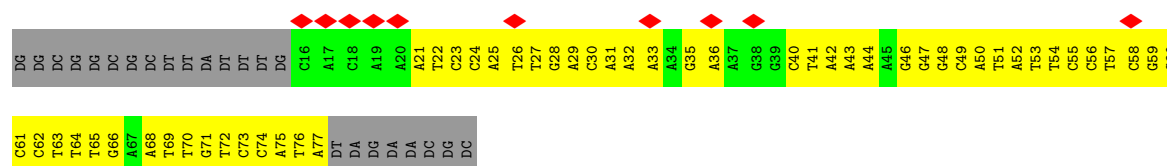
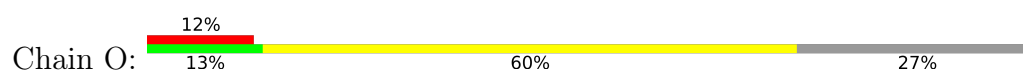




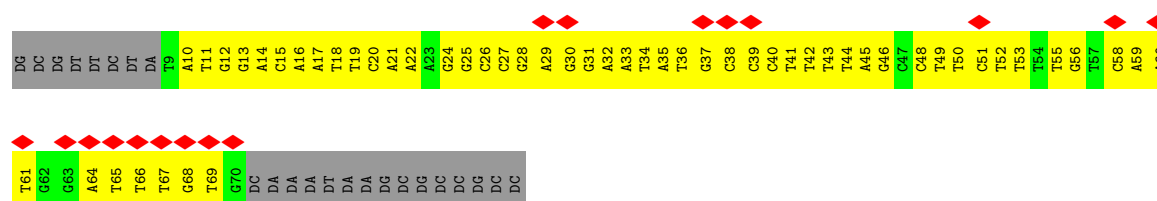
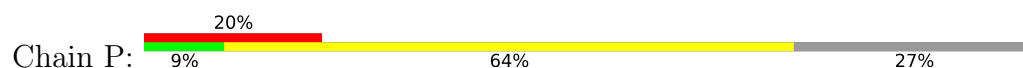
• Molecule 6: Protein TraR



• Molecule 7: DNA (85-MER)



• Molecule 8: DNA (85-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	46650	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.154	Depositor
Minimum map value	-0.109	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	332.8, 332.8, 332.8	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 1N7, 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	G	0.36	0/1784	0.55	0/2419
1	H	0.32	0/1697	0.53	0/2301
1	M	0.19	0/579	0.54	0/784
2	I	0.37	0/10740	0.57	0/14492
3	J	0.35	0/10619	0.55	0/14338
4	K	0.29	0/629	0.52	0/847
5	L	0.25	0/3906	0.53	2/5251 (0.0%)
6	N	0.24	0/581	0.64	1/785 (0.1%)
7	O	0.23	0/1426	0.40	0/2197
8	P	0.26	0/1424	0.45	0/2197
All	All	0.34	0/33385	0.54	3/45611 (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
2	I	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	N	27	ILE	N-CA-C	6.98	113.68	106.21
5	L	94	THR	CA-C-N	-6.16	113.32	122.56
5	L	94	THR	C-N-CA	-6.16	113.32	122.56

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	I	442	VAL	Peptide
2	I	545	PHE	Peptide
2	I	57	PHE	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	G	1762	0	1785	116	0
1	H	1678	0	1698	149	0
1	M	572	0	602	58	0
2	I	10571	0	10580	945	0
3	J	10460	0	10679	964	0
4	K	627	0	634	52	0
5	L	3854	0	3911	481	0
6	N	571	0	558	35	0
7	O	1270	0	698	88	0
8	P	1272	0	705	107	0
9	I	27	39	38	5	0
9	J	27	39	38	5	0
10	J	1	0	0	0	0
11	J	2	0	0	0	0
11	N	1	0	0	0	0
All	All	32695	78	31926	2753	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 43.

All (2753) 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)
9:J:1504:1N7:C19	9:J:1504:1N7:C3	1.84	1.54
9:I:1401:1N7:C3	9:I:1401:1N7:C19	1.82	1.52
5:L:146:GLU:O	5:L:150:ARG:HG3	1.48	1.10
3:J:145:VAL:HG23	3:J:159:ILE:HG22	1.36	1.05
3:J:965:SER:HB2	3:J:973:LEU:HD11	1.38	1.03
2:I:811:ASN:HA	2:I:815:SER:HB2	1.40	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:93:GLN:HB2	1:H:120:ASP:HB2	1.42	1.01
2:I:106:GLU:HB3	2:I:109:ALA:HB2	1.43	1.00
2:I:75:LEU:HD11	2:I:127:ILE:HD11	1.43	1.00
1:H:16:ILE:HD11	1:H:214:GLU:HG2	1.44	0.99
1:G:192:VAL:HG11	1:G:195:ARG:HB2	1.45	0.98
2:I:317:LEU:HA	2:I:321:LEU:HD12	1.46	0.98
3:J:885:VAL:HG13	3:J:894:VAL:HG21	1.40	0.98
2:I:255:ILE:HB	2:I:263:VAL:O	1.62	0.96
1:M:257:VAL:HG23	1:M:260:LEU:HD22	1.45	0.96
3:J:1272:SER:HB2	3:J:1300:ALA:HB2	1.46	0.96
3:J:1162:ILE:HA	3:J:1203:ARG:HA	1.42	0.96
3:J:556:GLU:O	3:J:563:LEU:HA	1.66	0.96
2:I:975:ILE:HA	2:I:978:VAL:HB	1.47	0.96
3:J:706:VAL:HG12	3:J:715:LYS:HG2	1.48	0.95
3:J:1215:GLU:HB2	3:J:1220:ILE:HD11	1.45	0.95
4:K:13:ILE:HD11	4:K:54:ILE:HD12	1.46	0.95
5:L:512:GLY:HA3	8:P:30:DG:H4'	1.46	0.95
3:J:1107:VAL:HG22	3:J:1122:ALA:HB2	1.48	0.94
3:J:697:MET:HE3	3:J:698:MET:HE3	1.47	0.93
3:J:1040:MET:HB3	3:J:1046:ILE:HD13	1.46	0.93
2:I:311:CYS:HB3	2:I:321:LEU:HD22	1.51	0.93
2:I:1141:LEU:HD22	2:I:1170:MET:HE1	1.51	0.93
3:J:1046:ILE:HG22	3:J:1061:VAL:HA	1.49	0.92
3:J:1081:VAL:HA	3:J:1087:ASP:HA	1.49	0.92
2:I:992:LEU:HD12	2:I:996:ARG:HB3	1.48	0.92
3:J:930:LEU:HD13	3:J:1244:GLN:HG3	1.51	0.92
1:G:113:ALA:HB2	1:G:126:PRO:HB3	1.51	0.92
2:I:159:SER:HB3	2:I:172:TYR:HA	1.50	0.92
2:I:463:GLN:HG3	2:I:505:PHE:HB2	1.50	0.92
5:L:576:VAL:HG11	5:L:587:ILE:HG21	1.52	0.92
2:I:599:VAL:HG22	2:I:627:GLY:HA2	1.52	0.91
3:J:516:ASP:HB3	3:J:573:THR:HG21	1.51	0.91
2:I:243:PRO:HA	2:I:246:LEU:HD13	1.51	0.91
3:J:690:ASN:HB2	3:J:743:MET:HE2	1.50	0.91
3:J:1178:THR:HA	3:J:1184:ASP:HB3	1.51	0.91
1:M:289:LEU:HD23	1:M:300:LEU:HD13	1.51	0.90
3:J:702:GLN:HG3	3:J:703:THR:HG23	1.52	0.90
1:M:257:VAL:HA	1:M:260:LEU:HD13	1.52	0.90
5:L:551:LEU:HD21	5:L:597:LYS:HD3	1.54	0.89
5:L:224:LEU:HG	5:L:252:LEU:HD11	1.52	0.89
2:I:59:ILE:HB	2:I:68:LEU:O	1.73	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:937:ILE:HG13	3:J:1134:ILE:HD12	1.51	0.88
7:O:71:DG:H1'	7:O:72:DT:H5'	1.53	0.88
3:J:518:VAL:HG12	3:J:707:ILE:HD11	1.55	0.88
2:I:699:LEU:HB2	2:I:799:ASN:HD22	1.36	0.88
2:I:1101:LEU:HD13	3:J:504:GLN:HB2	1.55	0.88
1:H:190:ALA:HB2	1:H:200:LYS:HB2	1.56	0.88
2:I:200:ARG:HD2	7:O:62:DC:H5''	1.55	0.88
5:L:134:VAL:HA	5:L:273:MET:HE1	1.56	0.88
1:H:107:ILE:HG23	1:H:135:ASP:HB3	1.56	0.88
2:I:718:ALA:HB2	2:I:783:LEU:HD21	1.54	0.88
2:I:803:ALA:HB2	2:I:1094:VAL:HG11	1.56	0.87
5:L:344:LEU:HA	5:L:347:ILE:HD12	1.55	0.87
2:I:99:LYS:HA	2:I:121:GLU:HA	1.55	0.87
2:I:496:LYS:HG2	8:P:34:DT:H4'	1.53	0.87
2:I:525:THR:HG21	2:I:687:ARG:HD2	1.56	0.87
3:J:401:VAL:HG22	3:J:408:VAL:HG21	1.56	0.87
5:L:273:MET:HA	5:L:276:MET:HE2	1.55	0.87
3:J:1024:THR:HA	3:J:1125:PRO:HA	1.57	0.87
2:I:277:LEU:HA	2:I:280:ASP:HB2	1.56	0.87
3:J:1050:THR:HG23	3:J:1057:SER:HB3	1.56	0.87
5:L:290:LEU:HD11	5:L:336:GLU:HG3	1.54	0.86
5:L:587:ILE:HD13	5:L:590:ILE:HD12	1.58	0.86
1:G:135:ASP:HB3	1:G:138:ALA:HB2	1.57	0.86
2:I:1333:LEU:HD22	3:J:307:LEU:HD13	1.56	0.86
2:I:483:ASP:HB2	2:I:487:LEU:HD22	1.58	0.86
8:P:21:DA:H1'	8:P:22:DA:H5'	1.58	0.86
3:J:936:HIS:HA	3:J:1134:ILE:O	1.75	0.86
5:L:305:LEU:HB3	5:L:315:TRP:HB2	1.56	0.85
2:I:292:ILE:HG22	2:I:317:LEU:HB2	1.58	0.85
1:H:61:ILE:HD12	1:H:142:MET:HE2	1.56	0.85
2:I:817:LEU:HD21	2:I:1085:MET:HE1	1.58	0.85
4:K:30:MET:HE1	4:K:49:ILE:HB	1.59	0.85
3:J:1144:LEU:HD11	3:J:1236:GLU:HG3	1.57	0.84
7:O:75:DA:H2''	7:O:76:DT:H71	1.59	0.84
1:G:43:LEU:HD13	1:G:217:ILE:HD11	1.57	0.84
3:J:975:ILE:H	3:J:1000:GLY:HA2	1.40	0.84
3:J:1261:LEU:HD13	3:J:1304:ARG:HD3	1.59	0.84
2:I:901:LEU:HD22	5:L:565:ILE:HD11	1.57	0.83
1:G:207:THR:HG22	1:G:209:GLY:H	1.42	0.83
2:I:103:VAL:HA	2:I:117:ILE:HG22	1.58	0.83
5:L:324:LYS:H	5:L:327:SER:HB3	1.41	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:309:ASN:HB2	3:J:326:SER:HB2	1.59	0.83
3:J:259:ARG:HH11	5:L:502:LYS:HD2	1.44	0.82
5:L:309:ASN:HD21	5:L:312:SER:HB2	1.42	0.82
3:J:641:ILE:HD12	3:J:644:MET:HE3	1.61	0.82
2:I:227:LYS:HZ3	2:I:298:ALA:HB1	1.43	0.82
2:I:1151:LEU:HD21	2:I:1198:LEU:HD13	1.61	0.82
2:I:251:ALA:HB3	2:I:266:GLY:H	1.45	0.82
2:I:960:LEU:HD11	2:I:1028:LYS:HE3	1.62	0.82
1:H:215:GLU:HA	1:H:218:ARG:HG2	1.63	0.81
3:J:552:ILE:HD11	3:J:570:LYS:HG3	1.62	0.81
3:J:527:LEU:HD23	3:J:532:GLU:HG3	1.59	0.81
2:I:884:VAL:HG11	2:I:1050:VAL:HG11	1.61	0.81
3:J:848:VAL:HG12	3:J:857:LEU:HB3	1.61	0.81
3:J:1163:VAL:HG23	3:J:1177:ILE:HG12	1.60	0.81
3:J:205:LEU:HD12	3:J:214:ARG:HD2	1.63	0.81
2:I:120:GLN:HB3	2:I:489:PRO:HG2	1.62	0.81
2:I:452:ARG:NH1	2:I:584:TYR:O	2.13	0.81
3:J:925:GLU:HG3	3:J:926:PRO:HD3	1.62	0.81
1:G:58:GLU:HG2	1:G:145:LYS:HE3	1.63	0.81
3:J:914:ALA:HB2	3:J:1359:ALA:HB1	1.63	0.81
2:I:1125:GLY:HA3	2:I:1179:GLY:HA2	1.61	0.81
1:H:183:ILE:HG22	1:H:205:MET:HG3	1.61	0.80
3:J:163:GLU:HA	3:J:166:LEU:HD12	1.64	0.80
3:J:975:ILE:HB	3:J:1000:GLY:H	1.46	0.80
2:I:98:VAL:HG21	2:I:124:MET:HE3	1.62	0.80
2:I:1333:LEU:HD21	3:J:327:LEU:HD22	1.63	0.80
1:M:300:LEU:HA	1:M:303:ILE:HD12	1.63	0.80
2:I:705:GLU:HB2	2:I:794:LEU:HB3	1.62	0.80
3:J:1078:LEU:HG	3:J:1101:LEU:HD21	1.64	0.80
5:L:116:GLU:HA	5:L:119:ILE:HD12	1.64	0.80
2:I:1304:MET:HE3	2:I:1308:ILE:HD11	1.63	0.80
1:G:83:LEU:HD23	2:I:694:ARG:HE	1.47	0.79
3:J:520:ALA:HB3	3:J:546:ALA:HB2	1.62	0.79
5:L:303:ILE:HA	5:L:306:PHE:HB3	1.61	0.79
3:J:342:LEU:HD23	3:J:1352:ILE:HG23	1.64	0.79
3:J:395:LYS:HD3	5:L:536:THR:HG21	1.63	0.79
2:I:960:LEU:HD23	2:I:1029:LEU:HB2	1.64	0.79
2:I:516:ASP:HB3	2:I:522:SER:OG	1.82	0.79
5:L:134:VAL:HG23	5:L:365:MET:HE1	1.62	0.79
2:I:1280:ALA:HB1	3:J:918:ILE:HG22	1.65	0.79
1:H:89:ALA:HB3	1:H:124:VAL:HG11	1.64	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:993:PRO:HD2	2:I:996:ARG:HG3	1.65	0.79
3:J:964:LYS:HB2	3:J:977:SER:HB2	1.65	0.79
2:I:975:ILE:HG23	2:I:1014:LEU:HG	1.64	0.79
1:H:205:MET:HE1	1:H:217:ILE:HG13	1.65	0.78
2:I:60:GLN:HA	2:I:67:GLU:HG2	1.64	0.78
2:I:964:LEU:HD21	2:I:1022:LYS:HG2	1.63	0.78
3:J:759:ILE:HG23	3:J:771:GLN:HG2	1.62	0.78
5:L:148:TYR:CE1	5:L:152:GLU:HG3	2.18	0.78
1:M:296:GLY:HA3	8:P:67:DT:H3'	1.63	0.78
2:I:870:ILE:HD13	2:I:944:ARG:HD3	1.65	0.78
3:J:513:MET:HE3	3:J:579:LEU:HB2	1.65	0.78
3:J:1029:THR:HB	3:J:1121:LEU:HD11	1.65	0.77
1:H:57:THR:HG21	1:H:147:GLN:HB3	1.65	0.77
6:N:47:ALA:HA	6:N:50:LYS:HE3	1.66	0.77
2:I:346:TYR:OH	2:I:437:ASN:OD1	2.02	0.77
5:L:166:VAL:H	5:L:259:PHE:HB3	1.50	0.77
5:L:426:LYS:HD3	7:O:52:DA:H5'	1.65	0.77
1:H:32:GLU:HA	1:H:198:LEU:HD12	1.64	0.77
2:I:225:PHE:HB2	2:I:336:LEU:HD13	1.67	0.77
2:I:4:SER:O	2:I:8:LYS:N	2.17	0.76
3:J:1271:SER:H	3:J:1299:GLY:HA3	1.50	0.76
1:G:90:VAL:HG23	1:G:123:ILE:HD13	1.66	0.76
1:H:74:VAL:HG22	1:H:133:LEU:HA	1.67	0.76
2:I:216:THR:OG1	2:I:219:GLN:OE1	2.03	0.76
5:L:262:VAL:HG12	5:L:265:GLN:H	1.51	0.76
2:I:1246:ARG:HH11	2:I:1266:GLY:HA2	1.50	0.76
3:J:260:PHE:HB2	5:L:504:PRO:HB3	1.67	0.76
2:I:249:GLU:O	2:I:269:ILE:N	2.17	0.76
2:I:1017:GLN:O	2:I:1021:LEU:HB2	1.87	0.75
5:L:354:THR:HG23	5:L:357:GLN:H	1.51	0.75
2:I:565:GLU:HA	2:I:569:ILE:HG12	1.68	0.75
2:I:1296:ASP:OD2	2:I:1322:SER:N	2.20	0.75
3:J:1067:ARG:HD2	3:J:1072:LYS:HA	1.67	0.75
3:J:1328:THR:O	3:J:1332:LEU:HB2	1.85	0.75
2:I:55:SER:OG	2:I:465:ARG:NH1	2.18	0.75
3:J:245:LEU:HG	3:J:246:PRO:HD2	1.68	0.75
3:J:515:ARG:HH21	3:J:717:VAL:HG23	1.51	0.75
5:L:583:THR:HG21	7:O:26:DT:H73	1.68	0.75
7:O:21:DA:H2''	7:O:22:DT:H71	1.69	0.75
1:G:45:ARG:NH2	2:I:1084:ASP:OD1	2.20	0.75
2:I:250:THR:HA	2:I:268:ARG:HA	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:668:PHE:HB2	3:J:678:ARG:HG3	1.69	0.74
2:I:321:LEU:HD23	2:I:324:LYS:HE3	1.68	0.74
2:I:901:LEU:HD11	2:I:905:ILE:HD11	1.69	0.74
2:I:942:ASP:OD2	2:I:1048:LYS:NZ	2.20	0.74
8:P:24:DG:H2'	8:P:25:DG:H8	1.52	0.74
2:I:1120:ALA:HB2	2:I:1199:LEU:HG	1.69	0.74
3:J:950:ILE:HD12	3:J:1018:ALA:HB3	1.68	0.74
3:J:1368:ASP:OD1	3:J:1372:ARG:NH1	2.20	0.74
2:I:238:GLN:HG2	2:I:286:GLU:HG3	1.68	0.74
2:I:980:VAL:HG13	2:I:984:VAL:HG23	1.68	0.74
3:J:325:LYS:HD3	5:L:508:GLU:HG3	1.70	0.74
5:L:148:TYR:HA	5:L:161:LEU:HD21	1.69	0.74
2:I:528:ARG:NH2	2:I:576:SER:O	2.19	0.74
2:I:1103:VAL:HG21	2:I:1112:ILE:HD11	1.68	0.74
5:L:148:TYR:HA	5:L:161:LEU:HD11	1.69	0.74
1:H:64:VAL:HG22	1:H:66:HIS:H	1.50	0.74
3:J:124:ILE:HG22	3:J:135:ILE:HD13	1.70	0.74
3:J:1314:LEU:HD13	3:J:1326:GLN:HB2	1.70	0.74
5:L:353:LEU:HD13	5:L:357:GLN:HB3	1.69	0.74
2:I:1004:ASP:HA	2:I:1008:GLN:HG2	1.69	0.74
3:J:1060:VAL:HG11	3:J:1106:ILE:HG12	1.69	0.74
3:J:1109:LEU:HD23	3:J:1113:VAL:HB	1.68	0.74
3:J:1105:ALA:HA	3:J:1123:ARG:O	1.88	0.73
3:J:1132:LYS:N	3:J:1132:LYS:HD2	2.02	0.73
2:I:232:ILE:HG12	2:I:237:LEU:HD22	1.69	0.73
2:I:842:ASP:HB2	2:I:1047:LEU:HD21	1.69	0.73
3:J:962:ASN:O	3:J:980:THR:OG1	2.06	0.73
3:J:554:GLU:OE2	3:J:570:LYS:NZ	2.22	0.73
3:J:1371:ARG:HD2	3:J:1372:ARG:HH22	1.53	0.73
2:I:221:LEU:HD13	2:I:336:LEU:HD11	1.70	0.73
3:J:698:MET:HE2	3:J:698:MET:HA	1.70	0.73
8:P:60:DA:H2'	8:P:61:DT:H71	1.70	0.73
2:I:472:GLU:HA	2:I:475:VAL:HG12	1.70	0.73
2:I:758:ARG:NH2	2:I:762:ASN:OD1	2.21	0.73
3:J:1148:ARG:HH21	7:O:66:DG:H4'	1.54	0.73
5:L:151:VAL:HG22	5:L:156:ALA:HB3	1.70	0.73
2:I:1281:TYR:OH	3:J:489:ASN:ND2	2.22	0.72
5:L:280:VAL:HG11	5:L:359:LYS:HG2	1.70	0.72
2:I:453:ILE:HD11	2:I:587:LEU:HD11	1.69	0.72
2:I:817:LEU:HD21	2:I:1080:ASN:HD22	1.52	0.72
3:J:218:THR:HA	3:J:221:ILE:HG22	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:848:VAL:HB	3:J:858:VAL:HG22	1.71	0.72
2:I:1105:SER:HB2	3:J:731:ARG:HB3	1.71	0.72
2:I:618:GLN:HE21	2:I:620:ASN:HB2	1.55	0.72
2:I:714:VAL:HG22	2:I:787:PRO:HD2	1.71	0.72
2:I:721:GLY:HA2	2:I:777:VAL:O	1.90	0.72
2:I:1297:ASP:OD1	2:I:1300:GLY:N	2.18	0.72
3:J:58:CYS:SG	3:J:59:ALA:N	2.63	0.72
3:J:781:LYS:NZ	3:J:785:ASP:OD2	2.22	0.72
2:I:292:ILE:HG21	2:I:317:LEU:HD12	1.69	0.72
2:I:27:LEU:N	2:I:711:ASP:OD2	2.21	0.72
2:I:197:ARG:HH12	2:I:200:ARG:HA	1.55	0.72
2:I:1212:LEU:HD22	2:I:1225:VAL:HG21	1.71	0.72
3:J:1004:ALA:N	3:J:1017:VAL:O	2.23	0.71
5:L:105:MET:HE3	5:L:388:ILE:HD12	1.70	0.71
2:I:800:MET:HE3	2:I:822:VAL:HG21	1.71	0.71
2:I:894:GLN:NE2	3:J:76:LYS:O	2.22	0.71
6:N:48:ARG:HA	6:N:51:ILE:HD12	1.70	0.71
1:G:158:ARG:NH2	1:G:177:TYR:OH	2.24	0.71
1:H:140:ILE:HD11	1:H:142:MET:HE3	1.71	0.71
2:I:179:TYR:OH	2:I:458:GLU:OE2	2.06	0.71
2:I:452:ARG:NH2	2:I:458:GLU:OE1	2.23	0.71
7:O:23:DC:H2'	7:O:24:DC:C6	2.26	0.71
3:J:202:ARG:HG3	3:J:221:ILE:HD11	1.72	0.71
2:I:102:LEU:N	2:I:118:LYS:O	2.22	0.71
3:J:58:CYS:HB3	3:J:61:ILE:HB	1.73	0.71
3:J:70:CYS:SG	3:J:71:LEU:N	2.63	0.71
3:J:287:ALA:HA	5:L:413:MET:HE1	1.73	0.71
3:J:130:MET:HE3	3:J:134:ASP:HB3	1.71	0.70
3:J:936:HIS:NE2	3:J:1133:ASP:HA	2.05	0.70
5:L:162:ILE:HA	5:L:262:VAL:HG23	1.72	0.70
5:L:385:ARG:HG3	7:O:55:DC:H5''	1.73	0.70
3:J:160:LEU:HB3	3:J:164:GLN:HB2	1.73	0.70
3:J:352:ARG:HH12	8:P:26:DC:H2''	1.55	0.70
3:J:1298:VAL:HG22	3:J:1300:ALA:H	1.55	0.70
5:L:136:GLU:OE1	5:L:364:ARG:NH2	2.24	0.70
2:I:31:GLN:NE2	2:I:527:LYS:O	2.24	0.70
2:I:1005:GLU:O	2:I:1009:ASN:N	2.20	0.70
5:L:234:THR:HG21	5:L:244:THR:H	1.56	0.70
1:H:28:LEU:HG	1:H:31:LEU:HD21	1.72	0.70
1:H:56:VAL:HG22	1:H:146:VAL:HG12	1.72	0.70
3:J:47:ARG:NH2	7:O:44:DA:OP1	2.23	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:299:LYS:HA	5:L:302:PHE:HB3	1.72	0.70
2:I:1117:LEU:HD21	2:I:1182:ILE:HG21	1.72	0.70
2:I:318:SER:OG	2:I:320:ASP:OD1	2.07	0.70
3:J:1194:ARG:NH2	3:J:1212:ASP:O	2.24	0.70
5:L:252:LEU:HA	5:L:255:VAL:HG22	1.74	0.70
1:H:111:THR:HG23	1:H:113:ALA:H	1.53	0.70
3:J:513:MET:HG3	3:J:544:LEU:HD11	1.72	0.70
3:J:733:SER:N	3:J:736:GLN:OE1	2.24	0.70
1:H:83:LEU:HD11	3:J:526:VAL:HG12	1.74	0.70
2:I:808:ASN:H	3:J:633:ALA:HB2	1.57	0.70
2:I:840:SER:HB3	2:I:850:ILE:HD11	1.72	0.70
4:K:56:GLU:HB2	4:K:58:LEU:HG	1.73	0.70
2:I:1123:GLY:HA3	2:I:1204:LEU:HD11	1.74	0.69
5:L:295:CYS:HB2	5:L:329:LYS:HB3	1.74	0.69
1:G:14:VAL:HG12	1:G:15:ASP:H	1.56	0.69
2:I:319:LEU:HG	2:I:322:LEU:HD13	1.72	0.69
2:I:714:VAL:O	2:I:767:GLN:NE2	2.25	0.69
5:L:362:ASN:HA	5:L:365:MET:HB2	1.73	0.69
2:I:36:GLN:NE2	2:I:40:GLU:OE2	2.25	0.69
2:I:62:TYR:OH	2:I:477:GLU:OE1	2.10	0.69
1:G:11:PRO:HA	1:G:30:PRO:HG2	1.75	0.69
1:G:118:ASP:OD1	1:G:118:ASP:N	2.26	0.69
2:I:903:ARG:HD2	2:I:908:GLU:H	1.56	0.69
2:I:27:LEU:HD13	2:I:663:VAL:HG21	1.74	0.69
3:J:111:THR:OG1	3:J:300:GLN:OE1	2.08	0.69
3:J:972:LYS:HD2	3:J:1002:VAL:HG11	1.74	0.69
1:M:253:LEU:O	1:M:279:GLY:N	2.25	0.69
6:N:8:ALA:O	6:N:12:THR:HG23	1.93	0.69
6:N:52:PHE:O	6:N:55:VAL:HG23	1.93	0.69
3:J:1174:ARG:HG2	3:J:1189:MET:HE1	1.74	0.69
1:H:100:LEU:HD23	1:H:115:ILE:HG21	1.75	0.69
3:J:161:THR:HG22	3:J:164:GLN:HG3	1.75	0.69
3:J:1155:ILE:H	3:J:1211:SER:HG	1.39	0.69
2:I:1246:ARG:NH2	2:I:1250:SER:O	2.18	0.68
1:H:111:THR:N	1:H:114:ASP:OD2	2.22	0.68
9:I:1401:1N7:C3	9:I:1401:1N7:C2	2.70	0.68
5:L:148:TYR:HA	5:L:161:LEU:CD2	2.23	0.68
3:J:821:MET:HA	3:J:881:LYS:HA	1.74	0.68
3:J:937:ILE:HG13	3:J:1134:ILE:CD1	2.24	0.68
2:I:575:LEU:HD21	2:I:579:ALA:HB3	1.76	0.68
2:I:1113:LEU:HD11	3:J:641:ILE:HD13	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:34:SER:OG	3:J:36:GLY:O	2.11	0.68
5:L:148:TYR:HA	5:L:161:LEU:CD1	2.23	0.68
2:I:744:GLY:O	2:I:1017:GLN:NE2	2.25	0.68
2:I:968:GLU:HB2	2:I:1018:TYR:HE1	1.58	0.68
5:L:147:GLN:HG3	5:L:265:GLN:HE22	1.58	0.68
5:L:387:VAL:HG22	5:L:435:ILE:HD13	1.74	0.68
8:P:68:DG:H1'	8:P:69:DT:H5'	1.75	0.68
2:I:813:GLU:HG2	3:J:460:ASP:HB2	1.76	0.68
2:I:957:LYS:HG2	2:I:1029:LEU:HD11	1.76	0.68
7:O:57:DT:H1'	7:O:58:DC:H5'	1.73	0.68
1:G:229:GLU:HA	1:G:232:VAL:HG12	1.75	0.68
3:J:34:SER:HA	3:J:102:MET:O	1.94	0.68
1:G:102:LEU:HD22	1:G:142:MET:HE2	1.74	0.68
1:H:69:SER:HB2	1:H:78:ILE:HD11	1.75	0.68
3:J:275:ARG:HH11	3:J:302:ALA:HB2	1.59	0.68
1:M:262:LEU:HD23	1:M:302:GLU:HB3	1.76	0.67
2:I:681:MET:HB3	2:I:685:MET:HE3	1.75	0.67
3:J:149:GLY:HA2	3:J:177:ASP:HB2	1.75	0.67
3:J:417:ARG:NE	4:K:43:ASN:O	2.27	0.67
5:L:363:ARG:O	5:L:367:ILE:HG13	1.95	0.67
2:I:159:SER:CB	2:I:172:TYR:HA	2.23	0.67
2:I:310:ILE:HG23	2:I:324:LYS:HB3	1.76	0.67
2:I:933:VAL:HG11	2:I:945:ALA:HB2	1.77	0.67
2:I:1069:ARG:NH2	2:I:1114:GLU:OE2	2.22	0.67
3:J:44:ILE:HD11	3:J:252:LEU:HD22	1.76	0.67
3:J:550:VAL:HG12	3:J:552:ILE:HG23	1.75	0.67
3:J:1060:VAL:HG21	3:J:1106:ILE:HG23	1.76	0.67
5:L:288:MET:HE2	5:L:299:LYS:NZ	2.09	0.67
5:L:466:ILE:HD11	5:L:486:ARG:HB3	1.77	0.67
4:K:38:LEU:N	4:K:53:GLU:OE2	2.20	0.67
2:I:732:ILE:HD13	2:I:783:LEU:HB3	1.77	0.67
2:I:1253:LEU:HD13	3:J:253:VAL:HG11	1.75	0.67
5:L:311:THR:HG22	5:L:344:LEU:HD21	1.75	0.67
7:O:40:DC:H2''	7:O:41:DT:H71	1.76	0.67
2:I:229:ILE:HD12	2:I:334:GLU:HG2	1.74	0.67
5:L:414:LYS:HE3	5:L:418:LYS:HE2	1.76	0.67
2:I:632:ASP:HA	2:I:647:ARG:CD	2.24	0.67
3:J:186:GLN:HB2	3:J:238:ILE:HG21	1.76	0.67
5:L:303:ILE:HG22	5:L:307:THR:HG23	1.77	0.67
5:L:586:ARG:HH21	7:O:24:DC:H3'	1.58	0.67
2:I:522:SER:HB2	2:I:687:ARG:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1293:VAL:HG11	2:I:1304:MET:HG2	1.77	0.67
2:I:903:ARG:NH1	2:I:908:GLU:O	2.28	0.66
2:I:1080:ASN:HB2	2:I:1085:MET:HE3	1.76	0.66
3:J:334:LYS:HD3	3:J:339:ARG:HH21	1.59	0.66
3:J:1036:ARG:HB2	3:J:1079:LYS:HB3	1.77	0.66
3:J:798:ARG:HH21	3:J:1325:PHE:HB2	1.60	0.66
5:L:445:ASP:OD1	5:L:451:ARG:NH2	2.29	0.66
5:L:133:SER:OG	5:L:365:MET:SD	2.49	0.66
2:I:257:ALA:N	2:I:260:LYS:O	2.27	0.66
1:G:11:PRO:HB3	1:G:31:LEU:HG	1.78	0.66
3:J:18:ASP:OD1	3:J:1373:ARG:NE	2.28	0.66
5:L:95:THR:HG23	5:L:96:ASP:H	1.61	0.66
2:I:598:VAL:HA	2:I:627:GLY:HA3	1.78	0.66
8:P:18:DT:H2'	8:P:19:DT:H71	1.77	0.66
3:J:1161:GLY:O	3:J:1204:VAL:N	2.24	0.66
5:L:101:TYR:HE2	5:L:405:ILE:HG21	1.59	0.66
1:H:84:ASN:ND2	1:H:129:VAL:O	2.26	0.66
2:I:130:MET:SD	2:I:134:GLY:HA2	2.36	0.66
2:I:145:ILE:HB	2:I:456:VAL:HG22	1.77	0.66
3:J:58:CYS:SG	3:J:61:ILE:N	2.69	0.66
5:L:573:LEU:HG	5:L:584:ARG:HE	1.60	0.66
3:J:1021:ASP:OD1	3:J:1024:THR:N	2.29	0.66
3:J:1346:GLY:O	3:J:1350:ASN:ND2	2.26	0.66
1:M:254:LEU:HD23	1:M:321:TRP:HH2	1.60	0.66
2:I:118:LYS:NZ	2:I:487:LEU:O	2.26	0.65
2:I:1184:THR:HG23	2:I:1189:GLY:HA3	1.77	0.65
3:J:423:LEU:CD1	3:J:468:VAL:HG12	2.26	0.65
3:J:1063:ASP:HA	3:J:1103:GLY:HA3	1.78	0.65
1:H:97:GLU:HG2	1:H:147:GLN:HG3	1.78	0.65
2:I:1070:HIS:NE2	2:I:1114:GLU:OE1	2.21	0.65
5:L:148:TYR:O	5:L:161:LEU:HD11	1.96	0.65
5:L:150:ARG:HB3	5:L:150:ARG:CZ	2.26	0.65
2:I:423:ASP:HA	2:I:426:ILE:HD11	1.78	0.65
2:I:545:PHE:O	2:I:547:VAL:HG22	1.97	0.65
3:J:76:LYS:O	3:J:77:ARG:NH1	2.27	0.65
3:J:93:THR:HG22	3:J:94:GLN:H	1.61	0.65
3:J:1270:GLY:HA3	3:J:1299:GLY:HA3	1.78	0.65
9:J:1504:1N7:C3	9:J:1504:1N7:C2	2.72	0.65
2:I:237:LEU:HD23	2:I:289:VAL:HG22	1.77	0.65
2:I:1101:LEU:HD23	3:J:725:MET:SD	2.36	0.65
2:I:1109:ILE:CG2	3:J:644:MET:HE1	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1313:HIS:HB2	3:J:474:LEU:HD23	1.78	0.65
3:J:288:PRO:HG3	5:L:380:VAL:HG21	1.78	0.65
3:J:368:LEU:HD22	3:J:373:ALA:HB2	1.78	0.65
3:J:414:GLU:OE1	3:J:417:ARG:NH1	2.23	0.65
3:J:647:PRO:HG3	3:J:697:MET:HA	1.78	0.65
5:L:375:ALA:HA	5:L:378:GLU:HB2	1.78	0.65
5:L:583:THR:HG22	5:L:586:ARG:H	1.61	0.65
1:M:289:LEU:O	1:M:295:LEU:HD13	1.96	0.65
3:J:114:ILE:HD12	3:J:304:ASP:HB3	1.77	0.65
3:J:1079:LYS:HG3	3:J:1087:ASP:OD1	1.97	0.65
5:L:295:CYS:HA	5:L:329:LYS:HE2	1.78	0.65
2:I:471:VAL:HG11	2:I:498:ILE:HD11	1.78	0.65
3:J:814:CYS:HB3	3:J:895:CYS:HB3	1.79	0.65
2:I:217:THR:HG23	2:I:351:LEU:HD13	1.79	0.65
3:J:538:ARG:NH2	3:J:631:TYR:OH	2.30	0.65
3:J:950:ILE:O	3:J:951:GLN:NE2	2.30	0.65
1:H:76:GLU:OE1	1:H:132:HIS:N	2.23	0.65
2:I:759:SER:OG	2:I:763:THR:OG1	2.14	0.65
4:K:76:GLU:O	4:K:80:LEU:N	2.30	0.64
5:L:303:ILE:O	5:L:307:THR:N	2.26	0.64
5:L:426:LYS:HE2	7:O:52:DA:H3'	1.78	0.64
1:G:61:ILE:HB	1:G:64:VAL:HG11	1.79	0.64
3:J:1050:THR:HA	3:J:1057:SER:HB3	1.79	0.64
5:L:309:ASN:ND2	5:L:312:SER:HB2	2.12	0.64
2:I:593:LYS:NZ	2:I:594:VAL:O	2.30	0.64
3:J:85:CYS:SG	3:J:86:GLU:N	2.70	0.64
3:J:210:SER:HB3	8:P:12:DG:H3'	1.79	0.64
3:J:948:SER:OG	3:J:1020:TRP:NE1	2.30	0.64
3:J:961:SER:HB3	3:J:981:GLU:HB2	1.79	0.64
3:J:1026:PRO:HB2	3:J:1028:ILE:HG13	1.79	0.64
2:I:271:ALA:HA	2:I:274:ILE:HD12	1.79	0.64
2:I:975:ILE:HG22	2:I:1011:LEU:HD23	1.79	0.64
3:J:44:ILE:HG22	3:J:45:ASN:H	1.59	0.64
5:L:96:ASP:O	5:L:99:ARG:N	2.25	0.64
5:L:311:THR:HA	5:L:344:LEU:HD22	1.80	0.64
6:N:32:ILE:O	6:N:54:GLY:HA2	1.97	0.64
5:L:151:VAL:HB	5:L:161:LEU:HG	1.77	0.64
1:H:73:GLY:O	1:H:134:THR:N	2.31	0.64
2:I:1257:GLN:NE2	2:I:1296:ASP:OD1	2.25	0.64
3:J:425:ARG:HD2	3:J:459:ALA:HB2	1.79	0.64
3:J:510:LEU:HD22	3:J:601:ILE:HD12	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1163:VAL:HG12	3:J:1202:GLU:O	1.98	0.64
5:L:114:GLU:HG3	5:L:117:ILE:HD12	1.78	0.64
2:I:469:VAL:O	2:I:472:GLU:HG3	1.98	0.64
3:J:405:GLU:O	3:J:408:VAL:HG12	1.98	0.64
3:J:984:LEU:HD23	3:J:993:GLU:HG3	1.80	0.64
3:J:1219:ASP:OD1	3:J:1222:ARG:NH2	2.21	0.64
1:G:41:ASN:O	1:G:45:ARG:HG3	1.98	0.64
2:I:20:GLN:OE1	2:I:20:GLN:N	2.27	0.64
2:I:870:ILE:HG21	2:I:931:VAL:HG11	1.78	0.64
3:J:513:MET:CE	3:J:579:LEU:HB2	2.27	0.64
3:J:259:ARG:HD3	5:L:502:LYS:HD2	1.79	0.64
2:I:153:PRO:O	2:I:401:GLY:HA2	1.97	0.64
5:L:470:MET:HE2	5:L:478:PRO:HB3	1.80	0.64
1:G:61:ILE:HB	1:G:64:VAL:CG1	2.28	0.63
1:H:64:VAL:HG21	1:H:78:ILE:HD13	1.79	0.63
2:I:150:HIS:CE1	2:I:452:ARG:HD3	2.32	0.63
2:I:1134:GLN:OE1	2:I:1134:GLN:N	2.32	0.63
3:J:137:ARG:HG2	3:J:142:GLU:OE1	1.98	0.63
3:J:966:VAL:HG23	3:J:974:VAL:HG23	1.79	0.63
2:I:813:GLU:HG2	3:J:460:ASP:CB	2.29	0.63
5:L:219:GLU:O	5:L:223:GLU:HG3	1.98	0.63
8:P:41:DT:H2"	8:P:42:DT:H71	1.80	0.63
2:I:346:TYR:HE2	2:I:437:ASN:HD21	1.47	0.63
2:I:898:GLU:HA	2:I:901:LEU:HB3	1.79	0.63
3:J:1038:THR:HG21	3:J:1079:LYS:NZ	2.14	0.63
5:L:141:ILE:HG23	5:L:224:LEU:HD21	1.80	0.63
5:L:333:VAL:O	5:L:337:VAL:HG23	1.98	0.63
2:I:314:ASN:O	2:I:352:ARG:NH1	2.31	0.63
3:J:1063:ASP:OD1	3:J:1103:GLY:HA3	1.97	0.63
5:L:525:ASP:OD2	5:L:528:LEU:HG	1.98	0.63
5:L:283:GLN:OE1	5:L:344:LEU:HB2	1.97	0.63
2:I:800:MET:HE2	2:I:1096:ILE:HG13	1.81	0.63
2:I:802:VAL:HG21	2:I:1098:LEU:HD13	1.80	0.63
3:J:1329:THR:O	3:J:1333:THR:HG23	1.98	0.63
4:K:60:ASN:HB2	4:K:63:ILE:CD1	2.29	0.63
4:K:60:ASN:HB2	4:K:63:ILE:HD12	1.79	0.63
1:H:61:ILE:HB	1:H:64:VAL:HG12	1.78	0.63
3:J:1034:PHE:HE1	3:J:1114:GLN:HB3	1.64	0.63
3:J:1144:LEU:HD11	3:J:1236:GLU:CG	2.29	0.63
5:L:385:ARG:HD2	7:O:54:DT:H2"	1.80	0.63
6:N:31:GLY:HA2	6:N:53:PRO:HB2	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:44:ARG:NH2	3:J:538:ARG:HG2	2.13	0.63
1:H:118:ASP:HB3	1:H:121:VAL:CG1	2.27	0.63
1:H:219:ARG:HA	1:H:222:THR:HG22	1.79	0.63
2:I:188:PHE:CE1	2:I:194:LEU:HD13	2.33	0.63
2:I:717:VAL:HG12	2:I:782:VAL:HG12	1.80	0.63
2:I:1033:ARG:O	2:I:1037:THR:HG22	1.98	0.63
3:J:1256:ILE:O	3:J:1260:MET:HG3	1.98	0.63
5:L:167:ASP:HA	5:L:216:LEU:HD22	1.79	0.63
1:G:11:PRO:HG3	1:G:31:LEU:HD21	1.80	0.63
1:G:83:LEU:HD21	2:I:693:LEU:CD2	2.29	0.63
2:I:232:ILE:CG1	2:I:237:LEU:HD22	2.29	0.63
2:I:1333:LEU:HD22	3:J:307:LEU:CD1	2.26	0.63
5:L:493:LYS:HA	5:L:496:LYS:HG2	1.80	0.63
1:M:254:LEU:HD23	1:M:321:TRP:CH2	2.34	0.63
2:I:273:HIS:O	2:I:277:LEU:HG	1.98	0.62
5:L:301:ASN:HA	5:L:304:THR:HB	1.81	0.62
2:I:488:MET:HE3	2:I:489:PRO:HD3	1.81	0.62
2:I:1223:ARG:NH2	3:J:719:PHE:O	2.32	0.62
3:J:212:THR:HA	3:J:215:LYS:HD3	1.80	0.62
3:J:1001:ALA:CB	3:J:1020:TRP:HB3	2.29	0.62
3:J:1038:THR:CG2	3:J:1077:ALA:HB3	2.29	0.62
7:O:68:DA:H2''	7:O:69:DT:H5'	1.80	0.62
3:J:279:LEU:HD12	3:J:295:GLU:HG3	1.81	0.62
3:J:1172:LYS:HB3	3:J:1190:ILE:O	1.99	0.62
3:J:1227:HIS:HA	3:J:1230:THR:HG22	1.82	0.62
8:P:30:DG:H5''	8:P:30:DG:H8	1.62	0.62
2:I:18:ARG:HE	2:I:620:ASN:HA	1.64	0.62
2:I:199:ASP:N	2:I:199:ASP:OD1	2.28	0.62
2:I:249:GLU:H	2:I:269:ILE:HB	1.64	0.62
2:I:960:LEU:HG	2:I:1025:PHE:HD1	1.63	0.62
2:I:1023:HIS:O	2:I:1027:LYS:HG3	2.00	0.62
3:J:1326:GLN:HB3	3:J:1327:GLU:OE1	1.99	0.62
5:L:316:PHE:CE2	5:L:320:ILE:HD11	2.33	0.62
5:L:453:PRO:HG3	7:O:44:DA:H5'	1.80	0.62
1:G:162:GLU:HG2	1:G:165:GLU:H	1.63	0.62
1:G:183:ILE:HD13	1:G:205:MET:HB2	1.80	0.62
2:I:87:ILE:HG23	2:I:932:GLN:HE22	1.64	0.62
5:L:267:ASP:O	5:L:271:ASN:ND2	2.32	0.62
3:J:208:THR:HG23	3:J:214:ARG:HD3	1.81	0.62
3:J:552:ILE:HD11	3:J:570:LYS:CG	2.29	0.62
5:L:288:MET:SD	5:L:289:LYS:HG3	2.40	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:179:PRO:HG3	1:G:211:ILE:HG13	1.82	0.62
2:I:71:VAL:HB	2:I:99:LYS:O	2.00	0.62
2:I:198:ILE:HG22	2:I:199:ASP:H	1.63	0.62
2:I:495:ALA:HB3	5:L:471:LEU:HD11	1.81	0.62
2:I:590:PRO:HG3	2:I:605:TYR:CE1	2.35	0.62
2:I:1336:ASN:HB2	3:J:25:ALA:HB2	1.80	0.62
3:J:197:GLU:O	3:J:201:LEU:HG	1.99	0.62
1:H:133:LEU:HD11	1:H:138:ALA:HB3	1.81	0.62
3:J:1063:ASP:HA	3:J:1103:GLY:CA	2.30	0.62
1:G:23:HIS:HB3	1:G:206:GLU:HG3	1.82	0.62
2:I:714:VAL:CG2	2:I:787:PRO:HD2	2.29	0.62
3:J:26:SER:HB3	3:J:236:TRP:CE2	2.34	0.62
5:L:586:ARG:O	5:L:590:ILE:HG13	2.00	0.62
1:G:86:LYS:NZ	2:I:826:ASP:OD2	2.32	0.61
2:I:523:GLU:HG2	2:I:527:LYS:HZ1	1.65	0.61
3:J:401:VAL:HG22	3:J:408:VAL:CG2	2.30	0.61
3:J:475:GLU:N	3:J:475:GLU:OE1	2.31	0.61
3:J:755:ILE:HD12	3:J:774:ILE:HG23	1.82	0.61
2:I:211:ARG:HD3	2:I:357:ASN:O	2.00	0.61
2:I:817:LEU:CD2	2:I:1085:MET:HE1	2.29	0.61
3:J:210:SER:CB	8:P:12:DG:H3'	2.30	0.61
3:J:914:ALA:HB2	3:J:1359:ALA:CB	2.30	0.61
3:J:1005:LYS:CG	3:J:1017:VAL:HG13	2.30	0.61
5:L:339:ARG:HA	5:L:342:GLN:HG2	1.82	0.61
5:L:444:ALA:HB1	5:L:457:ILE:HD12	1.81	0.61
2:I:322:LEU:O	2:I:325:LEU:HG	2.00	0.61
2:I:903:ARG:O	2:I:907:GLY:N	2.27	0.61
2:I:980:VAL:HA	2:I:984:VAL:HA	1.82	0.61
2:I:1109:ILE:HG23	3:J:644:MET:HE1	1.82	0.61
3:J:165:TYR:O	3:J:169:LEU:HB2	2.00	0.61
3:J:754:ILE:HD11	6:N:19:GLY:HA3	1.81	0.61
3:J:1167:LYS:HB3	3:J:1174:ARG:HD2	1.82	0.61
5:L:163:THR:HG23	5:L:262:VAL:HG22	1.81	0.61
5:L:253:SER:O	5:L:257:LYS:HB2	2.00	0.61
5:L:343:LYS:O	5:L:347:ILE:HG13	2.00	0.61
5:L:583:THR:O	5:L:587:ILE:HG12	2.01	0.61
2:I:525:THR:HG21	2:I:687:ARG:CD	2.30	0.61
2:I:575:LEU:CD2	2:I:579:ALA:HB3	2.30	0.61
1:M:254:LEU:HB3	1:M:321:TRP:CZ2	2.36	0.61
2:I:895:LEU:HD11	2:I:899:GLU:OE1	2.00	0.61
3:J:1325:PHE:CE2	3:J:1326:GLN:HG2	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:600:HIS:HB3	5:L:603:ARG:HB3	1.82	0.61
2:I:802:VAL:CG2	2:I:1098:LEU:HD13	2.30	0.61
9:I:1401:1N7:C3	9:I:1401:1N7:C18	2.64	0.61
3:J:1061:VAL:HG21	3:J:1101:LEU:HD13	1.83	0.61
3:J:1169:THR:HG22	3:J:1170:LYS:H	1.63	0.61
5:L:348:GLU:HG2	5:L:355:ILE:HG12	1.81	0.61
8:P:24:DG:H2'	8:P:25:DG:C8	2.36	0.61
3:J:697:MET:SD	3:J:741:ALA:HB3	2.41	0.61
3:J:735:ALA:HA	3:J:738:ARG:HG2	1.82	0.61
1:G:162:GLU:HG3	1:G:165:GLU:HB3	1.83	0.61
3:J:311:ARG:NH2	3:J:1329:THR:HG21	2.16	0.61
2:I:256:GLU:HA	2:I:261:VAL:HA	1.81	0.61
5:L:339:ARG:HB3	5:L:343:LYS:NZ	2.16	0.61
7:O:40:DC:H2''	7:O:41:DT:C7	2.31	0.61
2:I:239:MET:SD	2:I:241:LEU:HB2	2.40	0.61
3:J:557:LYS:HA	3:J:562:GLU:O	2.01	0.61
3:J:1000:GLY:HA3	3:J:1028:ILE:CD1	2.31	0.61
3:J:1036:ARG:HE	3:J:1081:VAL:HG11	1.64	0.60
1:H:112:ALA:HB1	1:H:123:ILE:HG21	1.83	0.60
2:I:238:GLN:HA	2:I:285:ILE:O	2.01	0.60
2:I:243:PRO:HG2	2:I:278:GLU:HG3	1.83	0.60
3:J:412:LEU:O	3:J:416:ILE:HG12	2.00	0.60
3:J:576:ARG:NH1	3:J:593:ASN:O	2.34	0.60
3:J:591:ILE:HG23	3:J:592:VAL:HG13	1.81	0.60
3:J:1162:ILE:HD12	3:J:1203:ARG:N	2.16	0.60
3:J:281:ARG:HH21	5:L:410:ILE:HD13	1.66	0.60
3:J:1001:ALA:HB2	3:J:1020:TRP:HB3	1.83	0.60
3:J:1272:SER:HB2	3:J:1300:ALA:CB	2.28	0.60
4:K:69:ARG:O	4:K:73:GLN:HG2	2.02	0.60
5:L:503:GLU:OE1	5:L:504:PRO:HD2	2.01	0.60
1:G:156:SER:O	1:G:159:ILE:HG22	2.01	0.60
2:I:105:TYR:CD1	2:I:114:VAL:HG12	2.37	0.60
3:J:210:SER:O	3:J:213:LYS:N	2.34	0.60
3:J:1078:LEU:CG	3:J:1101:LEU:HD21	2.31	0.60
3:J:1349:GLU:O	3:J:1353:VAL:HG23	2.01	0.60
5:L:216:LEU:O	5:L:220:LYS:HG2	2.01	0.60
2:I:296:VAL:HG12	2:I:352:ARG:HH22	1.67	0.60
2:I:594:VAL:HG11	2:I:650:VAL:HG23	1.82	0.60
5:L:114:GLU:HA	5:L:117:ILE:HD12	1.82	0.60
5:L:163:THR:HG23	5:L:262:VAL:HA	1.82	0.60
2:I:387:ASN:HA	2:I:391:SER:HB3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:678:ARG:NH2	6:N:3:ASP:OD2	2.31	0.60
3:J:72:CYS:SG	3:J:73:GLY:N	2.75	0.60
3:J:79:LYS:CB	5:L:569:THR:HB	2.31	0.60
3:J:515:ARG:NH2	3:J:717:VAL:HG23	2.17	0.60
3:J:1036:ARG:HG3	3:J:1081:VAL:HG11	1.83	0.60
5:L:595:LEU:O	5:L:599:ARG:HG2	2.01	0.60
1:G:162:GLU:O	1:G:165:GLU:N	2.33	0.60
2:I:296:VAL:HA	2:I:316:GLU:HA	1.84	0.60
2:I:1041:ASP:O	2:I:1042:LEU:HD23	2.01	0.60
2:I:1246:ARG:NH1	2:I:1266:GLY:HA2	2.16	0.60
3:J:208:THR:CG2	3:J:214:ARG:HD3	2.32	0.60
3:J:1042:ASP:OD1	3:J:1046:ILE:HG13	2.02	0.60
2:I:1117:LEU:HD21	2:I:1182:ILE:CG2	2.31	0.60
3:J:926:PRO:HB3	3:J:1246:VAL:HG11	1.82	0.60
5:L:281:ARG:HA	5:L:284:GLU:OE1	2.01	0.60
5:L:283:GLN:O	5:L:287:ILE:HG13	2.02	0.60
5:L:380:VAL:O	5:L:384:LEU:HG	2.01	0.60
2:I:1119:MET:HE2	2:I:1204:LEU:HD22	1.84	0.60
3:J:58:CYS:SG	3:J:60:ARG:N	2.75	0.60
3:J:457:TYR:CE2	3:J:466:MET:HE1	2.37	0.60
5:L:213:ASP:HB2	5:L:214:PRO:HD2	1.84	0.60
5:L:338:HIS:O	5:L:342:GLN:HG2	2.02	0.60
5:L:344:LEU:HA	5:L:347:ILE:CD1	2.29	0.60
5:L:540:LEU:O	5:L:544:THR:HG23	2.02	0.60
6:N:37:CYS:HB2	6:N:41:GLY:H	1.67	0.60
2:I:300:ASP:OD1	2:I:312:ALA:HA	2.01	0.60
3:J:72:CYS:HB2	3:J:87:LYS:HD3	1.84	0.60
3:J:429:LEU:HB3	3:J:925:GLU:HB2	1.84	0.60
3:J:490:ILE:HD11	3:J:609:TYR:CE1	2.37	0.60
3:J:555:TYR:HD2	3:J:585:LYS:HB3	1.66	0.60
2:I:11:ILE:HG22	2:I:1172:LEU:HD11	1.84	0.59
2:I:618:GLN:NE2	2:I:620:ASN:HB2	2.16	0.59
2:I:1217:THR:OG1	2:I:1219:GLU:HG2	2.02	0.59
3:J:821:MET:HG2	3:J:879:ALA:HB1	1.83	0.59
3:J:1149:ARG:HG2	3:J:1216:ALA:HB1	1.83	0.59
5:L:151:VAL:HG13	5:L:156:ALA:O	2.01	0.59
2:I:207:THR:HG23	2:I:350:THR:HG21	1.84	0.59
2:I:632:ASP:HA	2:I:647:ARG:HD2	1.84	0.59
3:J:208:THR:O	3:J:214:ARG:NH1	2.34	0.59
3:J:1323:ALA:HB2	3:J:1331:VAL:HG11	1.84	0.59
5:L:281:ARG:O	5:L:285:ARG:HG2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:93:GLN:HB2	1:H:120:ASP:CB	2.24	0.59
2:I:325:LEU:HD22	2:I:333:ILE:HG13	1.83	0.59
2:I:621:SER:HB2	2:I:653:MET:HE3	1.84	0.59
2:I:685:MET:CE	2:I:1073:LYS:HG3	2.32	0.59
2:I:1042:LEU:HD13	2:I:1049:ILE:HG13	1.82	0.59
3:J:709:ARG:NH1	3:J:710:ASP:HB3	2.17	0.59
3:J:846:GLU:OE2	3:J:881:LYS:HD3	2.03	0.59
1:H:56:VAL:HG21	1:H:144:ILE:HD11	1.85	0.59
2:I:257:ALA:HB3	2:I:262:TYR:CE2	2.37	0.59
2:I:557:ARG:NH2	2:I:607:SER:O	2.32	0.59
3:J:609:TYR:HE1	3:J:614:LEU:HD13	1.68	0.59
5:L:148:TYR:OH	5:L:218:ARG:HA	2.02	0.59
5:L:313:ASP:O	5:L:317:ASN:HB2	2.01	0.59
7:O:57:DT:C2'	7:O:58:DC:H5'	2.32	0.59
1:H:222:THR:O	1:H:226:GLU:HG2	2.03	0.59
2:I:1170:MET:HE2	2:I:1170:MET:HA	1.84	0.59
3:J:108:ALA:HB3	3:J:279:LEU:HD22	1.84	0.59
3:J:835:LEU:O	3:J:839:VAL:HG12	2.03	0.59
5:L:144:LEU:HD21	5:L:256:PHE:CZ	2.37	0.59
5:L:148:TYR:CA	5:L:161:LEU:HD21	2.31	0.59
5:L:562:ARG:HG2	5:L:591:GLU:OE1	2.02	0.59
7:O:58:DC:H2''	7:O:59:DG:N7	2.16	0.59
8:P:39:DC:H1'	8:P:40:DC:H5'	1.83	0.59
1:G:86:LYS:HE2	1:G:174:ASP:HB2	1.84	0.59
1:H:140:ILE:HD11	1:H:142:MET:CE	2.32	0.59
4:K:71:GLU:HA	4:K:74:GLU:CD	2.28	0.59
5:L:102:MET:HE3	7:O:56:DC:C6	2.38	0.59
1:M:266:SER:O	1:M:270:LEU:HG	2.03	0.59
2:I:120:GLN:OE1	2:I:121:GLU:N	2.35	0.59
2:I:178:PRO:HB3	2:I:397:LEU:HD12	1.84	0.59
2:I:360:LEU:HD13	2:I:378:ARG:HD3	1.85	0.59
2:I:444:ASP:CG	2:I:447:HIS:HB2	2.28	0.59
2:I:820:GLU:HB2	2:I:1080:ASN:O	2.02	0.59
2:I:972:PHE:CE2	2:I:994:ARG:HB3	2.37	0.59
3:J:103:GLY:O	3:J:244:VAL:HG22	2.02	0.59
3:J:516:ASP:HA	3:J:545:HIS:HB2	1.84	0.59
5:L:345:GLN:O	5:L:349:GLU:HG2	2.02	0.59
2:I:632:ASP:HA	2:I:647:ARG:HG3	1.84	0.59
2:I:1282:GLY:HA3	4:K:17:PHE:CE1	2.38	0.59
3:J:253:VAL:HG21	5:L:523:ILE:HD13	1.83	0.59
4:K:26:ARG:NH1	4:K:30:MET:HB2	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:141:ILE:CG2	5:L:224:LEU:HD21	2.32	0.59
5:L:224:LEU:HD13	5:L:256:PHE:CD1	2.38	0.59
6:N:46:GLU:OE1	6:N:49:ARG:NE	2.35	0.59
2:I:103:VAL:HG12	2:I:117:ILE:CG2	2.32	0.59
2:I:971:LEU:HD13	2:I:1018:TYR:HB2	1.83	0.59
2:I:1256:GLN:OE1	5:L:528:LEU:HD11	2.03	0.59
3:J:211:GLU:OE1	3:J:214:ARG:HG3	2.03	0.59
3:J:555:TYR:CE2	3:J:585:LYS:HD2	2.36	0.59
3:J:972:LYS:HD2	3:J:1002:VAL:CG1	2.33	0.59
3:J:1107:VAL:HG22	3:J:1122:ALA:CB	2.29	0.59
3:J:267:ASP:OD1	3:J:270:ARG:NH2	2.36	0.59
3:J:615:LYS:O	3:J:619:ILE:HG22	2.03	0.59
3:J:936:HIS:CD2	3:J:1134:ILE:H	2.21	0.59
3:J:1047:THR:HB	3:J:1062:LEU:HD21	1.84	0.59
8:P:37:DG:H1'	8:P:38:DC:H5'	1.85	0.59
1:H:205:MET:HE3	1:H:213:PRO:CB	2.33	0.58
2:I:60:GLN:O	2:I:476:LYS:HE3	2.03	0.58
2:I:238:GLN:HB3	2:I:284:LEU:HD11	1.84	0.58
2:I:301:TYR:HB2	2:I:311:CYS:SG	2.42	0.58
3:J:298:MET:SD	5:L:402:LEU:HB3	2.43	0.58
3:J:759:ILE:HG23	3:J:771:GLN:CG	2.32	0.58
3:J:986:ASP:OD2	3:J:992:LYS:NZ	2.36	0.58
3:J:1149:ARG:HG2	3:J:1216:ALA:CB	2.34	0.58
1:G:59:VAL:HG21	1:G:82:LEU:HD22	1.84	0.58
3:J:833:GLU:HG2	3:J:1242:ARG:NH1	2.18	0.58
3:J:891:ASP:OD2	3:J:1287:ILE:HD11	2.03	0.58
1:H:32:GLU:HA	1:H:198:LEU:CD1	2.33	0.58
2:I:165:HIS:CE1	2:I:190:PRO:HG3	2.38	0.58
2:I:741:MET:HG3	2:I:974:ARG:NH1	2.18	0.58
3:J:1186:TYR:CE2	3:J:1188:GLU:HB2	2.38	0.58
5:L:148:TYR:N	5:L:161:LEU:HD21	2.19	0.58
1:H:47:LEU:HD22	1:H:180:VAL:HG11	1.86	0.58
2:I:297:VAL:HG12	2:I:315:MET:O	2.02	0.58
2:I:356:THR:HB	2:I:365:GLU:CD	2.27	0.58
3:J:910:ASN:ND2	4:K:15:ASN:HA	2.18	0.58
2:I:523:GLU:HG2	2:I:527:LYS:NZ	2.18	0.58
3:J:259:ARG:HG3	8:P:31:DG:N2	2.18	0.58
3:J:269:TYR:CD1	3:J:306:LEU:HD11	2.39	0.58
3:J:309:ASN:ND2	3:J:324:LEU:O	2.35	0.58
3:J:1031:VAL:HG12	3:J:1032:SER:H	1.67	0.58
3:J:1330:ARG:HH22	8:P:21:DA:H5''	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:96:ASP:HB3	5:L:99:ARG:HG3	1.86	0.58
5:L:287:ILE:HG22	5:L:302:PHE:CE1	2.39	0.58
5:L:324:LYS:HB3	5:L:325:PRO:HD2	1.85	0.58
1:G:8:PHE:HE2	1:H:223:ILE:HD13	1.69	0.58
1:H:205:MET:HE3	1:H:213:PRO:HB3	1.86	0.58
2:I:198:ILE:HG21	2:I:370:MET:HE1	1.83	0.58
2:I:431:LYS:HE2	2:I:435:ILE:CG1	2.33	0.58
3:J:1148:ARG:NH2	7:O:66:DG:H4'	2.19	0.58
5:L:163:THR:HG21	5:L:263:PRO:HD3	1.86	0.58
5:L:246:GLN:O	5:L:249:ILE:HG22	2.04	0.58
1:G:231:PHE:HE2	1:H:39:LEU:HD13	1.68	0.58
1:H:62:ASP:OD1	1:H:141:SER:HB3	2.04	0.58
2:I:1333:LEU:CD2	3:J:327:LEU:HD22	2.31	0.58
3:J:950:ILE:CD1	3:J:1018:ALA:HB3	2.34	0.58
3:J:958:ILE:O	3:J:1008:GLY:HA2	2.04	0.58
9:J:1504:1N7:H34	8:P:29:DA:H3'	1.85	0.58
5:L:132:CYS:SG	5:L:257:LYS:NZ	2.61	0.58
2:I:621:SER:HB2	2:I:653:MET:CE	2.34	0.58
2:I:742:TYR:O	2:I:745:GLU:HG2	2.04	0.58
2:I:838:CYS:HB3	2:I:1050:VAL:CG1	2.33	0.58
3:J:210:SER:HB2	8:P:13:DG:OP2	2.03	0.58
3:J:661:VAL:HG23	3:J:682:VAL:HG22	1.83	0.58
1:G:99:ILE:HG21	1:G:143:ARG:NH2	2.19	0.58
2:I:22:LEU:HB3	2:I:655:VAL:HG21	1.86	0.58
2:I:557:ARG:NH1	2:I:611:GLU:OE2	2.28	0.58
2:I:672:GLU:HG3	2:I:673:HIS:CD2	2.39	0.58
3:J:160:LEU:HD11	3:J:176:PHE:HZ	1.68	0.58
3:J:452:LEU:HD13	3:J:500:ILE:CG2	2.34	0.58
3:J:623:GLN:O	3:J:627:THR:HG22	2.04	0.58
3:J:844:THR:HG23	3:J:864:LEU:HD11	1.84	0.58
3:J:1068:THR:O	3:J:1072:LYS:N	2.37	0.58
1:M:250:ASP:HB3	1:M:253:LEU:HD13	1.86	0.58
7:O:25:DA:H2'	7:O:26:DT:C7	2.34	0.58
1:G:207:THR:HG22	1:G:209:GLY:N	2.18	0.58
2:I:130:MET:HE2	2:I:134:GLY:O	2.04	0.58
2:I:561:ILE:HG21	3:J:772:TYR:HE2	1.67	0.58
2:I:877:VAL:HG11	2:I:883:LEU:HD21	1.86	0.58
5:L:305:LEU:HB3	5:L:315:TRP:CB	2.30	0.58
5:L:586:ARG:NH2	7:O:24:DC:H3'	2.19	0.58
8:P:30:DG:H5''	8:P:30:DG:C8	2.39	0.58
8:P:50:DT:H4'	8:P:51:DC:OP1	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1271:GLY:HA3	8:P:26:DC:OP1	2.03	0.57
3:J:663:GLU:O	3:J:666:GLU:HG2	2.04	0.57
5:L:420:GLU:HB2	7:O:50:DA:H61	1.69	0.57
5:L:432:THR:O	5:L:436:ARG:HG2	2.04	0.57
7:O:74:DC:C6	7:O:74:DC:H5'	2.39	0.57
2:I:275:ARG:HA	2:I:278:GLU:OE1	2.04	0.57
2:I:1004:ASP:HA	2:I:1008:GLN:CG	2.34	0.57
2:I:1269:ARG:NH1	3:J:344:GLY:O	2.36	0.57
2:I:1304:MET:O	2:I:1308:ILE:HG12	2.04	0.57
5:L:127:ILE:HA	5:L:130:VAL:HG22	1.86	0.57
1:M:256:PRO:HA	1:M:277:TYR:HD1	1.69	0.57
1:M:298:LYS:HB3	8:P:67:DT:OP1	2.03	0.57
6:N:37:CYS:HB2	6:N:41:GLY:N	2.19	0.57
8:P:48:DC:H2''	8:P:49:DT:H71	1.85	0.57
1:H:92:VAL:HG12	1:H:93:GLN:O	2.03	0.57
3:J:211:GLU:O	3:J:215:LYS:HG3	2.03	0.57
3:J:518:VAL:HA	3:J:547:ARG:NH1	2.18	0.57
3:J:701:LEU:HD21	3:J:723:TYR:HB2	1.86	0.57
5:L:306:PHE:CE1	5:L:310:GLU:HG3	2.39	0.57
1:H:27:THR:HG23	1:H:202:VAL:HG22	1.86	0.57
2:I:231:GLU:OE1	2:I:332:ARG:NH2	2.37	0.57
2:I:1121:ALA:HB2	2:I:1182:ILE:HD12	1.85	0.57
3:J:923:ILE:HD11	3:J:1252:HIS:O	2.04	0.57
3:J:1035:VAL:HG12	3:J:1111:ASP:OD2	2.04	0.57
5:L:606:VAL:O	5:L:609:SER:HB3	2.04	0.57
2:I:146:VAL:HG23	2:I:511:LEU:HD22	1.87	0.57
2:I:292:ILE:HG23	2:I:295:LYS:HB2	1.86	0.57
2:I:745:GLU:HA	2:I:1017:GLN:OE1	2.05	0.57
3:J:50:LYS:NZ	3:J:71:LEU:O	2.34	0.57
3:J:844:THR:CG2	3:J:864:LEU:HD11	2.34	0.57
3:J:846:GLU:CD	3:J:881:LYS:HD3	2.30	0.57
2:I:415:GLU:N	2:I:415:GLU:OE1	2.37	0.57
2:I:1313:HIS:HB2	3:J:474:LEU:CD2	2.35	0.57
3:J:1158:GLU:HG2	3:J:1186:TYR:CE1	2.40	0.57
5:L:98:VAL:O	5:L:102:MET:HG2	2.05	0.57
8:P:32:DA:H2''	8:P:33:DA:C8	2.39	0.57
1:G:234:LEU:HD12	1:H:218:ARG:HH11	1.68	0.57
3:J:1271:SER:O	3:J:1292:LEU:HD21	2.05	0.57
5:L:339:ARG:HB3	5:L:343:LYS:HZ3	1.69	0.57
1:G:90:VAL:CG2	1:G:123:ILE:HD13	2.34	0.57
1:H:22:THR:OG1	1:H:207:THR:N	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:85:LEU:HD21	1:H:130:ILE:HG23	1.86	0.57
2:I:237:LEU:HD23	2:I:289:VAL:CG2	2.34	0.57
2:I:746:ALA:HB2	2:I:971:LEU:HD23	1.87	0.57
2:I:983:GLY:HA3	2:I:1002:LEU:HD13	1.85	0.57
3:J:264:ASP:HB3	3:J:324:LEU:HD22	1.87	0.57
3:J:658:GLU:HA	3:J:661:VAL:HG12	1.86	0.57
3:J:957:SER:HA	3:J:1009:GLU:O	2.05	0.57
3:J:1209:VAL:O	3:J:1210:ILE:HD13	2.04	0.57
5:L:561:MET:HG3	5:L:571:TYR:CD2	2.40	0.57
2:I:288:PRO:HB2	2:I:290:GLU:CD	2.29	0.57
3:J:115:TRP:HB3	3:J:1333:THR:HG21	1.87	0.57
3:J:950:ILE:HD12	3:J:1018:ALA:CB	2.35	0.57
5:L:148:TYR:HB2	5:L:221:PHE:CZ	2.39	0.57
7:O:57:DT:H2''	7:O:58:DC:H5'	1.87	0.57
1:G:29:GLU:HB3	1:G:30:PRO:HD3	1.85	0.57
2:I:204:LEU:HD11	2:I:369:MET:HE2	1.87	0.57
2:I:231:GLU:HB3	2:I:233:ARG:HG3	1.87	0.57
2:I:445:ILE:O	2:I:451:ARG:HD2	2.04	0.57
2:I:559:CYS:HB2	2:I:662:SER:HB3	1.86	0.57
3:J:205:LEU:HD12	3:J:214:ARG:CD	2.34	0.57
3:J:519:ASN:HB2	3:J:709:ARG:HB2	1.87	0.57
3:J:1090:ILE:HG13	3:J:1093:THR:OG1	2.05	0.57
5:L:133:SER:HA	5:L:364:ARG:NH2	2.18	0.57
2:I:118:LYS:HD3	2:I:488:MET:SD	2.45	0.56
2:I:524:ILE:O	2:I:528:ARG:HG2	2.05	0.56
2:I:636:CYS:HB2	2:I:645:PHE:HD2	1.70	0.56
5:L:513:ASP:HB3	5:L:515:GLU:OE1	2.05	0.56
2:I:92:TYR:HB3	2:I:137:VAL:CG1	2.36	0.56
3:J:1143:ASP:OD1	3:J:1148:ARG:HD2	2.04	0.56
5:L:347:ILE:HG22	5:L:355:ILE:HD12	1.87	0.56
1:H:73:GLY:C	1:H:134:THR:HG22	2.31	0.56
2:I:798:GLN:HG3	2:I:827:ARG:O	2.05	0.56
2:I:1256:GLN:HB3	2:I:1301:ARG:NH2	2.20	0.56
2:I:1329:GLU:OE1	3:J:330:MET:HE2	2.05	0.56
3:J:80:HIS:O	3:J:83:VAL:HG12	2.05	0.56
3:J:250:ARG:O	3:J:266:ASN:ND2	2.38	0.56
3:J:269:TYR:O	3:J:273:ILE:HG13	2.04	0.56
3:J:697:MET:HE1	3:J:738:ARG:HB3	1.86	0.56
3:J:1024:THR:CG2	3:J:1123:ARG:HB3	2.35	0.56
3:J:1146:GLU:OE2	3:J:1310:THR:HG22	2.05	0.56
3:J:1368:ASP:O	3:J:1372:ARG:HG2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:303:ILE:CA	5:L:306:PHE:HB3	2.35	0.56
5:L:335:GLU:OE1	5:L:339:ARG:HD3	2.06	0.56
1:M:281:LEU:HD21	1:M:307:LEU:HD11	1.87	0.56
2:I:887:VAL:HB	2:I:913:VAL:CG1	2.35	0.56
5:L:98:VAL:HG23	5:L:402:LEU:HD11	1.87	0.56
5:L:414:LYS:HE2	5:L:434:TRP:CH2	2.40	0.56
7:O:52:DA:H2''	7:O:53:DT:H5'	1.86	0.56
1:H:89:ALA:O	1:H:124:VAL:HG12	2.06	0.56
2:I:979:LEU:HD22	2:I:989:LEU:CD1	2.36	0.56
3:J:518:VAL:HG12	3:J:707:ILE:CD1	2.32	0.56
3:J:807:LEU:HD12	3:J:1259:GLN:OE1	2.06	0.56
3:J:1032:SER:O	3:J:1088:VAL:HG21	2.05	0.56
5:L:142:THR:O	5:L:146:GLU:HG3	2.06	0.56
1:G:27:THR:C	1:G:28:LEU:HD12	2.30	0.56
2:I:231:GLU:O	2:I:238:GLN:N	2.39	0.56
2:I:870:ILE:H	2:I:870:ILE:HD12	1.71	0.56
2:I:1153:ALA:O	2:I:1155:VAL:HG13	2.05	0.56
3:J:46:TYR:OH	7:O:44:DA:OP2	2.24	0.56
3:J:700:ASN:HA	3:J:704:GLU:HG3	1.87	0.56
3:J:803:VAL:HA	3:J:1313:SER:HB3	1.88	0.56
3:J:1357:ILE:HD12	3:J:1359:ALA:HB3	1.87	0.56
5:L:127:ILE:HD12	5:L:130:VAL:CG2	2.36	0.56
5:L:390:ILE:HA	5:L:393:LYS:CG	2.36	0.56
2:I:110:PRO:HD2	2:I:111:GLU:OE1	2.06	0.56
2:I:856:ASN:ND2	5:L:612:ASP:O	2.39	0.56
2:I:1289:GLU:O	2:I:1294:LYS:HG3	2.04	0.56
3:J:213:LYS:O	3:J:217:LEU:HD23	2.06	0.56
5:L:279:ARG:HG2	5:L:347:ILE:HD11	1.88	0.56
5:L:303:ILE:O	5:L:307:THR:HG23	2.05	0.56
2:I:361:SER:O	2:I:365:GLU:HG3	2.06	0.56
2:I:421:SER:N	2:I:424:ASP:OD2	2.39	0.56
2:I:539:THR:O	2:I:543:ALA:HB2	2.06	0.56
3:J:426:ALA:HB3	3:J:427:PRO:HD3	1.88	0.56
3:J:1227:HIS:HA	3:J:1230:THR:CG2	2.36	0.56
5:L:281:ARG:HA	5:L:284:GLU:CD	2.31	0.56
1:H:88:LEU:HD21	1:H:115:ILE:HD11	1.88	0.56
1:H:118:ASP:HB3	1:H:121:VAL:HG12	1.87	0.56
2:I:413:GLU:OE1	2:I:413:GLU:N	2.39	0.56
2:I:545:PHE:O	2:I:547:VAL:N	2.38	0.56
2:I:625:GLU:HG2	2:I:626:GLU:OE2	2.06	0.56
3:J:866:GLU:N	3:J:866:GLU:OE1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1024:THR:HG21	3:J:1123:ARG:HB3	1.88	0.56
5:L:102:MET:HG3	7:O:56:DC:C4	2.40	0.56
5:L:162:ILE:CD1	5:L:261:LEU:HA	2.36	0.56
2:I:1004:ASP:HA	2:I:1008:GLN:CB	2.36	0.56
2:I:1111:GLN:HB2	2:I:1230:MET:CE	2.36	0.56
5:L:101:TYR:CE2	5:L:405:ILE:HG21	2.39	0.56
5:L:134:VAL:HG21	5:L:266:PHE:CE1	2.41	0.56
6:N:67:ARG:O	6:N:70:LYS:HB3	2.05	0.56
7:O:56:DC:H2''	7:O:57:DT:C6	2.41	0.56
1:H:133:LEU:HD11	1:H:138:ALA:CB	2.36	0.55
2:I:211:ARG:NH1	2:I:357:ASN:O	2.36	0.55
2:I:854:ILE:HG12	2:I:887:VAL:CG1	2.36	0.55
2:I:1154:ASP:N	2:I:1154:ASP:OD1	2.38	0.55
2:I:1274:GLU:HG2	3:J:424:ASN:ND2	2.20	0.55
3:J:555:TYR:CD2	3:J:585:LYS:HB3	2.40	0.55
5:L:137:TYR:CE2	5:L:276:MET:HE3	2.41	0.55
1:M:254:LEU:HB3	1:M:321:TRP:HZ2	1.71	0.55
7:O:25:DA:H2'	7:O:26:DT:H72	1.88	0.55
2:I:231:GLU:OE1	2:I:332:ARG:HD3	2.06	0.55
3:J:254:PRO:HA	3:J:260:PHE:HD1	1.70	0.55
3:J:1187:GLU:O	3:J:1187:GLU:HG3	2.06	0.55
4:K:52:ARG:O	4:K:56:GLU:HG2	2.06	0.55
4:K:67:ARG:O	4:K:70:GLN:HG3	2.07	0.55
1:M:281:LEU:HD21	1:M:307:LEU:CD1	2.35	0.55
1:G:169:GLY:O	1:G:171:LEU:HD22	2.07	0.55
1:H:22:THR:O	1:H:206:GLU:HA	2.06	0.55
1:H:89:ALA:HB1	1:H:210:THR:CG2	2.37	0.55
2:I:660:VAL:HG13	2:I:661:VAL:HG13	1.88	0.55
2:I:1121:ALA:HB1	2:I:1180:MET:O	2.06	0.55
3:J:48:THR:OG1	3:J:50:LYS:HG3	2.05	0.55
3:J:527:LEU:HD13	3:J:548:VAL:HG11	1.87	0.55
3:J:1012:ALA:N	3:J:1015:GLU:OE1	2.27	0.55
3:J:1064:SER:HA	3:J:1067:ARG:NH1	2.21	0.55
3:J:1154:ALA:N	3:J:1214:PRO:O	2.28	0.55
5:L:227:GLN:CG	5:L:252:LEU:HD13	2.36	0.55
5:L:353:LEU:HD13	5:L:357:GLN:CB	2.36	0.55
7:O:48:DG:H2''	7:O:49:DC:O4'	2.05	0.55
1:G:68:TYR:HB3	2:I:756:TYR:CD2	2.41	0.55
1:H:81:ILE:O	1:H:85:LEU:HG	2.06	0.55
2:I:515:MET:SD	2:I:527:LYS:NZ	2.79	0.55
2:I:1010:GLN:O	2:I:1013:GLN:HG2	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:218:THR:HA	3:J:221:ILE:CG2	2.37	0.55
3:J:252:LEU:O	3:J:252:LEU:HD23	2.07	0.55
3:J:334:LYS:HG3	3:J:335:GLN:HE21	1.71	0.55
3:J:652:GLU:O	3:J:656:GLU:HG3	2.06	0.55
3:J:1050:THR:CG2	3:J:1057:SER:HB3	2.32	0.55
3:J:1077:ALA:HB2	3:J:1100:PHE:CD1	2.42	0.55
5:L:355:ILE:O	5:L:359:LYS:HG3	2.07	0.55
1:H:99:ILE:HG13	1:H:144:ILE:O	2.07	0.55
1:H:109:PRO:HB3	1:H:132:HIS:CE1	2.42	0.55
1:H:215:GLU:HB2	1:H:218:ARG:NH2	2.21	0.55
2:I:746:ALA:HB2	2:I:971:LEU:CD2	2.36	0.55
2:I:818:VAL:HG22	2:I:1096:ILE:HG12	1.89	0.55
2:I:1326:LEU:O	2:I:1330:ILE:HG13	2.07	0.55
3:J:128:LEU:HD21	3:J:189:LEU:HD23	1.88	0.55
3:J:411:ILE:O	3:J:415:VAL:HG23	2.06	0.55
3:J:531:LYS:HD3	3:J:581:MET:HE3	1.89	0.55
5:L:143:TYR:O	5:L:147:GLN:HG2	2.07	0.55
1:M:263:THR:HG22	1:M:265:ARG:H	1.72	0.55
7:O:26:DT:H3'	7:O:27:DT:H6	1.71	0.55
7:O:31:DA:H2''	7:O:32:DA:C8	2.42	0.55
1:G:223:ILE:HG12	1:H:8:PHE:CE2	2.42	0.55
1:H:32:GLU:O	1:H:35:PHE:HB2	2.07	0.55
1:H:64:VAL:HG21	1:H:78:ILE:CD1	2.37	0.55
1:H:111:THR:HG23	1:H:113:ALA:N	2.20	0.55
2:I:821:ARG:HD3	2:I:1082:ILE:HG23	1.88	0.55
2:I:823:VAL:CG2	2:I:1079:ILE:HD11	2.37	0.55
2:I:1172:LEU:HD23	2:I:1176:LEU:HG	1.89	0.55
3:J:44:ILE:CD1	3:J:252:LEU:HD22	2.37	0.55
3:J:83:VAL:O	3:J:92:VAL:HG12	2.07	0.55
3:J:709:ARG:HB3	3:J:714:GLU:OE2	2.05	0.55
3:J:766:GLY:C	3:J:767:LEU:HD12	2.32	0.55
3:J:975:ILE:HG23	3:J:977:SER:HB3	1.87	0.55
3:J:1078:LEU:HD13	3:J:1121:LEU:HD22	1.88	0.55
5:L:137:TYR:CE2	5:L:139:GLU:HB2	2.41	0.55
8:P:13:DG:H2''	8:P:14:DA:C8	2.42	0.55
8:P:58:DC:H2''	8:P:59:DA:H5'	1.88	0.55
1:G:90:VAL:HG11	1:G:146:VAL:HG21	1.87	0.55
1:H:44:ARG:HH21	3:J:538:ARG:HG2	1.71	0.55
2:I:297:VAL:HB	2:I:317:LEU:HD21	1.88	0.55
2:I:556:GLY:HA2	2:I:659:GLN:O	2.06	0.55
2:I:561:ILE:HD12	2:I:679:ALA:HB1	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:636:CYS:HB2	2:I:645:PHE:CD2	2.42	0.55
2:I:1143:GLU:O	2:I:1147:ARG:HG3	2.06	0.55
3:J:588:PRO:O	3:J:591:ILE:HG22	2.06	0.55
3:J:1199:PHE:HB2	3:J:1202:GLU:OE2	2.06	0.55
8:P:39:DC:H1'	8:P:40:DC:C5'	2.37	0.55
1:G:228:LEU:HD12	1:H:221:ALA:O	2.07	0.55
2:I:186:PHE:CE1	2:I:196:VAL:HG23	2.41	0.55
2:I:1253:LEU:HD12	5:L:525:ASP:HA	1.88	0.55
3:J:364:HIS:HB3	3:J:487:THR:CG2	2.36	0.55
3:J:973:LEU:HG	3:J:1003:LEU:HD13	1.87	0.55
3:J:975:ILE:HB	3:J:1000:GLY:N	2.21	0.55
3:J:977:SER:OG	3:J:978:ARG:N	2.39	0.55
1:G:17:GLU:OE1	1:G:19:VAL:HB	2.07	0.55
2:I:210:LEU:O	2:I:215:TYR:HB2	2.07	0.55
2:I:1281:TYR:CD2	3:J:484:MET:HG2	2.42	0.55
2:I:1284:ALA:HB1	3:J:1356:LEU:HD22	1.89	0.55
5:L:165:PHE:HB3	5:L:259:PHE:CD2	2.41	0.55
5:L:279:ARG:HG2	5:L:347:ILE:CD1	2.37	0.55
5:L:507:MET:O	5:L:520:GLY:N	2.40	0.55
7:O:57:DT:C1'	7:O:58:DC:H5'	2.37	0.55
2:I:718:ALA:HB2	2:I:783:LEU:CD2	2.33	0.55
2:I:1016:GLU:OE2	2:I:1019:ASP:HB3	2.07	0.55
2:I:1319:MET:HG3	2:I:1320:PRO:HD2	1.89	0.55
3:J:194:LEU:HD12	3:J:228:VAL:HB	1.88	0.55
3:J:799:ARG:HB3	3:J:1309:ILE:HD12	1.88	0.55
3:J:894:VAL:HG11	3:J:915:ILE:HD11	1.88	0.55
3:J:1298:VAL:HG13	3:J:1299:GLY:H	1.71	0.55
2:I:253:PHE:CE2	2:I:255:ILE:HD13	2.42	0.54
2:I:319:LEU:HG	2:I:322:LEU:CD1	2.37	0.54
2:I:598:VAL:HG13	2:I:627:GLY:HA3	1.88	0.54
2:I:813:GLU:HA	3:J:504:GLN:NE2	2.20	0.54
2:I:1305:TYR:O	2:I:1309:VAL:HG23	2.07	0.54
3:J:651:HIS:O	3:J:655:SER:OG	2.22	0.54
5:L:136:GLU:O	5:L:249:ILE:HD11	2.06	0.54
5:L:390:ILE:HA	5:L:393:LYS:HG3	1.90	0.54
5:L:607:LEU:HA	5:L:610:PHE:HD2	1.72	0.54
1:G:40:GLY:HA3	1:G:185:TYR:CD2	2.43	0.54
2:I:163:LYS:HA	2:I:163:LYS:HE2	1.89	0.54
2:I:362:ALA:O	2:I:366:ILE:HG13	2.05	0.54
2:I:993:PRO:O	2:I:996:ARG:HB2	2.07	0.54
2:I:1086:PRO:HB2	2:I:1212:LEU:HD23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1260:GLY:O	2:I:1266:GLY:HA3	2.07	0.54
3:J:423:LEU:HD12	3:J:468:VAL:HG12	1.89	0.54
3:J:789:LYS:HD2	3:J:930:LEU:O	2.07	0.54
3:J:805:GLN:HG3	3:J:1348:LYS:HG2	1.89	0.54
3:J:968:ASN:HD21	3:J:972:LYS:HE3	1.71	0.54
3:J:975:ILE:N	3:J:1000:GLY:HA2	2.17	0.54
5:L:348:GLU:N	5:L:355:ILE:HD11	2.21	0.54
5:L:583:THR:HG21	7:O:26:DT:C7	2.37	0.54
1:H:22:THR:O	1:H:213:PRO:HG3	2.07	0.54
2:I:975:ILE:CG2	2:I:1011:LEU:HD23	2.36	0.54
2:I:1122:LYS:HG2	2:I:1229:TYR:CZ	2.42	0.54
5:L:131:GLN:O	5:L:257:LYS:HD2	2.07	0.54
5:L:303:ILE:HA	5:L:306:PHE:CB	2.32	0.54
2:I:471:VAL:CB	2:I:498:ILE:HD11	2.38	0.54
2:I:565:GLU:HA	2:I:569:ILE:CG1	2.34	0.54
2:I:771:VAL:HG21	2:I:783:LEU:CD1	2.37	0.54
3:J:813:ASP:OD2	3:J:897:HIS:ND1	2.41	0.54
5:L:299:LYS:HG3	5:L:302:PHE:HD2	1.72	0.54
2:I:933:VAL:HG22	2:I:1050:VAL:HG23	1.90	0.54
3:J:513:MET:CG	3:J:544:LEU:HD11	2.37	0.54
3:J:519:ASN:OD1	3:J:709:ARG:HD3	2.08	0.54
3:J:759:ILE:HD12	3:J:771:GLN:HA	1.88	0.54
3:J:1042:ASP:HA	3:J:1046:ILE:O	2.08	0.54
5:L:216:LEU:HD12	5:L:219:GLU:CD	2.32	0.54
1:H:100:LEU:HB2	1:H:144:ILE:CG2	2.37	0.54
2:I:21:VAL:HG21	2:I:592:ARG:NH1	2.23	0.54
2:I:950:GLU:O	2:I:954:LYS:HG3	2.07	0.54
2:I:1065:LYS:O	2:I:1235:LEU:HB2	2.07	0.54
3:J:355:ILE:HG21	3:J:466:MET:HG3	1.89	0.54
3:J:848:VAL:O	3:J:857:LEU:N	2.39	0.54
3:J:1237:VAL:CG1	3:J:1253:ILE:HD13	2.37	0.54
5:L:151:VAL:HB	5:L:161:LEU:CD1	2.38	0.54
5:L:311:THR:O	5:L:345:GLN:NE2	2.40	0.54
5:L:346:GLN:NE2	5:L:350:GLU:OE2	2.23	0.54
5:L:367:ILE:O	5:L:371:LYS:HG2	2.08	0.54
1:H:152:TYR:HE2	1:H:154:PRO:HG3	1.73	0.54
2:I:838:CYS:HB3	2:I:1050:VAL:HG12	1.90	0.54
2:I:960:LEU:CD1	2:I:1028:LYS:HE3	2.35	0.54
2:I:969:ALA:HB1	9:I:1401:1N7:C24	2.38	0.54
5:L:261:LEU:HD23	5:L:262:VAL:O	2.07	0.54
2:I:302:ILE:HG22	2:I:309:LEU:HD12	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:321:LEU:HD23	2:I:324:LYS:CE	2.37	0.54
2:I:757:THR:O	2:I:765:ILE:HG22	2.07	0.54
3:J:46:TYR:CE1	5:L:453:PRO:HD3	2.43	0.54
3:J:259:ARG:NH1	5:L:502:LYS:HD2	2.19	0.54
3:J:526:VAL:HG22	3:J:549:LYS:HB2	1.90	0.54
3:J:964:LYS:O	3:J:976:THR:HG22	2.08	0.54
5:L:105:MET:HE1	5:L:385:ARG:HB2	1.90	0.54
1:M:269:CYS:HB3	1:M:292:THR:HG21	1.90	0.54
1:G:23:HIS:HB2	1:G:205:MET:O	2.08	0.54
2:I:724:VAL:HG12	2:I:775:GLU:O	2.07	0.54
2:I:1304:MET:CE	3:J:472:LEU:HB3	2.38	0.54
2:I:1326:LEU:HD13	3:J:337:ARG:HB2	1.89	0.54
3:J:820:ILE:HG12	3:J:884:SER:OG	2.08	0.54
8:P:43:DT:H2'	8:P:44:DT:OP2	2.06	0.54
2:I:295:LYS:O	2:I:316:GLU:HA	2.07	0.54
2:I:1159:VAL:HG12	2:I:1161:LEU:HD22	1.90	0.54
3:J:664:ILE:HG22	3:J:678:ARG:HG2	1.89	0.54
5:L:141:ILE:O	5:L:145:LEU:HG	2.07	0.54
8:P:41:DT:C2'	8:P:42:DT:H71	2.37	0.54
1:G:113:ALA:HB2	1:G:126:PRO:CB	2.32	0.53
1:H:89:ALA:HB3	1:H:124:VAL:CG1	2.36	0.53
2:I:225:PHE:CB	2:I:336:LEU:HD13	2.37	0.53
2:I:347:ILE:O	2:I:351:LEU:HG	2.08	0.53
2:I:566:GLY:O	2:I:569:ILE:HG13	2.08	0.53
2:I:609:ILE:HG13	2:I:610:GLU:OE1	2.09	0.53
2:I:623:LEU:N	2:I:630:VAL:HG23	2.22	0.53
2:I:632:ASP:O	2:I:647:ARG:HG3	2.08	0.53
2:I:748:ILE:HG21	2:I:966:ILE:CG2	2.38	0.53
3:J:1110:GLU:O	3:J:1113:VAL:HG23	2.09	0.53
5:L:231:THR:HA	5:L:248:GLU:CD	2.34	0.53
1:G:192:VAL:HG21	1:G:195:ARG:CG	2.38	0.53
1:H:98:VAL:O	1:H:146:VAL:HG22	2.07	0.53
3:J:374:LEU:HD11	3:J:401:VAL:HG13	1.88	0.53
3:J:953:LYS:HB2	3:J:993:GLU:OE2	2.08	0.53
3:J:1003:LEU:HA	3:J:1018:ALA:HB2	1.90	0.53
3:J:1198:VAL:HG22	3:J:1202:GLU:HG3	1.88	0.53
1:H:149:GLY:HA3	1:H:177:TYR:CE2	2.43	0.53
2:I:230:PHE:HD1	2:I:239:MET:HB2	1.73	0.53
2:I:748:ILE:HG21	2:I:966:ILE:HG22	1.90	0.53
3:J:271:ARG:HH11	3:J:316:ILE:HD12	1.73	0.53
3:J:857:LEU:HD22	3:J:875:ASN:HD22	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:426:LYS:HD3	7:O:52:DA:C5'	2.36	0.53
5:L:552:THR:HG23	5:L:555:GLU:OE1	2.08	0.53
1:M:252:ILE:HG12	1:M:255:ARG:NH1	2.24	0.53
7:O:64:DT:OP2	7:O:64:DT:H2'	2.08	0.53
7:O:76:DT:H2''	7:O:77:DA:C8	2.44	0.53
2:I:49:LEU:HD12	2:I:73:TYR:CE2	2.43	0.53
2:I:478:ARG:NH1	2:I:478:ARG:O	2.41	0.53
2:I:632:ASP:HA	2:I:647:ARG:CG	2.39	0.53
3:J:520:ALA:HB3	3:J:546:ALA:CB	2.34	0.53
4:K:67:ARG:HA	4:K:70:GLN:HG2	1.90	0.53
5:L:162:ILE:CA	5:L:262:VAL:HG23	2.37	0.53
5:L:573:LEU:O	5:L:576:VAL:HB	2.09	0.53
8:P:59:DA:H2''	8:P:60:DA:O5'	2.07	0.53
1:G:211:ILE:CG2	1:G:216:ALA:HB2	2.38	0.53
2:I:317:LEU:HA	2:I:321:LEU:CD1	2.29	0.53
2:I:349:GLU:HA	2:I:352:ARG:HG3	1.90	0.53
2:I:472:GLU:O	2:I:475:VAL:HG12	2.08	0.53
2:I:705:GLU:HB2	2:I:794:LEU:H	1.73	0.53
2:I:771:VAL:HG23	2:I:783:LEU:O	2.09	0.53
2:I:810:TYR:HB3	2:I:817:LEU:HD12	1.90	0.53
2:I:975:ILE:HA	2:I:978:VAL:CB	2.31	0.53
2:I:1111:GLN:HB2	2:I:1230:MET:HE1	1.91	0.53
3:J:51:PRO:HB2	3:J:57:PHE:O	2.08	0.53
3:J:192:MET:HE2	3:J:197:GLU:OE2	2.09	0.53
2:I:253:PHE:CA	2:I:265:LYS:HG3	2.38	0.53
2:I:1134:GLN:O	2:I:1136:GLN:N	2.42	0.53
3:J:876:SER:OG	3:J:988:PHE:O	2.16	0.53
3:J:915:ILE:HA	3:J:918:ILE:HG12	1.90	0.53
3:J:1157:ALA:HB2	3:J:1210:ILE:HD11	1.90	0.53
5:L:292:VAL:HG13	5:L:297:MET:O	2.08	0.53
5:L:561:MET:O	5:L:571:TYR:HB2	2.09	0.53
3:J:26:SER:HB3	3:J:236:TRP:CZ2	2.44	0.53
3:J:661:VAL:HB	3:J:685:ILE:HD11	1.90	0.53
3:J:998:PRO:HG2	3:J:1020:TRP:CE2	2.43	0.53
3:J:1032:SER:CB	3:J:1116:SER:HA	2.39	0.53
4:K:63:ILE:HD12	4:K:63:ILE:H	1.73	0.53
5:L:279:ARG:NH2	5:L:343:LYS:O	2.42	0.53
5:L:496:LYS:O	5:L:500:ILE:HG12	2.09	0.53
5:L:507:MET:HG3	5:L:523:ILE:HD12	1.90	0.53
8:P:52:DT:H1'	8:P:53:DT:H5'	1.91	0.53
2:I:92:TYR:HB3	2:I:137:VAL:HG13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:255:ILE:CB	2:I:263:VAL:O	2.47	0.53
2:I:297:VAL:HG21	2:I:311:CYS:SG	2.49	0.53
2:I:1326:LEU:HD21	3:J:338:PHE:CZ	2.44	0.53
3:J:430:HIS:HB3	3:J:925:GLU:HG2	1.91	0.53
3:J:1046:ILE:HG22	3:J:1061:VAL:HG22	1.91	0.53
3:J:1098:GLN:OE1	3:J:1098:GLN:N	2.40	0.53
5:L:295:CYS:HB2	5:L:329:LYS:CB	2.37	0.53
6:N:52:PHE:HB2	6:N:55:VAL:CG2	2.39	0.53
2:I:253:PHE:HA	2:I:265:LYS:HG3	1.89	0.53
2:I:511:LEU:O	2:I:513:GLN:HG2	2.09	0.53
2:I:700:VAL:HG13	2:I:1117:LEU:HD22	1.91	0.53
2:I:1082:ILE:H	2:I:1082:ILE:HD12	1.74	0.53
3:J:123:ARG:NH2	3:J:1334:GLU:OE1	2.42	0.53
3:J:353:SER:OG	3:J:447:ILE:HG13	2.08	0.53
3:J:394:ILE:HG23	5:L:536:THR:HG22	1.90	0.53
3:J:697:MET:SD	3:J:738:ARG:HA	2.48	0.53
3:J:844:THR:OG1	3:J:860:ARG:O	2.13	0.53
3:J:950:ILE:O	3:J:1016:THR:HA	2.09	0.53
3:J:1076:PRO:C	3:J:1101:LEU:HD12	2.34	0.53
5:L:306:PHE:O	5:L:310:GLU:HB2	2.09	0.53
5:L:573:LEU:HA	5:L:576:VAL:CG2	2.39	0.53
2:I:217:THR:HG23	2:I:351:LEU:CD1	2.39	0.53
2:I:231:GLU:HB2	2:I:238:GLN:O	2.09	0.53
2:I:319:LEU:HA	2:I:322:LEU:HB2	1.90	0.53
2:I:1015:ALA:O	2:I:1018:TYR:HB3	2.09	0.53
3:J:357:VAL:HG13	3:J:358:GLY:H	1.73	0.53
3:J:423:LEU:HD23	3:J:449:LEU:HD13	1.89	0.53
3:J:580:TRP:CZ3	3:J:589:TYR:HA	2.44	0.53
5:L:144:LEU:HD11	5:L:221:PHE:HZ	1.74	0.53
5:L:165:PHE:O	5:L:260:ARG:NH2	2.32	0.53
5:L:252:LEU:HA	5:L:255:VAL:CG2	2.38	0.53
5:L:288:MET:HE2	5:L:299:LYS:HZ1	1.72	0.53
8:P:18:DT:C2'	8:P:19:DT:H71	2.39	0.53
1:G:178:SER:O	1:G:178:SER:OG	2.26	0.52
2:I:471:VAL:CG1	2:I:498:ILE:HD11	2.38	0.52
2:I:895:LEU:HD21	2:I:899:GLU:HG2	1.91	0.52
3:J:36:GLY:O	3:J:104:HIS:ND1	2.43	0.52
3:J:97:VAL:HG12	3:J:101:ARG:HG3	1.90	0.52
5:L:287:ILE:HG22	5:L:302:PHE:HE1	1.74	0.52
5:L:295:CYS:CA	5:L:329:LYS:HE2	2.39	0.52
5:L:461:ASN:O	5:L:465:ARG:HG3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:475:VAL:HG23	2:I:492:MET:HB2	1.91	0.52
2:I:886:LYS:H	2:I:917:SER:HB3	1.73	0.52
2:I:1086:PRO:HD2	2:I:1094:VAL:CG2	2.39	0.52
3:J:210:SER:HA	8:P:13:DG:OP1	2.09	0.52
3:J:952:VAL:CG2	3:J:1015:GLU:HB3	2.39	0.52
5:L:262:VAL:HB	5:L:265:GLN:HB2	1.91	0.52
5:L:575:GLU:HB3	5:L:579:GLN:HE22	1.73	0.52
5:L:588:ARG:NH1	5:L:591:GLU:OE2	2.30	0.52
6:N:33:PRO:HB3	6:N:49:ARG:NH1	2.23	0.52
1:H:69:SER:HB2	1:H:78:ILE:CD1	2.40	0.52
2:I:186:PHE:CD1	2:I:196:VAL:HG23	2.44	0.52
3:J:194:LEU:HD22	3:J:224:LEU:CD2	2.40	0.52
3:J:253:VAL:HG21	5:L:523:ILE:HG21	1.91	0.52
3:J:288:PRO:HB3	5:L:377:LYS:HG2	1.90	0.52
3:J:449:LEU:HD22	3:J:466:MET:SD	2.49	0.52
3:J:1044:GLN:NE2	3:J:1070:GLY:O	2.41	0.52
5:L:147:GLN:C	5:L:161:LEU:HD21	2.33	0.52
5:L:319:ALA:HB1	5:L:326:TRP:CH2	2.44	0.52
5:L:348:GLU:OE2	5:L:355:ILE:N	2.42	0.52
5:L:594:ALA:O	5:L:598:LEU:HD23	2.09	0.52
1:G:212:ASP:N	1:G:212:ASP:OD1	2.39	0.52
2:I:178:PRO:HB3	2:I:397:LEU:CD1	2.40	0.52
2:I:270:THR:HG22	2:I:271:ALA:H	1.74	0.52
2:I:501:ALA:O	2:I:504:GLU:HB3	2.10	0.52
2:I:941:LYS:NZ	2:I:949:GLU:OE1	2.31	0.52
2:I:976:ARG:HD2	2:I:997:TRP:CH2	2.45	0.52
2:I:1010:GLN:O	2:I:1014:LEU:HD23	2.08	0.52
3:J:429:LEU:HB3	3:J:925:GLU:CB	2.39	0.52
3:J:722:ILE:CG2	3:J:737:ILE:HD12	2.39	0.52
3:J:1036:ARG:NE	3:J:1081:VAL:HG11	2.25	0.52
5:L:286:LEU:O	5:L:290:LEU:HG	2.09	0.52
8:P:39:DC:H2''	8:P:40:DC:OP2	2.09	0.52
8:P:48:DC:H1'	8:P:49:DT:H5'	1.91	0.52
1:G:102:LEU:HD22	1:G:142:MET:CE	2.40	0.52
1:H:59:VAL:HG11	1:H:82:LEU:HD21	1.92	0.52
2:I:52:ALA:O	2:I:56:VAL:HG12	2.10	0.52
2:I:211:ARG:HD2	2:I:356:THR:HG23	1.90	0.52
2:I:243:PRO:CA	2:I:246:LEU:HD13	2.34	0.52
2:I:405:PHE:CZ	2:I:409:LEU:HD11	2.43	0.52
2:I:424:ASP:O	2:I:428:VAL:HG12	2.10	0.52
2:I:539:THR:OG1	2:I:542:ARG:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:150:ARG:CB	5:L:150:ARG:NH1	2.73	0.52
5:L:463:LEU:HA	5:L:466:ILE:HG22	1.91	0.52
2:I:12:ARG:NH1	2:I:1181:PRO:HB3	2.25	0.52
2:I:198:ILE:CG1	2:I:369:MET:HE1	2.39	0.52
2:I:771:VAL:HG21	2:I:783:LEU:HD12	1.90	0.52
2:I:1247:SER:HB3	3:J:375:GLU:O	2.10	0.52
3:J:31:ARG:NH1	3:J:106:GLU:OE2	2.43	0.52
3:J:196:GLN:O	3:J:200:GLN:HG3	2.10	0.52
3:J:212:THR:O	3:J:215:LYS:HB2	2.09	0.52
3:J:518:VAL:HA	3:J:547:ARG:HH12	1.74	0.52
3:J:1197:ASN:HD22	3:J:1209:VAL:HG13	1.75	0.52
5:L:298:PRO:HD3	5:L:326:TRP:CD1	2.45	0.52
5:L:316:PHE:CE1	5:L:337:VAL:HG11	2.44	0.52
1:H:107:ILE:HG23	1:H:135:ASP:CB	2.35	0.52
2:I:373:GLY:HA2	5:L:91:ILE:HD12	1.92	0.52
3:J:423:LEU:HD11	3:J:468:VAL:HG12	1.91	0.52
3:J:749:LYS:HD3	3:J:753:SER:HB2	1.91	0.52
3:J:952:VAL:HG22	3:J:1015:GLU:O	2.10	0.52
1:M:318:LEU:HG	1:M:319:GLU:H	1.75	0.52
8:P:49:DT:H1'	8:P:50:DT:H5'	1.92	0.52
2:I:617:ALA:HB3	2:I:653:MET:HA	1.92	0.52
2:I:628:HIS:HB3	2:I:647:ARG:NH2	2.25	0.52
2:I:658:GLN:HG2	2:I:1186:VAL:HG23	1.91	0.52
2:I:732:ILE:CD1	2:I:783:LEU:HB3	2.39	0.52
2:I:828:PHE:CB	2:I:1060:ILE:HD12	2.40	0.52
2:I:965:GLN:O	2:I:968:GLU:HG3	2.08	0.52
2:I:1339:LEU:HD23	3:J:17:PHE:CE2	2.44	0.52
3:J:117:LEU:HD11	3:J:135:ILE:HG21	1.92	0.52
1:G:38:THR:HG21	1:H:46:ILE:CD1	2.39	0.52
1:H:11:PRO:HB3	1:H:31:LEU:HD22	1.91	0.52
2:I:153:PRO:HA	2:I:177:ILE:O	2.09	0.52
2:I:680:LEU:HD13	3:J:783:LEU:CD1	2.40	0.52
2:I:1060:ILE:HD11	2:I:1066:MET:SD	2.49	0.52
2:I:1105:SER:OG	3:J:731:ARG:NH1	2.42	0.52
3:J:385:LEU:CD2	3:J:411:ILE:HG13	2.40	0.52
3:J:525:MET:O	3:J:548:VAL:HG13	2.10	0.52
3:J:582:ILE:HG22	3:J:620:PHE:CE1	2.44	0.52
3:J:598:LYS:HA	3:J:601:ILE:HG22	1.90	0.52
8:P:51:DC:H2''	8:P:52:DT:OP2	2.09	0.52
2:I:189:ASP:HB3	2:I:190:PRO:HD2	1.91	0.52
2:I:1157:GLN:O	2:I:1158:LYS:HD3	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:98:ARG:O	3:J:247:PRO:HD2	2.10	0.52
3:J:368:LEU:CD2	3:J:373:ALA:HB2	2.39	0.52
3:J:1229:VAL:O	3:J:1233:ILE:HG12	2.10	0.52
3:J:1326:GLN:OE1	3:J:1326:GLN:HA	2.10	0.52
5:L:216:LEU:O	5:L:219:GLU:HG2	2.10	0.52
5:L:280:VAL:CG1	5:L:359:LYS:HG2	2.37	0.52
2:I:77:GLU:OE1	2:I:78:PRO:HD2	2.10	0.51
2:I:671:LEU:HD23	2:I:1186:VAL:CG1	2.40	0.51
2:I:788:SER:O	2:I:788:SER:OG	2.24	0.51
2:I:800:MET:CE	2:I:822:VAL:HG21	2.39	0.51
2:I:1072:ASN:N	2:I:1072:ASN:OD1	2.44	0.51
3:J:816:THR:OG1	3:J:889:ASP:HB2	2.11	0.51
3:J:823:THR:HG23	3:J:824:PRO:HD2	1.92	0.51
3:J:978:ARG:NH2	3:J:1198:VAL:HA	2.25	0.51
3:J:1161:GLY:N	3:J:1204:VAL:O	2.42	0.51
1:G:193:GLU:HG3	1:G:194:GLN:H	1.73	0.51
1:H:190:ALA:HB2	1:H:200:LYS:CB	2.35	0.51
2:I:103:VAL:HG12	2:I:117:ILE:HG21	1.92	0.51
2:I:995:ASP:O	2:I:998:LEU:HD13	2.09	0.51
3:J:530:PRO:HB3	3:J:577:ALA:O	2.10	0.51
3:J:1132:LYS:N	3:J:1132:LYS:CD	2.73	0.51
3:J:1327:GLU:OE1	3:J:1327:GLU:N	2.25	0.51
5:L:463:LEU:O	5:L:466:ILE:HG22	2.10	0.51
5:L:573:LEU:HD12	5:L:576:VAL:HB	1.93	0.51
2:I:422:LYS:O	2:I:426:ILE:HG12	2.09	0.51
2:I:898:GLU:CD	5:L:544:THR:HG21	2.35	0.51
2:I:945:ALA:O	2:I:949:GLU:HG3	2.10	0.51
2:I:1210:ILE:HG22	2:I:1211:ARG:H	1.76	0.51
3:J:573:THR:OG1	3:J:576:ARG:HG3	2.09	0.51
3:J:1005:LYS:HG2	3:J:1017:VAL:HG13	1.92	0.51
3:J:1058:SER:O	3:J:1060:VAL:HG23	2.10	0.51
4:K:25:ARG:HD3	4:K:64:LEU:HD13	1.92	0.51
5:L:110:LEU:HD12	5:L:111:LEU:N	2.25	0.51
5:L:437:GLN:HB2	7:O:49:DC:N4	2.24	0.51
1:H:53:GLY:O	1:H:177:TYR:HB3	2.10	0.51
2:I:186:PHE:HE2	2:I:428:VAL:HG13	1.76	0.51
2:I:1113:LEU:CD1	3:J:641:ILE:HD13	2.41	0.51
5:L:148:TYR:CA	5:L:161:LEU:HD11	2.40	0.51
5:L:452:ILE:HD11	5:L:457:ILE:HG12	1.93	0.51
1:G:183:ILE:CD1	1:G:205:MET:HB2	2.38	0.51
1:H:73:GLY:O	1:H:134:THR:HG22	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:118:LYS:HD3	2:I:488:MET:CE	2.40	0.51
2:I:301:TYR:OH	2:I:334:GLU:HG3	2.10	0.51
2:I:901:LEU:HD22	5:L:565:ILE:CD1	2.34	0.51
3:J:37:GLU:HB2	3:J:104:HIS:CE1	2.46	0.51
3:J:50:LYS:HE2	3:J:71:LEU:HG	1.92	0.51
3:J:115:TRP:HB3	3:J:1333:THR:CG2	2.39	0.51
3:J:202:ARG:CG	3:J:221:ILE:HD11	2.41	0.51
3:J:1027:VAL:HG23	3:J:1122:ALA:O	2.10	0.51
5:L:425:TYR:OH	7:O:51:DT:O5'	2.29	0.51
5:L:453:PRO:CG	7:O:44:DA:H5'	2.40	0.51
5:L:470:MET:HG2	5:L:474:MET:HG2	1.92	0.51
5:L:605:GLU:HA	5:L:608:ARG:HG2	1.93	0.51
7:O:22:DT:C6	7:O:22:DT:H5'	2.44	0.51
1:G:186:ASN:HB2	1:G:202:VAL:CG1	2.41	0.51
1:H:27:THR:HG21	1:H:200:LYS:HE3	1.92	0.51
1:H:149:GLY:HA3	1:H:177:TYR:CD2	2.45	0.51
1:H:208:ASN:OD1	1:H:210:THR:HG23	2.10	0.51
2:I:122:VAL:HG21	2:I:493:ILE:CG2	2.40	0.51
2:I:255:ILE:HB	2:I:263:VAL:C	2.35	0.51
2:I:816:ILE:HD12	2:I:1074:GLY:HA3	1.92	0.51
2:I:908:GLU:OE1	5:L:611:LEU:HD22	2.11	0.51
3:J:978:ARG:HD2	3:J:1197:ASN:OD1	2.09	0.51
5:L:572:THR:O	5:L:576:VAL:N	2.41	0.51
1:H:196:THR:OG1	1:H:197:ASP:OD1	2.28	0.51
2:I:235:ASN:OD1	2:I:236:LYS:HG2	2.11	0.51
3:J:178:ALA:O	3:J:179:LYS:HD3	2.11	0.51
3:J:289:ASP:HA	3:J:292:VAL:CG2	2.41	0.51
3:J:1160:SER:HB3	3:J:1206:ARG:H	1.76	0.51
5:L:105:MET:HE3	5:L:388:ILE:CD1	2.39	0.51
5:L:262:VAL:CG1	5:L:265:GLN:H	2.23	0.51
5:L:479:THR:O	5:L:483:LEU:HD12	2.10	0.51
1:M:286:GLU:HA	1:M:300:LEU:HD21	1.92	0.51
8:P:38:DC:H1'	8:P:39:DC:H5'	1.93	0.51
2:I:204:LEU:CD1	2:I:369:MET:HE2	2.41	0.51
2:I:360:LEU:O	2:I:364:VAL:HG22	2.11	0.51
2:I:488:MET:O	2:I:492:MET:HE3	2.11	0.51
2:I:521:LEU:HD11	2:I:664:GLY:HA2	1.92	0.51
2:I:685:MET:HE2	2:I:1073:LYS:HE3	1.91	0.51
2:I:1296:ASP:OD2	2:I:1321:GLU:N	2.43	0.51
3:J:125:GLY:HA2	3:J:135:ILE:CD1	2.41	0.51
3:J:517:CYS:O	3:J:547:ARG:NH1	2.31	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:302:ILE:HG22	2:I:309:LEU:CD1	2.40	0.51
2:I:431:LYS:HE2	2:I:435:ILE:HG13	1.92	0.51
3:J:72:CYS:SG	3:J:74:LYS:HG3	2.51	0.51
3:J:146:VAL:HG13	3:J:177:ASP:O	2.10	0.51
3:J:1199:PHE:N	3:J:1202:GLU:HG3	2.26	0.51
4:K:18:ASP:O	4:K:22:VAL:HG13	2.10	0.51
5:L:124:GLU:HA	5:L:127:ILE:HG22	1.92	0.51
5:L:592:ALA:O	5:L:596:ARG:HG3	2.10	0.51
1:G:229:GLU:O	1:G:232:VAL:HG12	2.11	0.51
2:I:135:THR:HB	2:I:142:GLU:HG2	1.93	0.51
2:I:255:ILE:HB	2:I:263:VAL:HB	1.92	0.51
2:I:277:LEU:HB3	2:I:282:VAL:HG11	1.93	0.51
2:I:565:GLU:HA	2:I:569:ILE:CD1	2.41	0.51
2:I:856:ASN:ND2	5:L:613:ASP:HA	2.25	0.51
2:I:903:ARG:HD2	2:I:908:GLU:N	2.23	0.51
3:J:179:LYS:HB2	3:J:184:ALA:HB2	1.92	0.51
3:J:224:LEU:O	3:J:228:VAL:HG12	2.11	0.51
3:J:289:ASP:HA	3:J:292:VAL:HG22	1.93	0.51
3:J:449:LEU:HD21	3:J:457:TYR:CD2	2.46	0.51
5:L:387:VAL:HG22	5:L:435:ILE:CD1	2.40	0.51
1:G:99:ILE:HG21	1:G:143:ARG:CZ	2.40	0.50
1:H:76:GLU:OE2	1:H:132:HIS:HB2	2.11	0.50
1:H:197:ASP:C	1:H:198:LEU:HD22	2.36	0.50
2:I:623:LEU:CA	2:I:630:VAL:HG23	2.41	0.50
2:I:1321:GLU:OE2	3:J:99:ARG:NH2	2.40	0.50
2:I:1332:SER:O	3:J:243:PRO:HG2	2.11	0.50
4:K:30:MET:HE3	4:K:46:THR:HA	1.92	0.50
1:G:226:GLU:HB3	1:H:10:LYS:NZ	2.27	0.50
2:I:188:PHE:CE2	2:I:436:ARG:HG3	2.47	0.50
2:I:496:LYS:HB3	2:I:497:PRO:HD3	1.92	0.50
2:I:803:ALA:HB2	2:I:1094:VAL:CG1	2.37	0.50
2:I:1136:GLN:O	2:I:1137:GLU:HG3	2.11	0.50
2:I:1155:VAL:HG23	2:I:1157:GLN:H	1.76	0.50
3:J:108:ALA:HB2	3:J:280:LYS:CG	2.41	0.50
3:J:300:GLN:NE2	3:J:304:ASP:OD1	2.40	0.50
3:J:303:VAL:O	3:J:307:LEU:HD23	2.11	0.50
3:J:960:LEU:HA	3:J:981:GLU:O	2.12	0.50
5:L:151:VAL:HB	5:L:161:LEU:CG	2.41	0.50
5:L:289:LYS:O	5:L:294:GLN:HB2	2.10	0.50
5:L:353:LEU:HB2	5:L:357:GLN:OE1	2.11	0.50
1:H:107:ILE:HA	1:H:135:ASP:HA	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:106:GLU:HG3	2:I:107:ARG:O	2.11	0.50
2:I:230:PHE:CD1	2:I:239:MET:HB2	2.46	0.50
2:I:294:GLY:C	2:I:316:GLU:HB2	2.36	0.50
2:I:1023:HIS:O	2:I:1026:GLU:HG3	2.12	0.50
2:I:1182:ILE:HD11	2:I:1198:LEU:HD21	1.93	0.50
3:J:88:CYS:SG	3:J:89:GLY:N	2.84	0.50
3:J:839:VAL:HG22	3:J:864:LEU:HD12	1.92	0.50
3:J:857:LEU:HD11	3:J:871:LEU:CD2	2.42	0.50
3:J:1038:THR:HG21	3:J:1079:LYS:HZ3	1.75	0.50
6:N:11:VAL:O	6:N:14:GLN:HG3	2.12	0.50
2:I:205:PRO:O	2:I:208:ILE:HG22	2.10	0.50
2:I:1129:ASN:OD1	2:I:1177:ARG:NH2	2.38	0.50
3:J:306:LEU:HD23	3:J:307:LEU:HD22	1.93	0.50
3:J:378:LYS:HB2	3:J:379:PRO:HD3	1.92	0.50
3:J:488:ASN:HB3	4:K:16:ARG:HH22	1.75	0.50
3:J:1361:THR:HG23	4:K:21:LEU:HG	1.93	0.50
4:K:8:ASP:O	4:K:12:LYS:HG2	2.12	0.50
1:G:111:THR:HB	1:G:126:PRO:O	2.11	0.50
1:H:185:TYR:HA	1:H:202:VAL:O	2.11	0.50
1:H:201:LEU:HD12	1:H:202:VAL:H	1.76	0.50
2:I:238:GLN:HG2	2:I:286:GLU:CG	2.41	0.50
2:I:678:ARG:HG3	2:I:1108:ASN:HB3	1.94	0.50
2:I:887:VAL:HB	2:I:913:VAL:HG12	1.92	0.50
2:I:970:GLY:O	2:I:974:ARG:HG2	2.12	0.50
3:J:1266:ILE:HB	3:J:1276:GLU:O	2.12	0.50
4:K:40:PRO:HB2	4:K:42:GLU:OE2	2.10	0.50
5:L:158:LEU:O	5:L:162:ILE:N	2.33	0.50
5:L:226:ALA:O	5:L:230:VAL:HG23	2.11	0.50
5:L:310:GLU:OE1	5:L:356:GLU:HB2	2.12	0.50
5:L:429:THR:HG22	7:O:50:DA:H4'	1.93	0.50
8:P:10:DA:H1'	8:P:11:DT:O4'	2.12	0.50
2:I:854:ILE:HG12	2:I:887:VAL:HG13	1.93	0.50
3:J:130:MET:SD	3:J:157:GLN:NE2	2.84	0.50
3:J:582:ILE:HG23	3:J:623:GLN:HB3	1.93	0.50
3:J:749:LYS:CD	3:J:753:SER:HB2	2.42	0.50
3:J:1160:SER:HB3	3:J:1206:ARG:HB2	1.92	0.50
2:I:11:ILE:HG23	2:I:1149:TYR:OH	2.12	0.50
2:I:221:LEU:HD22	2:I:336:LEU:CD1	2.42	0.50
2:I:295:LYS:C	2:I:316:GLU:HA	2.37	0.50
2:I:800:MET:HE3	2:I:822:VAL:CG2	2.39	0.50
2:I:1220:GLN:HG2	2:I:1221:PHE:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:782:GLY:HA2	6:N:11:VAL:CG2	2.42	0.50
5:L:290:LEU:HB3	5:L:333:VAL:HG21	1.93	0.50
1:G:67:GLU:HB3	1:G:171:LEU:HD12	1.93	0.50
2:I:463:GLN:HG3	2:I:505:PHE:CB	2.32	0.50
3:J:259:ARG:HD3	5:L:502:LYS:CD	2.41	0.50
3:J:705:THR:HG21	3:J:718:SER:HA	1.94	0.50
3:J:733:SER:O	3:J:737:ILE:HG12	2.12	0.50
3:J:822:MET:O	3:J:879:ALA:HA	2.12	0.50
5:L:114:GLU:HA	5:L:117:ILE:CD1	2.41	0.50
5:L:556:ALA:O	5:L:560:ARG:HG3	2.11	0.50
1:M:253:LEU:CD2	1:M:318:LEU:HD22	2.41	0.50
1:G:175:ALA:HB1	1:G:177:TYR:CZ	2.47	0.50
1:G:192:VAL:HG21	1:G:195:ARG:HG3	1.92	0.50
2:I:545:PHE:HZ	3:J:781:LYS:HD3	1.76	0.50
2:I:979:LEU:HD22	2:I:989:LEU:HD11	1.93	0.50
2:I:988:LYS:HA	2:I:991:LYS:HD2	1.92	0.50
2:I:1005:GLU:N	2:I:1008:GLN:HB3	2.27	0.50
3:J:951:GLN:NE2	3:J:1016:THR:OG1	2.45	0.50
4:K:71:GLU:HA	4:K:74:GLU:OE2	2.11	0.50
1:M:255:ARG:HB3	1:M:278:ILE:HD12	1.92	0.50
8:P:41:DT:H1'	8:P:42:DT:H5'	1.94	0.50
1:H:41:ASN:HA	1:H:44:ARG:HG2	1.94	0.49
1:H:118:ASP:OD1	1:H:119:GLY:N	2.39	0.49
2:I:588:GLU:HA	2:I:606:LEU:O	2.11	0.49
2:I:705:GLU:CB	2:I:794:LEU:HB3	2.39	0.49
2:I:906:PHE:HA	5:L:599:ARG:NH1	2.27	0.49
2:I:1212:LEU:HD13	2:I:1225:VAL:HG22	1.94	0.49
3:J:326:SER:OG	3:J:327:LEU:N	2.45	0.49
3:J:385:LEU:HD23	3:J:411:ILE:HG13	1.94	0.49
3:J:684:ASP:OD2	6:N:27:ILE:HD11	2.12	0.49
7:O:30:DC:H2''	7:O:31:DA:C8	2.47	0.49
2:I:17:LYS:NZ	2:I:1194:GLU:OE2	2.27	0.49
2:I:66:SER:OG	2:I:104:ILE:HA	2.11	0.49
2:I:78:PRO:HB3	2:I:92:TYR:HE1	1.77	0.49
2:I:177:ILE:HG23	2:I:183:TRP:NE1	2.27	0.49
2:I:187:GLU:CD	2:I:197:ARG:HD2	2.37	0.49
2:I:375:PRO:HD3	5:L:103:ARG:HD3	1.94	0.49
2:I:724:VAL:HG12	2:I:775:GLU:H	1.77	0.49
2:I:944:ARG:O	2:I:948:ILE:HG13	2.12	0.49
3:J:253:VAL:HG23	3:J:261:ALA:HB3	1.93	0.49
3:J:334:LYS:HD3	3:J:339:ARG:NH2	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1282:TYR:O	3:J:1285:VAL:HG12	2.13	0.49
5:L:515:GLU:OE1	8:P:29:DA:H2''	2.12	0.49
7:O:63:DT:H2'	7:O:64:DT:H71	1.94	0.49
2:I:196:VAL:HB	2:I:206:ALA:HA	1.94	0.49
2:I:204:LEU:HD21	2:I:369:MET:HG3	1.93	0.49
2:I:595:THR:OG1	2:I:598:VAL:HB	2.13	0.49
2:I:895:LEU:HD21	2:I:899:GLU:CG	2.42	0.49
2:I:902:LEU:HD21	5:L:611:LEU:HG	1.93	0.49
2:I:1000:LEU:HD23	2:I:1002:LEU:HG	1.92	0.49
2:I:1246:ARG:NH1	2:I:1258:PRO:HB3	2.27	0.49
3:J:1216:ALA:O	3:J:1220:ILE:HG12	2.12	0.49
2:I:135:THR:CG2	2:I:527:LYS:HE3	2.42	0.49
2:I:153:PRO:HG2	2:I:179:TYR:HD1	1.77	0.49
2:I:208:ILE:HG12	2:I:366:ILE:HD11	1.95	0.49
2:I:230:PHE:O	2:I:332:ARG:HA	2.13	0.49
2:I:400:VAL:HG21	2:I:452:ARG:NH1	2.27	0.49
2:I:972:PHE:O	2:I:976:ARG:HB3	2.12	0.49
2:I:976:ARG:HD2	2:I:997:TRP:CZ3	2.47	0.49
2:I:1124:ILE:O	2:I:1128:ILE:HG13	2.12	0.49
3:J:807:LEU:HD13	3:J:1255:VAL:HG13	1.94	0.49
3:J:926:PRO:CB	3:J:1246:VAL:HG11	2.42	0.49
4:K:10:VAL:O	4:K:14:GLY:N	2.39	0.49
5:L:166:VAL:HB	5:L:259:PHE:CD1	2.47	0.49
5:L:347:ILE:O	5:L:351:THR:HG23	2.13	0.49
6:N:22:ARG:O	6:N:26:LYS:HG3	2.12	0.49
1:G:31:LEU:HB2	1:G:199:ASP:O	2.12	0.49
1:H:204:GLU:HG2	1:H:205:MET:N	2.28	0.49
2:I:232:ILE:HG12	2:I:237:LEU:H	1.78	0.49
2:I:465:ARG:O	2:I:469:VAL:HG13	2.12	0.49
2:I:605:TYR:C	2:I:606:LEU:HD12	2.37	0.49
2:I:901:LEU:O	2:I:905:ILE:HG13	2.12	0.49
3:J:291:ILE:HG12	5:L:409:ASN:ND2	2.26	0.49
3:J:533:ALA:HB1	3:J:574:VAL:HG13	1.92	0.49
3:J:986:ASP:CG	3:J:990:ARG:HG2	2.38	0.49
3:J:1320:ILE:O	3:J:1324:SER:OG	2.30	0.49
4:K:75:GLN:O	4:K:79:GLU:N	2.45	0.49
5:L:305:LEU:CD2	5:L:315:TRP:HA	2.43	0.49
5:L:389:SER:O	5:L:392:LYS:HG2	2.13	0.49
1:M:262:LEU:HD11	1:M:306:VAL:HG21	1.93	0.49
8:P:55:DT:H2''	8:P:56:DG:O5'	2.11	0.49
2:I:176:ILE:O	2:I:178:PRO:HD3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:472:GLU:CA	2:I:475:VAL:HG12	2.41	0.49
2:I:496:LYS:HD3	8:P:35:DA:P	2.52	0.49
2:I:1040:ASP:OD1	2:I:1041:ASP:N	2.45	0.49
3:J:475:GLU:OE1	4:K:28:ARG:NH2	2.45	0.49
3:J:615:LYS:HB2	3:J:616:PRO:HD3	1.95	0.49
3:J:1174:ARG:HG2	3:J:1189:MET:CE	2.42	0.49
3:J:1331:VAL:HG12	3:J:1332:LEU:HD22	1.95	0.49
2:I:60:GLN:HB3	2:I:67:GLU:OE2	2.13	0.49
2:I:301:TYR:O	2:I:309:LEU:HD12	2.13	0.49
2:I:472:GLU:O	2:I:476:LYS:HG2	2.13	0.49
2:I:738:GLU:HG2	2:I:974:ARG:HH22	1.77	0.49
2:I:905:ILE:HG21	5:L:598:LEU:HB3	1.93	0.49
2:I:1204:LEU:HB3	2:I:1205:PRO:HD2	1.94	0.49
2:I:1339:LEU:HD23	3:J:17:PHE:CD2	2.46	0.49
3:J:202:ARG:HG3	3:J:221:ILE:CD1	2.42	0.49
3:J:450:HIS:HE1	3:J:452:LEU:HD12	1.78	0.49
3:J:789:LYS:HG3	3:J:932:MET:HB3	1.94	0.49
3:J:932:MET:O	3:J:933:ARG:HD3	2.12	0.49
3:J:1251:LYS:O	3:J:1255:VAL:HG23	2.13	0.49
3:J:1330:ARG:NH2	8:P:21:DA:H5"	2.27	0.49
4:K:32:VAL:O	4:K:34:GLY:N	2.44	0.49
5:L:108:VAL:HG21	5:L:381:GLU:O	2.13	0.49
5:L:159:SER:HA	5:L:162:ILE:O	2.12	0.49
5:L:280:VAL:O	5:L:284:GLU:HG3	2.12	0.49
7:O:21:DA:C2'	7:O:22:DT:H71	2.42	0.49
1:G:71:LYS:HB3	1:G:74:VAL:CG1	2.42	0.49
1:H:78:ILE:O	1:H:81:ILE:HB	2.13	0.49
2:I:158:ASP:HA	2:I:442:VAL:HG13	1.95	0.49
2:I:165:HIS:NE2	2:I:190:PRO:HG3	2.28	0.49
2:I:931:VAL:O	2:I:948:ILE:HD13	2.13	0.49
2:I:1000:LEU:CD2	2:I:1002:LEU:HG	2.43	0.49
3:J:125:GLY:HA2	3:J:135:ILE:HD11	1.95	0.49
8:P:15:DC:H2"	8:P:16:DA:C8	2.47	0.49
1:G:18:GLN:NE2	1:G:20:SER:O	2.27	0.49
2:I:162:GLY:O	2:I:163:LYS:HE2	2.13	0.49
2:I:443:ASP:N	2:I:443:ASP:OD1	2.45	0.49
2:I:470:ARG:NE	8:P:34:DT:O2	2.45	0.49
2:I:519:ASN:HD21	2:I:689:ALA:HB3	1.77	0.49
2:I:593:LYS:HB2	2:I:604:HIS:CE1	2.47	0.49
3:J:78:LEU:O	3:J:78:LEU:HD23	2.13	0.49
3:J:278:ARG:NH2	5:L:407:GLU:OE2	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:555:TYR:HB2	3:J:585:LYS:O	2.13	0.49
3:J:937:ILE:HG12	3:J:1134:ILE:HG21	1.94	0.49
3:J:1067:ARG:CD	3:J:1072:LYS:HA	2.42	0.49
3:J:1172:LYS:HE3	3:J:1192:LYS:HG2	1.94	0.49
5:L:142:THR:HA	5:L:145:LEU:HD12	1.95	0.49
5:L:251:LYS:HD2	5:L:255:VAL:HG13	1.94	0.49
7:O:28:DG:H2'	7:O:29:DA:C8	2.48	0.49
7:O:41:DT:H2''	7:O:42:DA:C8	2.47	0.49
2:I:122:VAL:HG21	2:I:493:ILE:HG21	1.95	0.49
2:I:963:GLU:O	2:I:967:LEU:HG	2.13	0.49
3:J:705:THR:CG2	3:J:718:SER:HA	2.43	0.49
5:L:166:VAL:N	5:L:259:PHE:HB3	2.25	0.49
1:H:105:SER:OG	1:H:139:SER:HA	2.13	0.48
2:I:13:LYS:HB2	2:I:1180:MET:HE2	1.95	0.48
2:I:99:LYS:HE3	2:I:119:GLU:OE2	2.13	0.48
2:I:805:MET:HE1	2:I:1221:PHE:CZ	2.48	0.48
3:J:218:THR:CA	3:J:221:ILE:HG22	2.42	0.48
3:J:1050:THR:HA	3:J:1057:SER:CB	2.42	0.48
3:J:1116:SER:OG	3:J:1117:SER:N	2.44	0.48
5:L:266:PHE:O	5:L:270:VAL:HG12	2.13	0.48
1:M:287:VAL:HA	1:M:290:LEU:HB3	1.94	0.48
1:G:46:ILE:HD12	1:G:224:LEU:HD12	1.95	0.48
1:G:211:ILE:HG21	1:G:216:ALA:HB2	1.94	0.48
1:H:182:ARG:HD2	3:J:531:LYS:HD2	1.94	0.48
2:I:198:ILE:HG13	2:I:370:MET:CE	2.43	0.48
2:I:487:LEU:HD12	2:I:492:MET:HE1	1.95	0.48
2:I:551:HIS:CD2	2:I:552:PRO:HD2	2.48	0.48
2:I:664:GLY:O	2:I:686:GLN:NE2	2.46	0.48
2:I:794:LEU:HG	2:I:796:LEU:HD11	1.95	0.48
2:I:815:SER:HB3	2:I:1077:SER:OG	2.13	0.48
2:I:992:LEU:HD23	2:I:992:LEU:H	1.78	0.48
2:I:1104:PRO:HG3	3:J:725:MET:CE	2.43	0.48
2:I:1168:GLU:OE1	2:I:1171:ARG:NH1	2.46	0.48
3:J:215:LYS:O	3:J:219:LYS:HG3	2.12	0.48
3:J:441:LEU:O	3:J:442:ILE:HD13	2.12	0.48
3:J:1237:VAL:HG13	3:J:1253:ILE:HD13	1.95	0.48
4:K:45:LYS:O	4:K:49:ILE:HG13	2.13	0.48
5:L:297:MET:SD	5:L:302:PHE:HB2	2.53	0.48
5:L:408:GLY:CA	5:L:435:ILE:HG23	2.43	0.48
5:L:419:PHE:HA	5:L:430:TYR:CE2	2.49	0.48
1:H:80:GLU:HG2	3:J:569:LEU:HD21	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:238:GLN:HG2	2:I:286:GLU:HA	1.94	0.48
2:I:519:ASN:HD21	2:I:796:LEU:HD23	1.78	0.48
2:I:617:ALA:HB3	2:I:653:MET:HG3	1.96	0.48
2:I:1109:ILE:HG21	3:J:644:MET:HE1	1.95	0.48
3:J:708:ASN:HA	3:J:714:GLU:OE1	2.13	0.48
3:J:1080:ILE:CD1	3:J:1115:ILE:HD11	2.43	0.48
3:J:1321:SER:OG	3:J:1322:ALA:N	2.45	0.48
5:L:476:ARG:H	5:L:476:ARG:HD3	1.78	0.48
8:P:18:DT:H5'	8:P:18:DT:C6	2.48	0.48
1:H:74:VAL:HG12	1:H:76:GLU:N	2.27	0.48
2:I:349:GLU:O	2:I:352:ARG:HB2	2.13	0.48
2:I:618:GLN:OE1	3:J:770:LEU:HD23	2.13	0.48
2:I:727:VAL:HG12	2:I:728:ASP:H	1.77	0.48
2:I:1079:ILE:HG23	2:I:1079:ILE:O	2.14	0.48
2:I:1122:LYS:HG2	2:I:1229:TYR:CE1	2.48	0.48
3:J:372:MET:O	3:J:376:LEU:HG	2.13	0.48
3:J:425:ARG:HG2	3:J:426:ALA:H	1.78	0.48
3:J:436:ALA:O	3:J:485:MET:HA	2.13	0.48
3:J:925:GLU:CG	3:J:926:PRO:HD3	2.37	0.48
5:L:279:ARG:HH12	5:L:346:GLN:HG2	1.78	0.48
8:P:39:DC:P	8:P:39:DC:H3'	2.54	0.48
2:I:662:SER:O	2:I:666:SER:HB3	2.13	0.48
2:I:1091:GLY:O	2:I:1093:PRO:HD3	2.13	0.48
3:J:68:TYR:O	3:J:69:GLU:HG3	2.13	0.48
3:J:132:LEU:HD12	3:J:132:LEU:O	2.13	0.48
3:J:509:GLY:CA	3:J:632:ALA:HB2	2.43	0.48
3:J:1107:VAL:HG13	3:J:1121:LEU:O	2.14	0.48
5:L:547:VAL:HG21	5:L:607:LEU:HD21	1.96	0.48
1:M:250:ASP:OD2	1:M:252:ILE:HD12	2.13	0.48
8:P:48:DC:H1'	8:P:49:DT:C5'	2.43	0.48
1:G:113:ALA:CB	1:G:126:PRO:HB3	2.36	0.48
2:I:138:ILE:HG23	2:I:503:LYS:NZ	2.27	0.48
2:I:242:VAL:HG13	2:I:243:PRO:HD2	1.96	0.48
2:I:968:GLU:HB2	2:I:1018:TYR:CE1	2.42	0.48
2:I:993:PRO:CD	2:I:996:ARG:HG3	2.38	0.48
3:J:364:HIS:HB3	3:J:487:THR:HG21	1.95	0.48
3:J:479:GLU:O	3:J:483:LEU:N	2.40	0.48
3:J:1060:VAL:HG13	3:J:1106:ILE:HA	1.96	0.48
4:K:41:GLU:CG	4:K:49:ILE:HD11	2.43	0.48
5:L:150:ARG:CZ	5:L:150:ARG:CB	2.91	0.48
5:L:231:THR:OG1	5:L:248:GLU:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:257:VAL:O	1:M:260:LEU:HB2	2.13	0.48
2:I:289:VAL:HG11	2:I:322:LEU:HG	1.94	0.48
2:I:898:GLU:OE2	5:L:544:THR:HG21	2.14	0.48
2:I:1086:PRO:HB3	2:I:1221:PHE:HE2	1.79	0.48
2:I:1304:MET:CE	2:I:1308:ILE:HD11	2.37	0.48
3:J:29:MET:O	3:J:32:SER:HB3	2.13	0.48
3:J:269:TYR:CE1	3:J:306:LEU:HD11	2.48	0.48
3:J:500:ILE:HG22	3:J:500:ILE:O	2.14	0.48
5:L:96:ASP:OD2	5:L:99:ARG:HG3	2.13	0.48
5:L:409:ASN:O	5:L:413:MET:HG3	2.14	0.48
8:P:20:DC:N3	8:P:21:DA:N6	2.62	0.48
2:I:325:LEU:O	2:I:329:GLY:N	2.47	0.48
2:I:339:ASN:O	2:I:343:HIS:N	2.47	0.48
2:I:728:ASP:OD1	2:I:729:ALA:N	2.46	0.48
3:J:42:GLU:OE1	3:J:42:GLU:N	2.47	0.48
3:J:527:LEU:HD21	3:J:536:LEU:CD2	2.44	0.48
3:J:901:ARG:H	3:J:1251:LYS:HE2	1.79	0.48
3:J:1198:VAL:HG22	3:J:1202:GLU:CG	2.44	0.48
5:L:251:LYS:O	5:L:255:VAL:HG13	2.14	0.48
7:O:65:DT:H2''	7:O:66:DG:O5'	2.13	0.48
1:G:20:SER:OG	1:G:21:SER:N	2.45	0.48
1:H:152:TYR:CE2	1:H:154:PRO:HG3	2.49	0.48
2:I:74:ARG:CZ	2:I:97:ARG:HG3	2.44	0.48
2:I:287:VAL:HB	2:I:288:PRO:HD2	1.96	0.48
2:I:472:GLU:HA	2:I:475:VAL:CG1	2.42	0.48
2:I:542:ARG:HH11	7:O:63:DT:H5''	1.78	0.48
2:I:905:ILE:CG2	5:L:598:LEU:HB3	2.43	0.48
2:I:971:LEU:O	2:I:974:ARG:HB2	2.14	0.48
2:I:1306:LYS:NZ	2:I:1310:ASP:OD2	2.42	0.48
3:J:356:THR:OG1	3:J:448:GLN:HG2	2.13	0.48
3:J:513:MET:O	3:J:575:GLY:HA3	2.14	0.48
3:J:966:VAL:CG2	3:J:974:VAL:HG23	2.43	0.48
3:J:1307:LEU:HB2	3:J:1312:ALA:HB2	1.96	0.48
4:K:34:GLY:O	4:K:35:LYS:HD3	2.13	0.48
5:L:232:ARG:HG2	5:L:232:ARG:O	2.13	0.48
5:L:421:TYR:CZ	5:L:422:ARG:HG3	2.49	0.48
5:L:580:PHE:C	5:L:582:VAL:HG13	2.38	0.48
1:G:57:THR:O	1:G:173:VAL:HG22	2.14	0.48
2:I:78:PRO:HB3	2:I:92:TYR:CE1	2.48	0.48
2:I:138:ILE:CG1	2:I:143:ARG:HG3	2.44	0.48
2:I:188:PHE:CD1	2:I:194:LEU:HD13	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:453:ILE:HG22	2:I:454:ARG:O	2.14	0.48
2:I:895:LEU:HD21	2:I:899:GLU:CD	2.38	0.48
3:J:30:ILE:HG23	3:J:243:PRO:HB3	1.95	0.48
3:J:111:THR:OG1	3:J:300:GLN:HA	2.14	0.48
3:J:986:ASP:OD2	3:J:988:PHE:HB2	2.14	0.48
3:J:1046:ILE:HG22	3:J:1061:VAL:CA	2.31	0.48
5:L:431:ALA:O	5:L:435:ILE:HG13	2.13	0.48
7:O:53:DT:H4'	7:O:54:DT:OP2	2.14	0.48
7:O:63:DT:H2''	7:O:64:DT:C6	2.48	0.48
8:P:13:DG:H2''	8:P:14:DA:H8	1.78	0.48
1:G:218:ARG:NH1	1:H:231:PHE:O	2.43	0.47
1:H:211:ILE:HG12	1:H:219:ARG:HH22	1.79	0.47
2:I:136:PHE:HZ	2:I:456:VAL:HG11	1.78	0.47
2:I:594:VAL:HG12	2:I:595:THR:O	2.14	0.47
2:I:671:LEU:CD1	2:I:679:ALA:HB2	2.44	0.47
2:I:971:LEU:HD12	2:I:1018:TYR:HD1	1.79	0.47
3:J:1080:ILE:HB	3:J:1097:ALA:O	2.14	0.47
3:J:1320:ILE:HG22	3:J:1349:GLU:HG3	1.95	0.47
5:L:134:VAL:HA	5:L:273:MET:CE	2.35	0.47
5:L:423:ARG:HG2	5:L:425:TYR:HB2	1.96	0.47
1:M:250:ASP:HB3	1:M:253:LEU:CD1	2.43	0.47
1:H:211:ILE:HD11	1:H:215:GLU:OE1	2.13	0.47
2:I:69:GLN:HE21	2:I:101:ARG:HD2	1.80	0.47
2:I:1225:VAL:HG12	3:J:636:GLY:O	2.15	0.47
3:J:497:GLU:HG3	3:J:498:PRO:HD2	1.95	0.47
3:J:1081:VAL:HG12	3:J:1087:ASP:OD1	2.14	0.47
3:J:1183:SER:C	3:J:1185:PRO:HD3	2.39	0.47
3:J:1270:GLY:HA3	3:J:1299:GLY:CA	2.43	0.47
3:J:1314:LEU:CD1	3:J:1326:GLN:HB2	2.42	0.47
5:L:421:TYR:CE1	5:L:422:ARG:HG3	2.49	0.47
5:L:580:PHE:O	5:L:582:VAL:HG13	2.14	0.47
2:I:370:MET:HE3	2:I:388:LEU:CD1	2.43	0.47
2:I:375:PRO:HD3	5:L:103:ARG:HG2	1.97	0.47
2:I:867:GLU:OE2	2:I:943:LYS:HG2	2.14	0.47
2:I:1080:ASN:CB	2:I:1085:MET:HE3	2.43	0.47
2:I:1247:SER:OG	2:I:1248:THR:N	2.46	0.47
3:J:394:ILE:CG2	5:L:536:THR:HG22	2.44	0.47
3:J:783:LEU:O	3:J:786:THR:HG22	2.14	0.47
3:J:826:ILE:HA	3:J:830:ASP:O	2.15	0.47
5:L:463:LEU:HD12	5:L:497:VAL:HG11	1.96	0.47
5:L:492:ASP:O	5:L:495:ARG:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:183:ILE:CG2	1:H:205:MET:HG3	2.39	0.47
2:I:243:PRO:O	2:I:246:LEU:HB2	2.14	0.47
2:I:1101:LEU:HB3	3:J:731:ARG:CG	2.44	0.47
3:J:403:ARG:NE	3:J:405:GLU:OE2	2.33	0.47
4:K:41:GLU:HG2	4:K:49:ILE:HD11	1.96	0.47
1:H:19:VAL:HB	1:H:23:HIS:HB3	1.96	0.47
1:H:183:ILE:HG22	1:H:205:MET:CG	2.38	0.47
2:I:232:ILE:CD1	2:I:325:LEU:HD11	2.44	0.47
2:I:473:ARG:HD2	2:I:473:ARG:HA	1.73	0.47
2:I:898:GLU:OE2	5:L:540:LEU:HG	2.15	0.47
2:I:1034:ARG:O	2:I:1038:GLN:HB3	2.14	0.47
2:I:1261:GLY:H	8:P:29:DA:N6	2.13	0.47
2:I:1294:LYS:NZ	3:J:470:VAL:O	2.46	0.47
3:J:126:LEU:HD11	3:J:223:LEU:HD22	1.96	0.47
3:J:248:ASP:C	3:J:249:LEU:HD23	2.39	0.47
3:J:495:ASN:OD1	3:J:495:ASN:N	2.47	0.47
3:J:850:LYS:CG	3:J:851:PRO:HD2	2.45	0.47
3:J:997:VAL:HG12	3:J:1001:ALA:HB3	1.95	0.47
3:J:998:PRO:HG2	3:J:1020:TRP:CD2	2.49	0.47
3:J:1078:LEU:HD13	3:J:1121:LEU:CD2	2.45	0.47
5:L:452:ILE:HG13	5:L:457:ILE:HG13	1.96	0.47
8:P:21:DA:C1'	8:P:22:DA:H5'	2.38	0.47
2:I:319:LEU:HA	2:I:322:LEU:CB	2.45	0.47
2:I:356:THR:HB	2:I:365:GLU:OE2	2.15	0.47
2:I:810:TYR:CB	2:I:817:LEU:HD12	2.45	0.47
2:I:908:GLU:CD	5:L:611:LEU:HD13	2.39	0.47
2:I:1021:LEU:O	2:I:1024:GLU:HG3	2.14	0.47
2:I:1282:GLY:O	3:J:1360:GLY:HA3	2.15	0.47
3:J:259:ARG:HD3	5:L:502:LYS:HE3	1.95	0.47
3:J:620:PHE:CZ	3:J:624:ILE:HD11	2.49	0.47
3:J:754:ILE:HD11	6:N:19:GLY:CA	2.44	0.47
3:J:1271:SER:N	3:J:1299:GLY:HA3	2.24	0.47
5:L:252:LEU:CA	5:L:255:VAL:HG22	2.44	0.47
5:L:331:HIS:HA	5:L:334:SER:OG	2.14	0.47
7:O:56:DC:O2	7:O:57:DT:N3	2.47	0.47
1:G:54:CYS:SG	1:G:92:VAL:HG13	2.55	0.47
2:I:229:ILE:CG2	2:I:332:ARG:HB3	2.45	0.47
2:I:425:ILE:HA	2:I:428:VAL:HG12	1.96	0.47
2:I:519:ASN:ND2	2:I:689:ALA:HB3	2.29	0.47
2:I:831:ILE:HG22	2:I:833:ILE:HD12	1.97	0.47
2:I:833:ILE:HA	2:I:1054:LEU:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:960:LEU:HG	2:I:1025:PHE:CD1	2.48	0.47
2:I:982:GLY:HA3	2:I:1007:LYS:HD3	1.96	0.47
3:J:73:GLY:O	3:J:76:LYS:HE3	2.14	0.47
3:J:232:ASN:HA	3:J:236:TRP:CZ3	2.50	0.47
3:J:373:ALA:O	3:J:377:PHE:HB2	2.14	0.47
3:J:502:PRO:HB3	3:J:506:VAL:HG11	1.96	0.47
3:J:536:LEU:HD12	3:J:541:LEU:HB2	1.96	0.47
3:J:798:ARG:HH21	3:J:1325:PHE:CB	2.27	0.47
3:J:850:LYS:HG2	3:J:851:PRO:HD2	1.97	0.47
3:J:935:PHE:O	3:J:1135:THR:HA	2.15	0.47
3:J:937:ILE:HG12	3:J:1134:ILE:CG2	2.44	0.47
3:J:950:ILE:HB	3:J:1018:ALA:H	1.79	0.47
3:J:1038:THR:HG22	3:J:1077:ALA:HB3	1.97	0.47
3:J:1087:ASP:HB2	3:J:1096:PRO:HB3	1.95	0.47
3:J:1178:THR:HA	3:J:1184:ASP:CB	2.33	0.47
3:J:1230:THR:O	3:J:1234:VAL:HG13	2.14	0.47
4:K:39:VAL:CG2	4:K:40:PRO:HD2	2.44	0.47
5:L:493:LYS:HA	5:L:496:LYS:CG	2.44	0.47
5:L:507:MET:HG2	5:L:520:GLY:HA2	1.95	0.47
5:L:601:PRO:HG2	1:M:259:ASP:OD1	2.14	0.47
7:O:40:DC:H2''	7:O:41:DT:C5	2.50	0.47
1:G:47:LEU:O	1:G:180:VAL:HG21	2.15	0.47
1:H:23:HIS:O	1:H:213:PRO:HG2	2.15	0.47
1:H:99:ILE:C	1:H:100:LEU:HD12	2.39	0.47
2:I:233:ARG:HB2	2:I:238:GLN:HG3	1.97	0.47
2:I:1291:LEU:CD2	3:J:1351:VAL:HG13	2.45	0.47
3:J:233:LYS:HB2	3:J:236:TRP:CE2	2.49	0.47
3:J:490:ILE:HD11	3:J:609:TYR:CD1	2.50	0.47
3:J:961:SER:O	3:J:980:THR:HA	2.15	0.47
8:P:36:DT:H1'	8:P:37:DG:OP2	2.14	0.47
2:I:349:GLU:HA	2:I:352:ARG:CG	2.45	0.47
2:I:522:SER:O	2:I:525:THR:HG22	2.15	0.47
2:I:558:VAL:HG13	2:I:573:ASN:HB3	1.97	0.47
2:I:773:LEU:HD23	2:I:774:GLY:N	2.30	0.47
2:I:1151:LEU:CD2	2:I:1198:LEU:HD22	2.44	0.47
2:I:1258:PRO:HD2	3:J:346:ARG:O	2.15	0.47
2:I:1304:MET:HE2	3:J:472:LEU:HB3	1.97	0.47
3:J:56:LEU:HB3	3:J:250:ARG:HH12	1.79	0.47
3:J:174:ASP:O	3:J:175:GLU:HG2	2.14	0.47
3:J:259:ARG:HD3	5:L:502:LYS:CE	2.44	0.47
3:J:399:LYS:O	3:J:403:ARG:HG3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:504:GLN:OE1	3:J:731:ARG:HD3	2.15	0.47
3:J:1107:VAL:HG12	3:J:1109:LEU:H	1.80	0.47
5:L:561:MET:SD	5:L:576:VAL:HA	2.55	0.47
1:M:284:ARG:CZ	1:M:284:ARG:HA	2.45	0.47
8:P:44:DT:H2''	8:P:45:DA:C8	2.50	0.47
1:H:74:VAL:HG12	1:H:76:GLU:H	1.80	0.47
2:I:758:ARG:NE	2:I:835:GLU:HG3	2.29	0.47
2:I:1281:TYR:CE2	3:J:484:MET:HG2	2.49	0.47
3:J:130:MET:CE	3:J:134:ASP:HB3	2.43	0.47
3:J:747:MET:HG2	3:J:759:ILE:HG12	1.95	0.47
3:J:759:ILE:HG23	3:J:771:GLN:HB3	1.96	0.47
3:J:964:LYS:HE2	3:J:977:SER:HA	1.96	0.47
3:J:1163:VAL:HG23	3:J:1177:ILE:CG1	2.39	0.47
4:K:72:GLN:O	4:K:75:GLN:HB3	2.15	0.47
5:L:163:THR:CG2	5:L:262:VAL:HG22	2.44	0.47
6:N:29:ALA:O	6:N:30:HIS:HB3	2.15	0.47
8:P:65:DT:H2''	8:P:66:DT:H71	1.97	0.47
2:I:8:LYS:HG3	2:I:1168:GLU:OE2	2.15	0.46
2:I:432:LEU:HA	2:I:435:ILE:HD12	1.97	0.46
2:I:607:SER:OG	2:I:608:ALA:N	2.46	0.46
3:J:474:LEU:HB2	4:K:28:ARG:HH22	1.80	0.46
3:J:488:ASN:HB3	4:K:16:ARG:NH2	2.30	0.46
3:J:534:GLU:HA	3:J:578:ILE:HD11	1.97	0.46
3:J:649:LYS:O	3:J:653:ILE:HG13	2.15	0.46
9:J:1504:1N7:C3	9:J:1504:1N7:C18	2.74	0.46
5:L:285:ARG:O	5:L:288:MET:HG3	2.15	0.46
5:L:326:TRP:HE3	5:L:330:LEU:HD13	1.80	0.46
5:L:532:LEU:O	5:L:536:THR:HG23	2.15	0.46
1:M:307:LEU:HD23	1:M:312:LEU:HD12	1.97	0.46
1:H:92:VAL:HG13	1:H:120:ASP:OD2	2.16	0.46
2:I:26:TYR:HE2	2:I:32:LEU:HD12	1.80	0.46
3:J:350:SER:HA	3:J:468:VAL:O	2.15	0.46
3:J:644:MET:HG2	3:J:722:ILE:HD12	1.97	0.46
3:J:663:GLU:O	3:J:667:GLN:HG3	2.14	0.46
3:J:1147:ALA:O	3:J:1218:HIS:NE2	2.47	0.46
5:L:120:ALA:HB1	5:L:421:TYR:HB3	1.96	0.46
5:L:132:CYS:HB3	5:L:364:ARG:NH1	2.29	0.46
5:L:362:ASN:CA	5:L:365:MET:HB2	2.44	0.46
5:L:602:SER:H	5:L:605:GLU:HG3	1.80	0.46
8:P:27:DC:H2'	8:P:28:DG:C8	2.51	0.46
2:I:3:TYR:HB2	2:I:8:LYS:HE3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:209:ILE:O	2:I:213:LEU:HG	2.15	0.46
2:I:475:VAL:HG23	2:I:492:MET:O	2.16	0.46
2:I:884:VAL:CG1	2:I:1050:VAL:HG11	2.41	0.46
2:I:960:LEU:HD11	2:I:1028:LYS:CE	2.39	0.46
2:I:1285:TYR:CZ	3:J:1356:LEU:HD11	2.51	0.46
3:J:287:ALA:HB1	3:J:288:PRO:HD2	1.97	0.46
3:J:644:MET:HG2	3:J:722:ILE:CD1	2.45	0.46
3:J:804:ALA:O	3:J:916:GLY:HA3	2.15	0.46
3:J:1027:VAL:HA	3:J:1199:PHE:CZ	2.50	0.46
3:J:1123:ARG:CZ	3:J:1123:ARG:HB2	2.45	0.46
1:G:9:LEU:HD23	1:G:9:LEU:HA	1.82	0.46
1:H:124:VAL:HG21	1:H:209:GLY:HA3	1.97	0.46
2:I:277:LEU:O	2:I:282:VAL:HG22	2.15	0.46
2:I:810:TYR:CE1	3:J:359:PRO:HD2	2.50	0.46
2:I:1005:GLU:H	2:I:1008:GLN:HB3	1.79	0.46
2:I:1043:ALA:O	2:I:1046:VAL:HG12	2.15	0.46
3:J:31:ARG:NH2	3:J:106:GLU:OE1	2.48	0.46
3:J:122:SER:OG	3:J:125:GLY:HA3	2.16	0.46
3:J:450:HIS:NE2	3:J:625:MET:SD	2.88	0.46
3:J:937:ILE:CG1	3:J:1134:ILE:HG21	2.45	0.46
5:L:448:ARG:HD2	5:L:452:ILE:HG12	1.97	0.46
1:G:46:ILE:CD1	1:G:224:LEU:HD12	2.46	0.46
1:G:186:ASN:HB2	1:G:202:VAL:HG13	1.97	0.46
1:H:56:VAL:CG2	1:H:144:ILE:HD11	2.45	0.46
2:I:232:ILE:HD12	2:I:325:LEU:HD11	1.96	0.46
2:I:302:ILE:HG22	2:I:309:LEU:HA	1.96	0.46
2:I:699:LEU:HB2	2:I:799:ASN:ND2	2.19	0.46
2:I:1307:ASN:HB3	2:I:1312:ASN:O	2.16	0.46
3:J:41:PRO:HG3	3:J:274:ASN:OD1	2.16	0.46
3:J:416:ILE:CG2	3:J:439:PRO:HB2	2.45	0.46
3:J:582:ILE:HD11	3:J:627:THR:HB	1.96	0.46
3:J:664:ILE:CG2	3:J:678:ARG:HG2	2.45	0.46
5:L:394:TYR:HB2	5:L:404:LEU:HD13	1.98	0.46
6:N:28:ASN:O	6:N:30:HIS:N	2.36	0.46
8:P:37:DG:H2''	8:P:38:DC:H5'	1.98	0.46
1:G:8:PHE:HE1	1:H:150:ARG:HH11	1.64	0.46
1:G:38:THR:HG21	1:H:46:ILE:HD12	1.98	0.46
2:I:69:GLN:NE2	2:I:101:ARG:HD2	2.30	0.46
2:I:255:ILE:CB	2:I:263:VAL:HB	2.46	0.46
2:I:478:ARG:NH2	2:I:483:ASP:OD2	2.47	0.46
2:I:498:ILE:H	2:I:498:ILE:HD12	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:560:PRO:CB	3:J:776:THR:HG21	2.44	0.46
2:I:599:VAL:H	2:I:627:GLY:HA2	1.80	0.46
2:I:672:GLU:O	3:J:767:LEU:HD13	2.15	0.46
2:I:823:VAL:HG22	2:I:1060:ILE:HG22	1.97	0.46
2:I:862:LEU:HD22	2:I:865:LEU:HD12	1.96	0.46
2:I:865:LEU:HD21	2:I:882:ILE:O	2.16	0.46
2:I:1065:LYS:HD2	2:I:1235:LEU:HD12	1.98	0.46
2:I:1274:GLU:HG2	3:J:424:ASN:HD21	1.81	0.46
2:I:1290:MET:HE2	2:I:1290:MET:HB2	1.77	0.46
3:J:536:LEU:CD1	3:J:541:LEU:HB2	2.45	0.46
3:J:909:ILE:HD11	3:J:913:GLU:HB3	1.98	0.46
3:J:990:ARG:HD2	3:J:992:LYS:NZ	2.31	0.46
5:L:292:VAL:HG21	5:L:299:LYS:HE3	1.95	0.46
5:L:348:GLU:OE2	5:L:354:THR:HA	2.16	0.46
1:M:300:LEU:HD12	1:M:303:ILE:HB	1.96	0.46
2:I:56:VAL:HG13	2:I:57:PHE:HD2	1.81	0.46
2:I:1004:ASP:HA	2:I:1008:GLN:HB3	1.98	0.46
2:I:1282:GLY:HA3	4:K:17:PHE:HE1	1.79	0.46
3:J:253:VAL:CG2	5:L:523:ILE:HD13	2.45	0.46
3:J:576:ARG:HD3	3:J:593:ASN:HA	1.98	0.46
3:J:997:VAL:CG1	3:J:1001:ALA:HB3	2.45	0.46
5:L:257:LYS:HB3	5:L:257:LYS:HE2	1.75	0.46
5:L:353:LEU:HD21	5:L:361:ILE:HD11	1.98	0.46
5:L:586:ARG:NH2	7:O:25:DA:OP2	2.49	0.46
8:P:37:DG:C2'	8:P:38:DC:H5'	2.46	0.46
8:P:64:DA:H2''	8:P:65:DT:OP2	2.15	0.46
1:G:83:LEU:HD21	2:I:693:LEU:HD23	1.97	0.46
1:G:102:LEU:HD12	1:G:115:ILE:HG12	1.97	0.46
2:I:221:LEU:HD12	2:I:298:ALA:O	2.14	0.46
2:I:288:PRO:HB2	2:I:290:GLU:OE2	2.15	0.46
2:I:823:VAL:HG23	2:I:1079:ILE:HD11	1.98	0.46
2:I:989:LEU:O	2:I:997:TRP:NE1	2.45	0.46
3:J:502:PRO:HB3	3:J:506:VAL:CG1	2.45	0.46
3:J:638:SER:OG	3:J:639:VAL:N	2.49	0.46
3:J:755:ILE:CD1	3:J:774:ILE:HG23	2.45	0.46
3:J:1027:VAL:O	3:J:1027:VAL:HG12	2.16	0.46
5:L:279:ARG:NH1	5:L:350:GLU:OE1	2.49	0.46
6:N:28:ASN:HD21	6:N:54:GLY:C	2.24	0.46
7:O:64:DT:H2''	7:O:65:DT:OP2	2.16	0.46
8:P:25:DG:C2'	8:P:26:DC:H5''	2.46	0.46
1:H:49:SER:O	1:H:151:GLY:HA3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:145:ILE:HB	2:I:456:VAL:CG2	2.45	0.46
2:I:182:SER:HB3	2:I:199:ASP:OD2	2.15	0.46
2:I:227:LYS:NZ	2:I:298:ALA:HB1	2.24	0.46
2:I:680:LEU:HD13	3:J:783:LEU:HD13	1.97	0.46
3:J:282:LEU:HD13	3:J:291:ILE:HG22	1.97	0.46
3:J:479:GLU:CG	4:K:20:VAL:HG11	2.46	0.46
3:J:536:LEU:HD12	3:J:541:LEU:HD12	1.98	0.46
3:J:968:ASN:ND2	3:J:972:LYS:HE3	2.31	0.46
3:J:1138:LEU:HB3	3:J:1139:PRO:HD3	1.98	0.46
5:L:127:ILE:HA	5:L:130:VAL:CG2	2.46	0.46
5:L:297:MET:HG2	5:L:302:PHE:HB2	1.98	0.46
2:I:197:ARG:NH1	2:I:200:ARG:HA	2.27	0.46
2:I:563:THR:OG1	2:I:564:PRO:HD2	2.16	0.46
3:J:126:LEU:C	3:J:129:ASP:H	2.23	0.46
3:J:845:ALA:HB3	3:J:881:LYS:O	2.15	0.46
3:J:1263:LYS:HD3	3:J:1281:GLU:HA	1.98	0.46
5:L:224:LEU:CD1	5:L:256:PHE:HB2	2.46	0.46
1:G:152:TYR:CD1	2:I:824:GLN:HG2	2.51	0.45
1:H:197:ASP:OD1	1:H:197:ASP:N	2.47	0.45
2:I:22:LEU:HB3	2:I:655:VAL:CG2	2.46	0.45
2:I:238:GLN:HA	2:I:286:GLU:HA	1.98	0.45
2:I:700:VAL:CG1	2:I:1117:LEU:HD22	2.46	0.45
2:I:720:ARG:HG2	2:I:740:GLU:OE1	2.16	0.45
3:J:108:ALA:HB2	3:J:280:LYS:HG3	1.99	0.45
3:J:796:LEU:O	3:J:800:LEU:HD13	2.15	0.45
3:J:1029:THR:OG1	3:J:1030:GLU:N	2.49	0.45
3:J:1291:GLU:OE2	3:J:1292:LEU:HD12	2.16	0.45
1:M:291:LYS:HE2	1:M:291:LYS:HB3	1.84	0.45
8:P:18:DT:H5'	8:P:18:DT:H6	1.81	0.45
1:G:226:GLU:HB3	1:H:10:LYS:HZ1	1.80	0.45
1:H:74:VAL:CG2	1:H:133:LEU:HA	2.44	0.45
2:I:103:VAL:HG12	2:I:117:ILE:HG22	1.96	0.45
2:I:345:PRO:HB2	2:I:348:SER:OG	2.15	0.45
2:I:557:ARG:HB3	2:I:587:LEU:HB3	1.97	0.45
2:I:794:LEU:HG	2:I:796:LEU:CD1	2.46	0.45
2:I:1148:ALA:O	2:I:1151:LEU:HD13	2.16	0.45
2:I:1288:GLN:O	2:I:1292:THR:HB	2.17	0.45
3:J:212:THR:HA	3:J:215:LYS:CD	2.46	0.45
3:J:311:ARG:HH21	3:J:1329:THR:HG21	1.81	0.45
3:J:686:TRP:HA	3:J:686:TRP:CE3	2.50	0.45
3:J:733:SER:OG	3:J:734:ALA:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1003:LEU:HA	3:J:1018:ALA:CB	2.46	0.45
5:L:362:ASN:O	5:L:365:MET:HB2	2.16	0.45
5:L:454:VAL:O	5:L:458:GLU:HG2	2.17	0.45
1:M:252:ILE:HG21	1:M:312:LEU:HD21	1.99	0.45
8:P:31:DG:C8	8:P:31:DG:H5''	2.51	0.45
8:P:39:DC:H3'	8:P:39:DC:OP2	2.16	0.45
1:H:42:ALA:HB1	1:H:224:LEU:CD2	2.46	0.45
1:H:192:VAL:HB	1:H:195:ARG:HB2	1.98	0.45
2:I:144:VAL:HG21	2:I:515:MET:HG3	1.98	0.45
2:I:155:VAL:HA	2:I:175:ARG:O	2.17	0.45
2:I:224:PHE:CD1	2:I:347:ILE:HG13	2.50	0.45
2:I:488:MET:HE3	2:I:489:PRO:CD	2.44	0.45
2:I:561:ILE:CD1	2:I:671:LEU:HD21	2.46	0.45
3:J:309:ASN:CB	3:J:326:SER:HB2	2.38	0.45
3:J:791:ALA:HA	8:P:24:DG:C8	2.51	0.45
5:L:330:LEU:O	5:L:334:SER:OG	2.19	0.45
7:O:26:DT:H5''	7:O:27:DT:H71	1.98	0.45
1:H:50:SER:O	1:H:50:SER:OG	2.34	0.45
2:I:444:ASP:OD2	2:I:447:HIS:HB2	2.15	0.45
2:I:982:GLY:HA3	2:I:1007:LYS:CD	2.46	0.45
2:I:1077:SER:HB3	3:J:357:VAL:HG12	1.97	0.45
3:J:807:LEU:HD22	3:J:915:ILE:HG13	1.99	0.45
3:J:876:SER:CB	3:J:990:ARG:HH21	2.28	0.45
3:J:966:VAL:HG23	3:J:974:VAL:CG2	2.47	0.45
3:J:1044:GLN:HG2	3:J:1071:GLY:CA	2.46	0.45
5:L:130:VAL:HA	5:L:365:MET:SD	2.56	0.45
5:L:145:LEU:HD23	5:L:221:PHE:CD1	2.52	0.45
5:L:314:THR:O	5:L:318:ALA:HB3	2.15	0.45
1:M:255:ARG:CB	1:M:278:ILE:HD12	2.46	0.45
8:P:48:DC:H2''	8:P:49:DT:OP2	2.15	0.45
8:P:51:DC:H1'	8:P:52:DT:O5'	2.16	0.45
2:I:136:PHE:CE2	2:I:145:ILE:HD13	2.52	0.45
2:I:180:ARG:O	2:I:395:TYR:HA	2.16	0.45
2:I:317:LEU:HD11	2:I:333:ILE:HG21	1.99	0.45
2:I:821:ARG:HD3	2:I:1082:ILE:CG2	2.46	0.45
2:I:828:PHE:HB2	2:I:1060:ILE:HD12	1.98	0.45
3:J:973:LEU:HD12	3:J:974:VAL:H	1.81	0.45
5:L:230:VAL:HG12	5:L:248:GLU:OE2	2.16	0.45
5:L:279:ARG:CD	5:L:347:ILE:HG12	2.47	0.45
5:L:348:GLU:HG2	5:L:355:ILE:CG1	2.47	0.45
1:M:286:GLU:HG2	1:M:300:LEU:CD2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:61:ILE:HD12	1:G:78:ILE:HD12	1.98	0.45
1:H:18:GLN:HG3	1:H:20:SER:H	1.81	0.45
1:H:73:GLY:O	1:H:133:LEU:HD12	2.17	0.45
2:I:36:GLN:NE2	2:I:40:GLU:HB2	2.32	0.45
2:I:76:GLY:N	2:I:95:PRO:O	2.47	0.45
2:I:1271:GLY:N	2:I:1274:GLU:OE1	2.50	0.45
3:J:287:ALA:CA	5:L:413:MET:HE1	2.46	0.45
3:J:846:GLU:HA	3:J:860:ARG:HG3	1.98	0.45
3:J:878:ASP:HB3	3:J:990:ARG:HA	1.97	0.45
3:J:1150:PRO:HG2	3:J:1153:PRO:HB3	1.99	0.45
3:J:1320:ILE:CG2	3:J:1349:GLU:HG3	2.47	0.45
3:J:1356:LEU:HD23	3:J:1356:LEU:HA	1.79	0.45
4:K:6:VAL:HG11	4:K:51:LEU:HD22	1.97	0.45
5:L:162:ILE:HG13	5:L:164:GLY:N	2.31	0.45
5:L:319:ALA:HB1	5:L:326:TRP:CZ3	2.50	0.45
5:L:473:GLU:HB3	5:L:474:MET:HE2	1.98	0.45
1:M:298:LYS:HB2	1:M:298:LYS:HE3	1.72	0.45
1:M:311:GLY:O	1:M:312:LEU:HD23	2.16	0.45
7:O:31:DA:H2''	7:O:32:DA:H8	1.78	0.45
2:I:128:PRO:HD2	2:I:506:PHE:CE2	2.51	0.45
2:I:204:LEU:HD11	2:I:369:MET:HG3	1.99	0.45
2:I:320:ASP:OD1	2:I:321:LEU:HG	2.16	0.45
2:I:469:VAL:HA	2:I:472:GLU:CG	2.47	0.45
3:J:352:ARG:HH11	8:P:27:DC:H4'	1.81	0.45
3:J:568:SER:OG	3:J:569:LEU:N	2.49	0.45
4:K:18:ASP:O	4:K:22:VAL:HG22	2.17	0.45
5:L:267:ASP:HA	5:L:270:VAL:HG12	1.99	0.45
5:L:292:VAL:HA	5:L:297:MET:H	1.81	0.45
5:L:348:GLU:CA	5:L:355:ILE:HD11	2.46	0.45
5:L:412:LEU:HB2	5:L:435:ILE:HD11	1.98	0.45
8:P:44:DT:H4'	8:P:45:DA:OP1	2.17	0.45
1:G:7:GLU:HG3	1:G:8:PHE:H	1.81	0.45
1:H:100:LEU:HB2	1:H:144:ILE:HG23	1.97	0.45
2:I:870:ILE:HB	2:I:944:ARG:HD3	1.99	0.45
3:J:24:LEU:HD11	3:J:116:PHE:CZ	2.52	0.45
3:J:79:LYS:CG	5:L:569:THR:HB	2.47	0.45
3:J:392:THR:OG1	3:J:393:THR:N	2.50	0.45
3:J:903:LEU:HD11	3:J:1249:ASN:HD22	1.82	0.45
3:J:1158:GLU:O	3:J:1206:ARG:HG3	2.16	0.45
3:J:1267:VAL:HG22	3:J:1301:THR:O	2.17	0.45
4:K:52:ARG:O	4:K:55:GLU:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:114:GLU:HA	5:L:117:ILE:CG1	2.47	0.45
2:I:128:PRO:HG2	2:I:506:PHE:CD2	2.52	0.45
2:I:198:ILE:HG13	2:I:370:MET:HE2	1.99	0.45
2:I:296:VAL:HA	2:I:315:MET:C	2.42	0.45
2:I:802:VAL:HA	2:I:1096:ILE:O	2.17	0.45
2:I:1262:LYS:HG2	2:I:1262:LYS:O	2.15	0.45
3:J:532:GLU:OE1	3:J:535:ARG:NH2	2.50	0.45
3:J:611:ILE:HG22	3:J:612:LEU:HD12	1.99	0.45
3:J:855:ASP:OD1	3:J:855:ASP:N	2.50	0.45
5:L:604:SER:O	5:L:607:LEU:HB2	2.17	0.45
1:M:298:LYS:HB3	8:P:67:DT:P	2.57	0.45
1:G:99:ILE:C	1:G:100:LEU:HD23	2.42	0.45
2:I:27:LEU:CD1	2:I:663:VAL:HG21	2.46	0.45
2:I:75:LEU:HD11	2:I:127:ILE:CD1	2.31	0.45
2:I:551:HIS:CE1	2:I:553:THR:HG23	2.52	0.45
2:I:1151:LEU:HD21	2:I:1198:LEU:CD1	2.40	0.45
3:J:104:HIS:NE2	3:J:106:GLU:OE2	2.50	0.45
3:J:128:LEU:HA	3:J:192:MET:HE1	1.99	0.45
3:J:363:LEU:HD12	3:J:363:LEU:O	2.16	0.45
3:J:686:TRP:HB3	3:J:746:LEU:HD21	1.98	0.45
5:L:290:LEU:HB3	5:L:333:VAL:CG2	2.47	0.45
5:L:394:TYR:OH	5:L:436:ARG:NH2	2.43	0.45
5:L:492:ASP:OD1	5:L:495:ARG:HD3	2.16	0.45
1:G:214:GLU:O	1:G:217:ILE:HG22	2.18	0.44
2:I:346:TYR:OH	2:I:436:ARG:HD2	2.17	0.44
2:I:423:ASP:HA	2:I:426:ILE:CD1	2.45	0.44
2:I:548:ARG:HD3	2:I:569:ILE:O	2.16	0.44
2:I:678:ARG:HA	2:I:678:ARG:HD3	1.35	0.44
2:I:697:LYS:HA	2:I:795:ALA:HB2	1.98	0.44
2:I:1297:ASP:O	2:I:1301:ARG:HG2	2.17	0.44
3:J:34:SER:HB2	3:J:104:HIS:HB3	2.00	0.44
3:J:260:PHE:CB	5:L:504:PRO:HB3	2.44	0.44
3:J:686:TRP:CB	3:J:746:LEU:HD21	2.47	0.44
3:J:697:MET:HE1	3:J:738:ARG:CA	2.47	0.44
3:J:866:GLU:HA	3:J:869:CYS:HB2	1.98	0.44
3:J:1073:ASP:O	3:J:1074:LEU:HG	2.17	0.44
3:J:1079:LYS:HG3	3:J:1087:ASP:CG	2.42	0.44
4:K:63:ILE:HG22	4:K:67:ARG:HD3	1.99	0.44
5:L:148:TYR:CD2	5:L:221:PHE:CG	3.05	0.44
1:G:55:ALA:HB3	1:G:177:TYR:CD1	2.52	0.44
2:I:62:TYR:HD1	2:I:476:LYS:HE2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:375:PRO:HG3	5:L:103:ARG:HD3	1.99	0.44
2:I:499:SER:HA	2:I:502:VAL:HG12	1.98	0.44
2:I:598:VAL:HA	2:I:627:GLY:CA	2.46	0.44
2:I:599:VAL:HG21	2:I:623:LEU:HD22	1.98	0.44
2:I:727:VAL:HG21	2:I:772:SER:O	2.17	0.44
2:I:1085:MET:HE2	2:I:1085:MET:HA	1.99	0.44
2:I:1166:ASP:N	2:I:1166:ASP:OD1	2.50	0.44
2:I:1335:ILE:CG2	3:J:22:ILE:HD11	2.47	0.44
3:J:964:LYS:HE2	3:J:977:SER:CB	2.47	0.44
3:J:1173:ARG:NH2	3:J:1192:LYS:HA	2.32	0.44
5:L:291:CYS:HB3	5:L:297:MET:SD	2.57	0.44
1:M:257:VAL:CA	1:M:260:LEU:HD13	2.35	0.44
1:M:265:ARG:NH2	8:P:67:DT:O3'	2.51	0.44
1:H:88:LEU:HD13	1:H:128:HIS:ND1	2.33	0.44
1:H:182:ARG:HD3	3:J:531:LYS:HE3	2.00	0.44
2:I:231:GLU:HA	2:I:331:LYS:O	2.17	0.44
2:I:835:GLU:OE1	2:I:1051:LYS:HD3	2.16	0.44
3:J:214:ARG:O	3:J:218:THR:HG22	2.17	0.44
3:J:349:TYR:OH	3:J:379:PRO:HG2	2.17	0.44
3:J:1061:VAL:CG2	3:J:1101:LEU:HD13	2.45	0.44
3:J:1079:LYS:O	3:J:1081:VAL:HG13	2.16	0.44
3:J:1270:GLY:HA3	3:J:1299:GLY:O	2.18	0.44
9:J:1504:1N7:H17	5:L:522:PHE:HB3	1.98	0.44
4:K:10:VAL:HG21	4:K:16:ARG:HD2	1.98	0.44
5:L:476:ARG:HG2	5:L:477:GLU:N	2.32	0.44
8:P:25:DG:H2'	8:P:26:DC:H6	1.83	0.44
8:P:39:DC:H1'	8:P:40:DC:O5'	2.17	0.44
2:I:182:SER:HA	7:O:61:DC:H42	1.81	0.44
2:I:823:VAL:HG21	2:I:1079:ILE:HD11	1.98	0.44
2:I:903:ARG:HD2	2:I:908:GLU:O	2.16	0.44
3:J:124:ILE:HG22	3:J:135:ILE:CD1	2.42	0.44
3:J:153:ASN:HB3	3:J:154:LEU:HD12	2.00	0.44
3:J:357:VAL:HG13	3:J:358:GLY:N	2.33	0.44
3:J:447:ILE:HD13	3:J:468:VAL:HG13	1.99	0.44
3:J:447:ILE:HD13	3:J:468:VAL:CG1	2.48	0.44
3:J:566:LYS:HG3	3:J:566:LYS:O	2.17	0.44
3:J:1198:VAL:HG22	3:J:1199:PHE:H	1.81	0.44
5:L:118:ASP:O	5:L:121:LYS:HB3	2.17	0.44
5:L:279:ARG:HH21	5:L:343:LYS:CB	2.31	0.44
1:M:269:CYS:SG	1:M:295:LEU:HD12	2.57	0.44
1:M:302:GLU:O	1:M:306:VAL:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:N:52:PHE:HB2	6:N:55:VAL:HG22	1.99	0.44
2:I:594:VAL:HB	2:I:651:ASP:C	2.43	0.44
3:J:144:TYR:CD2	3:J:180:MET:HE3	2.53	0.44
3:J:251:PRO:HG2	5:L:507:MET:HE1	2.00	0.44
3:J:262:THR:O	5:L:507:MET:N	2.46	0.44
3:J:388:ARG:HG2	3:J:390:LEU:CD1	2.48	0.44
3:J:510:LEU:CD2	3:J:601:ILE:HD12	2.48	0.44
3:J:598:LYS:HA	3:J:601:ILE:CG2	2.48	0.44
3:J:1037:PHE:CD2	3:J:1111:ASP:HB2	2.53	0.44
5:L:303:ILE:HG23	5:L:306:PHE:CD2	2.52	0.44
5:L:316:PHE:O	5:L:319:ALA:HB3	2.17	0.44
2:I:243:PRO:CB	2:I:278:GLU:HG3	2.47	0.44
2:I:592:ARG:HG2	2:I:653:MET:O	2.18	0.44
2:I:610:GLU:OE1	2:I:610:GLU:N	2.51	0.44
2:I:842:ASP:HB2	2:I:1047:LEU:CD2	2.44	0.44
2:I:971:LEU:O	2:I:975:ILE:HG12	2.18	0.44
3:J:103:GLY:C	3:J:244:VAL:HG22	2.43	0.44
3:J:212:THR:HA	3:J:215:LYS:HG3	2.00	0.44
3:J:292:VAL:O	3:J:296:LYS:HG3	2.17	0.44
3:J:519:ASN:CG	3:J:709:ARG:HD3	2.42	0.44
3:J:682:VAL:O	3:J:685:ILE:HG12	2.18	0.44
3:J:1154:ALA:HB2	3:J:1213:GLY:O	2.18	0.44
3:J:1167:LYS:HD3	3:J:1169:THR:HB	1.99	0.44
5:L:116:GLU:OE1	5:L:116:GLU:N	2.44	0.44
5:L:290:LEU:HB3	5:L:337:VAL:HG22	2.00	0.44
5:L:363:ARG:NH1	5:L:367:ILE:HD11	2.33	0.44
5:L:408:GLY:HA2	5:L:435:ILE:HG23	2.00	0.44
5:L:486:ARG:HD2	5:L:486:ARG:HA	1.74	0.44
5:L:586:ARG:HD2	7:O:25:DA:H8	1.83	0.44
1:M:279:GLY:HA3	1:M:321:TRP:HE1	1.82	0.44
7:O:32:DA:H2''	7:O:33:DA:C8	2.53	0.44
8:P:51:DC:H1'	8:P:52:DT:C5'	2.47	0.44
2:I:453:ILE:HD13	2:I:530:ILE:HD12	2.00	0.44
2:I:698:PRO:HA	2:I:1231:TYR:CE1	2.52	0.44
2:I:883:LEU:HD11	2:I:1054:LEU:HD11	1.99	0.44
2:I:894:GLN:HG2	3:J:69:GLU:OE2	2.18	0.44
2:I:1146:GLN:OE1	2:I:1161:LEU:HD23	2.18	0.44
9:I:1401:1N7:H31	9:I:1401:1N7:H5	1.98	0.44
3:J:46:TYR:CZ	5:L:453:PRO:HD3	2.53	0.44
3:J:59:ALA:HA	3:J:63:GLY:O	2.17	0.44
3:J:452:LEU:HD13	3:J:500:ILE:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:853:THR:O	3:J:853:THR:HG22	2.18	0.44
3:J:1067:ARG:HD3	3:J:1071:GLY:O	2.17	0.44
5:L:166:VAL:H	5:L:259:PHE:CB	2.26	0.44
5:L:326:TRP:HA	5:L:329:LYS:HB2	1.99	0.44
5:L:348:GLU:OE2	5:L:355:ILE:HG12	2.18	0.44
5:L:490:PRO:HG2	5:L:493:LYS:HE3	2.00	0.44
7:O:61:DC:H2''	7:O:62:DC:O5'	2.17	0.44
2:I:38:PHE:HA	2:I:48:GLY:HA2	1.99	0.44
2:I:885:GLY:HA2	2:I:917:SER:CB	2.47	0.44
3:J:254:PRO:HA	3:J:260:PHE:CD1	2.49	0.44
3:J:261:ALA:CB	5:L:523:ILE:HD11	2.48	0.44
3:J:762:ASN:OD1	3:J:764:ARG:N	2.50	0.44
3:J:1046:ILE:HA	3:J:1062:LEU:HG	1.99	0.44
5:L:339:ARG:HA	5:L:342:GLN:CG	2.47	0.44
7:O:63:DT:C2'	7:O:64:DT:H71	2.48	0.44
1:H:205:MET:HE1	1:H:217:ILE:CG1	2.43	0.44
1:H:213:PRO:O	1:H:216:ALA:HB3	2.18	0.44
2:I:226:GLU:O	2:I:336:LEU:HD22	2.17	0.44
2:I:243:PRO:CG	2:I:278:GLU:HG3	2.48	0.44
2:I:243:PRO:HG3	2:I:282:VAL:HG21	1.98	0.44
2:I:546:GLU:OE1	2:I:546:GLU:N	2.37	0.44
2:I:660:VAL:HG11	3:J:769:VAL:HG13	2.00	0.44
2:I:671:LEU:HD23	2:I:1186:VAL:HG11	1.99	0.44
2:I:884:VAL:HG11	2:I:1050:VAL:CG1	2.42	0.44
2:I:1132:LEU:O	2:I:1132:LEU:HD23	2.18	0.44
3:J:736:GLN:O	3:J:740:LEU:HD13	2.18	0.44
3:J:1298:VAL:HG13	3:J:1299:GLY:N	2.33	0.44
5:L:288:MET:HB2	5:L:299:LYS:NZ	2.33	0.44
5:L:385:ARG:HG2	7:O:54:DT:H1'	1.99	0.44
5:L:426:LYS:HE2	7:O:53:DT:OP2	2.18	0.44
1:G:14:VAL:HG21	1:G:29:GLU:HB2	1.99	0.43
1:G:48:LEU:HA	1:G:180:VAL:HG21	2.00	0.43
1:G:57:THR:C	1:G:173:VAL:HG22	2.42	0.43
1:H:19:VAL:CG2	1:H:23:HIS:HB3	2.48	0.43
2:I:138:ILE:HG23	2:I:503:LYS:HZ1	1.83	0.43
2:I:195:PHE:CD1	2:I:203:LYS:HG2	2.52	0.43
2:I:808:ASN:N	3:J:633:ALA:HB2	2.28	0.43
2:I:829:THR:HG23	2:I:1057:LYS:HG2	2.00	0.43
2:I:1235:LEU:HD23	2:I:1235:LEU:HA	1.65	0.43
3:J:62:PHE:HE1	3:J:103:GLY:H	1.66	0.43
3:J:114:ILE:HB	3:J:304:ASP:OD2	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:161:THR:CG2	3:J:164:GLN:HG3	2.46	0.43
3:J:337:ARG:HB3	3:J:342:LEU:HD13	1.99	0.43
3:J:712:GLN:O	3:J:713:GLU:HG3	2.18	0.43
3:J:1082:ASP:N	3:J:1086:ASN:O	2.39	0.43
3:J:1167:LYS:HG2	3:J:1169:THR:OG1	2.18	0.43
5:L:110:LEU:O	5:L:111:LEU:HG	2.18	0.43
5:L:298:PRO:HD3	5:L:326:TRP:NE1	2.33	0.43
5:L:538:GLU:O	5:L:541:ARG:HB2	2.18	0.43
5:L:551:LEU:HD23	5:L:551:LEU:HA	1.82	0.43
5:L:602:SER:H	5:L:605:GLU:CD	2.26	0.43
1:M:291:LYS:O	1:M:291:LYS:HG2	2.15	0.43
1:M:318:LEU:O	1:M:319:GLU:HG2	2.18	0.43
7:O:75:DA:H2"	7:O:76:DT:C7	2.40	0.43
1:G:66:HIS:C	1:G:171:LEU:HD11	2.43	0.43
1:G:83:LEU:HD21	2:I:693:LEU:HD21	1.99	0.43
1:H:44:ARG:HA	1:H:183:ILE:CD1	2.48	0.43
1:H:196:THR:HG1	1:H:197:ASP:CG	2.26	0.43
2:I:3:TYR:CB	2:I:8:LYS:HE3	2.49	0.43
2:I:107:ARG:O	2:I:108:GLU:HB3	2.18	0.43
2:I:207:THR:HA	2:I:210:LEU:HD12	2.00	0.43
2:I:277:LEU:HA	2:I:280:ASP:CB	2.36	0.43
2:I:532:ALA:O	2:I:533:LEU:HD23	2.17	0.43
2:I:726:TYR:CZ	2:I:728:ASP:HB2	2.54	0.43
2:I:1086:PRO:HD2	2:I:1094:VAL:HG22	1.99	0.43
2:I:1116:HIS:HE1	3:J:641:ILE:H	1.65	0.43
2:I:1256:GLN:HB3	2:I:1301:ARG:HH21	1.82	0.43
3:J:94:GLN:OE1	3:J:96:LYS:HD3	2.18	0.43
3:J:154:LEU:HD22	3:J:160:LEU:HD21	1.99	0.43
3:J:355:ILE:HG21	3:J:466:MET:SD	2.58	0.43
3:J:1271:SER:HB3	3:J:1298:VAL:C	2.43	0.43
5:L:120:ALA:CB	5:L:421:TYR:HB3	2.48	0.43
8:P:15:DC:H2"	8:P:16:DA:N7	2.33	0.43
8:P:67:DT:H2"	8:P:68:DG:C8	2.53	0.43
1:G:17:GLU:HB3	1:G:25:LYS:HB2	2.00	0.43
1:H:51:MET:O	1:H:150:ARG:HG2	2.18	0.43
2:I:3:TYR:CE1	2:I:11:ILE:HD13	2.53	0.43
2:I:138:ILE:HG13	2:I:143:ARG:HG3	2.00	0.43
2:I:724:VAL:HG13	2:I:724:VAL:O	2.18	0.43
2:I:764:CYS:HB2	2:I:833:ILE:CD1	2.48	0.43
2:I:975:ILE:HG21	2:I:1014:LEU:HB2	2.00	0.43
3:J:58:CYS:HB2	3:J:61:ILE:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:390:LEU:HD23	3:J:407:VAL:HG21	2.00	0.43
3:J:768:ASN:N	3:J:771:GLN:OE1	2.50	0.43
3:J:811:GLU:O	3:J:895:CYS:HA	2.19	0.43
3:J:888:CYS:HB3	3:J:1258:ARG:HH12	1.84	0.43
3:J:1046:ILE:CG2	3:J:1061:VAL:HG22	2.48	0.43
3:J:1163:VAL:HG22	3:J:1164:SER:H	1.83	0.43
1:M:265:ARG:HE	1:M:294:ASN:C	2.24	0.43
7:O:70:DT:H2''	7:O:71:DG:N7	2.34	0.43
2:I:105:TYR:HA	2:I:114:VAL:HA	2.00	0.43
2:I:106:GLU:CB	2:I:109:ALA:HB2	2.31	0.43
2:I:251:ALA:N	2:I:267:ARG:O	2.51	0.43
2:I:842:ASP:CB	2:I:1047:LEU:HD11	2.48	0.43
2:I:887:VAL:HB	2:I:913:VAL:HG11	2.00	0.43
2:I:1214:ASP:HB2	2:I:1221:PHE:CE1	2.53	0.43
3:J:126:LEU:CD1	3:J:223:LEU:HD22	2.49	0.43
3:J:355:ILE:CG2	3:J:466:MET:HG3	2.48	0.43
3:J:370:LYS:NZ	3:J:443:GLU:OE2	2.25	0.43
3:J:425:ARG:NH1	3:J:464:ASP:HB3	2.33	0.43
4:K:54:ILE:HD13	4:K:59:ILE:O	2.18	0.43
5:L:448:ARG:H	5:L:448:ARG:HG2	1.62	0.43
5:L:572:THR:O	5:L:576:VAL:HG23	2.17	0.43
8:P:36:DT:H2''	8:P:37:DG:OP1	2.18	0.43
2:I:137:VAL:HG13	2:I:137:VAL:O	2.18	0.43
2:I:487:LEU:HD12	2:I:492:MET:CE	2.49	0.43
2:I:575:LEU:HD23	2:I:576:SER:N	2.33	0.43
2:I:724:VAL:CG2	2:I:727:VAL:HG22	2.48	0.43
2:I:870:ILE:HG21	2:I:931:VAL:CG1	2.46	0.43
2:I:1041:ASP:C	2:I:1042:LEU:HD23	2.44	0.43
3:J:789:LYS:HE2	3:J:789:LYS:HB3	1.86	0.43
3:J:1061:VAL:HG21	3:J:1101:LEU:HB3	2.00	0.43
5:L:96:ASP:CB	5:L:99:ARG:HG3	2.49	0.43
5:L:533:ASP:O	5:L:536:THR:OG1	2.31	0.43
8:P:48:DC:H1'	8:P:49:DT:O5'	2.18	0.43
8:P:52:DT:H1'	8:P:53:DT:C5'	2.48	0.43
2:I:93:SER:HA	2:I:128:PRO:HA	2.00	0.43
2:I:206:ALA:O	2:I:209:ILE:HG22	2.19	0.43
2:I:284:LEU:HD12	2:I:285:ILE:N	2.32	0.43
2:I:335:THR:C	2:I:336:LEU:HD23	2.44	0.43
2:I:455:SER:O	2:I:459:MET:HE2	2.19	0.43
2:I:902:LEU:CD2	5:L:611:LEU:HG	2.48	0.43
2:I:1018:TYR:CE2	2:I:1022:LYS:HD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:138:VAL:HG21	3:J:145:VAL:HB	2.00	0.43
3:J:527:LEU:HB2	3:J:550:VAL:HG22	2.00	0.43
3:J:875:ASN:O	3:J:876:SER:OG	2.36	0.43
3:J:968:ASN:OD1	3:J:972:LYS:N	2.52	0.43
5:L:492:ASP:HA	5:L:495:ARG:HD3	2.01	0.43
5:L:587:ILE:CD1	5:L:590:ILE:HD12	2.40	0.43
5:L:597:LYS:O	5:L:600:HIS:HB2	2.17	0.43
8:P:44:DT:P	8:P:44:DT:H2'	2.59	0.43
1:G:162:GLU:O	1:G:165:GLU:HB2	2.19	0.43
1:H:76:GLU:HA	1:H:80:GLU:OE2	2.18	0.43
1:H:211:ILE:HD12	1:H:211:ILE:HA	1.79	0.43
2:I:130:MET:HE2	2:I:134:GLY:HA2	2.00	0.43
2:I:833:ILE:HD12	2:I:833:ILE:H	1.83	0.43
2:I:1159:VAL:HG12	2:I:1161:LEU:CD2	2.48	0.43
3:J:334:LYS:HZ3	3:J:334:LYS:HG2	1.74	0.43
3:J:950:ILE:O	3:J:1016:THR:HG23	2.18	0.43
3:J:985:ILE:HD13	3:J:991:THR:HG22	2.01	0.43
5:L:279:ARG:HD3	5:L:347:ILE:HG12	2.00	0.43
5:L:355:ILE:HA	5:L:358:VAL:HB	2.00	0.43
5:L:608:ARG:O	5:L:611:LEU:HB2	2.19	0.43
1:M:264:VAL:HG13	1:M:267:ALA:HB3	2.01	0.43
8:P:11:DT:H2''	8:P:12:DG:C8	2.54	0.43
2:I:306:THR:OG1	2:I:308:GLU:HG2	2.19	0.43
2:I:359:ARG:CZ	2:I:363:LEU:HD11	2.49	0.43
2:I:690:VAL:HG23	2:I:763:THR:HG21	1.99	0.43
2:I:992:LEU:CD1	2:I:996:ARG:HB3	2.35	0.43
3:J:67:ASP:OD1	3:J:95:THR:N	2.40	0.43
3:J:238:ILE:HD13	3:J:238:ILE:HA	1.81	0.43
3:J:810:THR:O	3:J:911:LYS:HD2	2.18	0.43
3:J:1034:PHE:CE1	3:J:1114:GLN:HB3	2.51	0.43
4:K:71:GLU:O	4:K:74:GLU:HG2	2.19	0.43
5:L:426:LYS:CE	7:O:52:DA:H3'	2.47	0.43
5:L:441:ARG:O	5:L:445:ASP:HB2	2.19	0.43
7:O:60:DG:H4'	7:O:61:DC:OP1	2.19	0.43
8:P:38:DC:C1'	8:P:39:DC:H5'	2.49	0.43
8:P:45:DA:H1'	8:P:46:DG:C8	2.53	0.43
8:P:50:DT:H2''	8:P:51:DC:C5	2.54	0.43
1:G:83:LEU:HB3	2:I:694:ARG:HH21	1.83	0.43
1:G:184:ALA:HB2	2:I:1090:ASN:O	2.18	0.43
1:H:27:THR:HG22	1:H:28:LEU:H	1.84	0.43
2:I:149:LEU:HD12	2:I:453:ILE:HG12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:183:TRP:HZ3	7:O:62:DC:H5'	1.84	0.43
2:I:215:TYR:HE1	2:I:223:LEU:HD11	1.84	0.43
2:I:936:ARG:O	2:I:939:VAL:N	2.51	0.43
3:J:212:THR:HA	3:J:215:LYS:CG	2.47	0.43
3:J:416:ILE:O	3:J:416:ILE:HG22	2.18	0.43
5:L:150:ARG:NH1	5:L:150:ARG:HB2	2.34	0.43
5:L:485:GLU:N	5:L:485:GLU:OE1	2.52	0.43
5:L:605:GLU:HA	5:L:608:ARG:CG	2.49	0.43
1:H:153:VAL:HG23	1:H:153:VAL:O	2.18	0.43
2:I:103:VAL:HG23	2:I:103:VAL:O	2.19	0.43
2:I:157:PHE:HD1	2:I:174:ALA:HB2	1.84	0.43
2:I:216:THR:H	2:I:219:GLN:NE2	2.16	0.43
2:I:233:ARG:HE	2:I:238:GLN:CD	2.26	0.43
2:I:236:LYS:HA	2:I:236:LYS:HD3	1.72	0.43
2:I:817:LEU:HD11	2:I:1080:ASN:HD21	1.84	0.43
2:I:1246:ARG:HD2	2:I:1267:GLY:N	2.33	0.43
3:J:282:LEU:HD21	5:L:410:ILE:HG12	2.01	0.43
3:J:531:LYS:HD3	3:J:581:MET:CE	2.49	0.43
3:J:586:GLY:C	3:J:587:LEU:HD12	2.43	0.43
3:J:1045:THR:O	3:J:1062:LEU:HG	2.18	0.43
5:L:110:LEU:O	5:L:382:ALA:HB1	2.18	0.43
5:L:231:THR:HA	5:L:248:GLU:OE1	2.19	0.43
5:L:330:LEU:HA	5:L:333:VAL:HG12	2.01	0.43
5:L:607:LEU:O	5:L:610:PHE:HB2	2.18	0.43
1:G:58:GLU:OE1	1:G:170:ARG:HD3	2.19	0.42
1:G:231:PHE:CE2	1:H:39:LEU:HD13	2.53	0.42
2:I:98:VAL:O	2:I:122:VAL:N	2.40	0.42
2:I:166:SER:O	2:I:167:SER:OG	2.32	0.42
2:I:529:ARG:NH1	2:I:574:SER:HB3	2.34	0.42
2:I:702:THR:HA	2:I:1184:THR:H	1.84	0.42
2:I:885:GLY:HA2	2:I:917:SER:HB2	2.00	0.42
2:I:901:LEU:CD1	2:I:905:ILE:HD11	2.43	0.42
2:I:903:ARG:HH22	2:I:910:ALA:HA	1.82	0.42
2:I:957:LYS:O	2:I:961:SER:OG	2.26	0.42
3:J:432:LEU:HD23	3:J:489:ASN:ND2	2.34	0.42
3:J:480:ALA:HA	3:J:484:MET:HE3	2.01	0.42
3:J:993:GLU:HB3	3:J:995:TYR:HE2	1.84	0.42
3:J:1162:ILE:HD12	3:J:1202:GLU:C	2.44	0.42
5:L:139:GLU:HG3	5:L:350:GLU:O	2.19	0.42
5:L:290:LEU:CB	5:L:337:VAL:HG22	2.48	0.42
5:L:299:LYS:HG3	5:L:302:PHE:CD2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:305:ASP:OD1	1:M:306:VAL:N	2.53	0.42
7:O:63:DT:H3'	7:O:63:DT:OP2	2.18	0.42
7:O:73:DC:H2''	7:O:74:DC:C6	2.53	0.42
8:P:55:DT:H2''	8:P:56:DG:C5'	2.49	0.42
8:P:65:DT:C2'	8:P:66:DT:H71	2.49	0.42
2:I:212:ALA:HB2	2:I:362:ALA:HB1	2.01	0.42
2:I:719:LYS:O	2:I:720:ARG:HG3	2.19	0.42
2:I:753:LEU:CD2	2:I:769:PRO:HG3	2.49	0.42
2:I:847:PRO:O	2:I:889:PRO:HD3	2.19	0.42
2:I:1263:ALA:HB3	2:I:1264:GLN:NE2	2.35	0.42
3:J:210:SER:HB2	8:P:12:DG:H3'	2.00	0.42
3:J:265:LEU:HD23	3:J:265:LEU:HA	1.68	0.42
3:J:611:ILE:HG22	3:J:612:LEU:CD1	2.49	0.42
3:J:1021:ASP:OD2	3:J:1024:THR:HB	2.19	0.42
3:J:1075:ARG:NH2	3:J:1168:GLU:OE2	2.52	0.42
5:L:134:VAL:HG22	5:L:269:LEU:HD11	2.01	0.42
5:L:436:ARG:HG3	5:L:436:ARG:HH11	1.85	0.42
7:O:42:DA:H2''	7:O:43:DA:H5'	2.00	0.42
8:P:38:DC:C4'	8:P:39:DC:H5'	2.49	0.42
1:G:99:ILE:HD13	1:G:143:ARG:HH22	1.84	0.42
1:H:182:ARG:HD2	3:J:581:MET:HE1	2.01	0.42
2:I:298:ALA:HB3	2:I:334:GLU:HB2	2.01	0.42
2:I:425:ILE:HA	2:I:428:VAL:CG1	2.50	0.42
2:I:471:VAL:HB	2:I:498:ILE:HD11	2.00	0.42
3:J:200:GLN:O	3:J:204:GLU:HG3	2.19	0.42
3:J:352:ARG:HH11	8:P:27:DC:C4'	2.32	0.42
3:J:522:GLY:O	3:J:525:MET:HG2	2.20	0.42
5:L:290:LEU:CD1	5:L:336:GLU:HG3	2.37	0.42
5:L:384:LEU:O	5:L:387:VAL:HB	2.20	0.42
5:L:426:LYS:HD3	7:O:52:DA:C4'	2.49	0.42
5:L:426:LYS:HD3	7:O:52:DA:H3'	2.01	0.42
5:L:575:GLU:HB3	5:L:579:GLN:NE2	2.34	0.42
1:G:16:ILE:CD1	1:G:214:GLU:HB2	2.49	0.42
1:H:100:LEU:HD23	1:H:115:ILE:CG2	2.46	0.42
2:I:15:PHE:CG	2:I:1190:ALA:HB2	2.54	0.42
2:I:848:GLU:CD	2:I:888:THR:HG22	2.44	0.42
3:J:138:VAL:CG2	3:J:145:VAL:HB	2.49	0.42
3:J:147:ILE:O	3:J:177:ASP:HB3	2.20	0.42
3:J:294:ASN:HB3	5:L:406:GLN:HE22	1.84	0.42
3:J:364:HIS:HB3	3:J:487:THR:HG23	2.01	0.42
3:J:530:PRO:HB2	3:J:581:MET:HG2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:970:SER:HB3	3:J:972:LYS:CE	2.50	0.42
4:K:31:GLN:HA	4:K:46:THR:HG21	2.01	0.42
5:L:560:ARG:NH1	5:L:566:ASP:OD2	2.52	0.42
1:H:48:LEU:HD22	3:J:535:ARG:HG3	2.01	0.42
2:I:159:SER:O	2:I:161:LYS:HD3	2.18	0.42
2:I:349:GLU:O	2:I:353:VAL:HG22	2.20	0.42
2:I:592:ARG:HG3	2:I:653:MET:HB3	2.01	0.42
3:J:93:THR:HG22	3:J:94:GLN:N	2.31	0.42
3:J:672:LEU:HD23	6:N:48:ARG:HB2	2.01	0.42
3:J:697:MET:HE2	3:J:697:MET:HB3	1.82	0.42
3:J:1280:VAL:HG21	3:J:1285:VAL:HB	2.02	0.42
1:M:311:GLY:C	1:M:312:LEU:HD23	2.45	0.42
2:I:55:SER:CB	2:I:465:ARG:HH12	2.33	0.42
2:I:230:PHE:HB3	2:I:237:LEU:CD1	2.50	0.42
2:I:824:GLN:HE22	2:I:1082:ILE:HD11	1.83	0.42
2:I:840:SER:OG	2:I:1048:LYS:HG2	2.20	0.42
2:I:1291:LEU:HD21	3:J:1351:VAL:HG13	2.02	0.42
3:J:426:ALA:HB1	8:P:26:DC:H1'	2.02	0.42
5:L:135:ALA:HB1	5:L:253:SER:HA	2.02	0.42
8:P:58:DC:H2''	8:P:59:DA:C5'	2.49	0.42
2:I:241:LEU:CD1	2:I:245:ARG:HB2	2.50	0.42
2:I:247:ARG:HH12	2:I:271:ALA:HB2	1.84	0.42
2:I:447:HIS:NE2	2:I:553:THR:HG21	2.35	0.42
2:I:816:ILE:O	2:I:1076:ILE:HA	2.19	0.42
2:I:836:LEU:HD12	2:I:1054:LEU:CD1	2.50	0.42
2:I:1254:VAL:HG13	2:I:1255:THR:H	1.84	0.42
2:I:1327:LEU:HG	2:I:1331:ARG:HH21	1.84	0.42
3:J:150:GLY:HA3	3:J:175:GLU:O	2.19	0.42
3:J:154:LEU:HD23	3:J:158:GLN:NE2	2.35	0.42
3:J:294:ASN:HB3	5:L:406:GLN:NE2	2.35	0.42
3:J:339:ARG:HH12	3:J:798:ARG:HD2	1.83	0.42
3:J:615:LYS:H	3:J:615:LYS:HD3	1.84	0.42
3:J:643:ASP:OD2	3:J:721:SER:HB3	2.20	0.42
3:J:829:GLY:HA2	3:J:993:GLU:HA	2.02	0.42
3:J:931:THR:O	3:J:932:MET:HG2	2.19	0.42
3:J:961:SER:O	3:J:980:THR:HG23	2.19	0.42
3:J:973:LEU:HD12	3:J:974:VAL:N	2.35	0.42
3:J:1063:ASP:HA	3:J:1103:GLY:HA2	2.02	0.42
3:J:1080:ILE:HG13	3:J:1099:TYR:CE2	2.55	0.42
3:J:1135:THR:O	3:J:1135:THR:OG1	2.33	0.42
3:J:1188:GLU:HA	3:J:1188:GLU:OE2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1327:GLU:HG2	3:J:1327:GLU:O	2.18	0.42
5:L:251:LYS:O	5:L:255:VAL:HG22	2.19	0.42
5:L:444:ALA:HA	5:L:457:ILE:HD13	2.01	0.42
5:L:559:LEU:HA	5:L:559:LEU:HD12	1.74	0.42
5:L:586:ARG:HE	7:O:24:DC:H3'	1.84	0.42
5:L:602:SER:N	5:L:605:GLU:OE2	2.53	0.42
1:M:275:ILE:HG23	1:M:280:ASP:HB3	2.02	0.42
7:O:46:DG:H2''	7:O:47:DG:H5'	2.02	0.42
1:H:8:PHE:HD1	1:H:32:GLU:OE2	2.02	0.42
2:I:127:ILE:HG13	2:I:127:ILE:O	2.20	0.42
2:I:257:ALA:HB3	2:I:262:TYR:CD2	2.55	0.42
2:I:270:THR:O	2:I:274:ILE:HG13	2.19	0.42
2:I:618:GLN:O	2:I:621:SER:OG	2.23	0.42
2:I:1101:LEU:HA	3:J:725:MET:SD	2.59	0.42
2:I:1151:LEU:HD21	2:I:1198:LEU:HB2	2.02	0.42
3:J:40:LYS:HE3	3:J:42:GLU:OE2	2.20	0.42
3:J:517:CYS:SG	3:J:518:VAL:N	2.91	0.42
3:J:969:SER:HB3	3:J:1116:SER:CB	2.50	0.42
3:J:1024:THR:HG23	3:J:1125:PRO:CA	2.49	0.42
5:L:376:LYS:O	5:L:380:VAL:HG22	2.19	0.42
7:O:51:DT:C6	7:O:51:DT:H5'	2.55	0.42
8:P:25:DG:C3'	8:P:26:DC:H5''	2.50	0.42
8:P:26:DC:H2'	8:P:27:DC:C6	2.54	0.42
8:P:68:DG:H1'	8:P:69:DT:C5'	2.45	0.42
2:I:623:LEU:HD12	2:I:625:GLU:H	1.85	0.42
3:J:375:GLU:OE1	3:J:378:LYS:HD2	2.19	0.42
3:J:1036:ARG:HA	3:J:1111:ASP:OD1	2.20	0.42
5:L:127:ILE:HD12	5:L:130:VAL:HG23	2.01	0.42
5:L:133:SER:O	5:L:273:MET:HE1	2.20	0.42
5:L:150:ARG:HB2	5:L:150:ARG:HH11	1.85	0.42
1:M:252:ILE:O	1:M:252:ILE:HG22	2.19	0.42
6:N:47:ALA:O	6:N:50:LYS:HB3	2.20	0.42
7:O:35:DG:H2''	7:O:36:DA:N7	2.34	0.42
1:G:14:VAL:HG12	1:G:15:ASP:OD1	2.20	0.42
1:G:59:VAL:CG2	1:G:82:LEU:HD22	2.50	0.42
1:H:19:VAL:O	1:H:19:VAL:HG12	2.20	0.42
2:I:854:ILE:HD11	2:I:885:GLY:HA3	2.02	0.42
2:I:886:LYS:H	2:I:917:SER:CB	2.32	0.42
2:I:1077:SER:CB	3:J:357:VAL:HG12	2.50	0.42
2:I:1258:PRO:HG3	3:J:348:ASP:OD1	2.18	0.42
3:J:162:GLU:O	3:J:166:LEU:HG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:848:VAL:CB	3:J:858:VAL:HG22	2.46	0.42
5:L:295:CYS:SG	5:L:330:LEU:HD12	2.60	0.42
5:L:296:LYS:HD2	5:L:296:LYS:HA	1.81	0.42
5:L:312:SER:O	5:L:341:LEU:HD13	2.19	0.42
6:N:48:ARG:NH1	6:N:55:VAL:HG11	2.33	0.42
8:P:37:DG:C1'	8:P:38:DC:H5'	2.49	0.42
2:I:592:ARG:NH2	2:I:601:ASP:OD2	2.52	0.41
2:I:1117:LEU:HD12	2:I:1195:ILE:HG12	2.02	0.41
3:J:491:LEU:HB2	3:J:904:ALA:O	2.19	0.41
3:J:557:LYS:HE3	3:J:557:LYS:HB2	1.65	0.41
3:J:798:ARG:NH2	3:J:1325:PHE:HB2	2.29	0.41
3:J:1047:THR:CB	3:J:1062:LEU:HD21	2.49	0.41
5:L:102:MET:SD	5:L:388:ILE:HD13	2.60	0.41
5:L:290:LEU:HD22	5:L:333:VAL:CG2	2.50	0.41
5:L:390:ILE:HD11	5:L:435:ILE:CG2	2.50	0.41
7:O:32:DA:H2''	7:O:33:DA:H8	1.85	0.41
1:G:23:HIS:CB	1:G:206:GLU:HA	2.50	0.41
1:G:134:THR:OG1	2:I:773:LEU:HD12	2.20	0.41
1:H:16:ILE:HG23	1:H:16:ILE:O	2.21	0.41
2:I:454:ARG:HG2	2:I:458:GLU:CD	2.45	0.41
2:I:817:LEU:HD21	2:I:1080:ASN:ND2	2.28	0.41
2:I:839:VAL:HG12	2:I:1049:ILE:HG23	2.01	0.41
2:I:928:VAL:HG13	2:I:1052:VAL:CG1	2.50	0.41
3:J:288:PRO:HG3	5:L:380:VAL:CG2	2.48	0.41
3:J:968:ASN:HB3	3:J:1118:GLY:HA3	2.01	0.41
3:J:1167:LYS:HE3	3:J:1174:ARG:CD	2.50	0.41
3:J:1178:THR:HA	3:J:1179:PRO:HD3	1.89	0.41
3:J:1282:TYR:OH	3:J:1286:LYS:HD3	2.19	0.41
7:O:49:DC:H4'	7:O:49:DC:OP1	2.20	0.41
7:O:76:DT:H2''	7:O:77:DA:N7	2.35	0.41
8:P:16:DA:H2''	8:P:17:DA:H8	1.85	0.41
8:P:51:DC:H1'	8:P:52:DT:H5'	2.01	0.41
1:H:11:PRO:HG2	1:H:28:LEU:HD11	2.02	0.41
1:H:208:ASN:CG	1:H:210:THR:HG23	2.45	0.41
2:I:81:ASP:O	2:I:85:CYS:HB2	2.20	0.41
2:I:216:THR:HG1	2:I:219:GLN:CD	2.16	0.41
2:I:232:ILE:HG23	2:I:236:LYS:H	1.85	0.41
2:I:243:PRO:HB2	2:I:278:GLU:HG3	2.01	0.41
2:I:560:PRO:HB3	3:J:776:THR:HG21	2.03	0.41
2:I:718:ALA:HA	2:I:751:TYR:OH	2.20	0.41
3:J:334:LYS:HE3	8:P:25:DG:OP1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:417:ARG:HG2	3:J:418:GLU:HG3	2.01	0.41
3:J:527:LEU:HD13	3:J:548:VAL:CG1	2.50	0.41
3:J:749:LYS:HB2	3:J:750:PRO:CD	2.50	0.41
3:J:1144:LEU:HD23	3:J:1144:LEU:HA	1.72	0.41
3:J:1162:ILE:HD12	3:J:1203:ARG:CA	2.50	0.41
3:J:1172:LYS:HA	3:J:1172:LYS:HD3	1.64	0.41
5:L:96:ASP:CG	5:L:99:ARG:HG3	2.45	0.41
5:L:119:ILE:HG23	5:L:375:ALA:HB1	2.01	0.41
5:L:165:PHE:CD1	5:L:259:PHE:HB2	2.55	0.41
2:I:158:ASP:HA	2:I:442:VAL:CG1	2.49	0.41
2:I:506:PHE:O	2:I:512:SER:OG	2.16	0.41
2:I:658:GLN:O	2:I:661:VAL:HG22	2.20	0.41
2:I:669:PRO:HG3	2:I:1069:ARG:NH2	2.36	0.41
2:I:805:MET:HE1	2:I:1221:PHE:CE1	2.56	0.41
2:I:871:VAL:HG11	2:I:928:VAL:HG21	2.02	0.41
2:I:1303:LYS:HE2	2:I:1303:LYS:HA	2.02	0.41
3:J:143:SER:N	3:J:180:MET:HE2	2.35	0.41
3:J:351:GLY:O	3:J:467:ALA:HA	2.21	0.41
3:J:449:LEU:HD21	3:J:457:TYR:CE2	2.55	0.41
5:L:131:GLN:C	5:L:257:LYS:HD2	2.45	0.41
5:L:290:LEU:CD1	5:L:337:VAL:HG22	2.50	0.41
6:N:32:ILE:O	6:N:32:ILE:HG13	2.20	0.41
1:G:83:LEU:HD23	2:I:694:ARG:NE	2.26	0.41
1:H:44:ARG:HA	1:H:183:ILE:HD12	2.03	0.41
2:I:193:ASN:HB2	2:I:195:PHE:HE2	1.86	0.41
2:I:232:ILE:HG23	2:I:236:LYS:N	2.35	0.41
2:I:699:LEU:HD22	2:I:799:ASN:ND2	2.35	0.41
2:I:839:VAL:HG21	2:I:841:ARG:NH2	2.35	0.41
2:I:865:LEU:HD22	2:I:869:GLY:O	2.20	0.41
2:I:1246:ARG:CZ	2:I:1258:PRO:HB3	2.50	0.41
2:I:1295:SER:OG	3:J:347:VAL:HG22	2.20	0.41
2:I:1341:ASP:HB2	3:J:18:ASP:H	1.84	0.41
3:J:68:TYR:HA	3:J:92:VAL:CG2	2.50	0.41
3:J:148:GLU:HG3	3:J:148:GLU:O	2.20	0.41
3:J:262:THR:O	5:L:507:MET:HB2	2.19	0.41
3:J:423:LEU:HD23	3:J:449:LEU:CD1	2.49	0.41
3:J:681:LYS:HA	3:J:681:LYS:HD2	1.84	0.41
3:J:708:ASN:HB2	3:J:711:GLY:O	2.21	0.41
3:J:754:ILE:HD13	6:N:23:ILE:HD12	2.02	0.41
3:J:1346:GLY:HA3	3:J:1349:GLU:OE1	2.20	0.41
5:L:98:VAL:HG23	5:L:402:LEU:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:150:ARG:HB3	5:L:150:ARG:NH1	2.35	0.41
5:L:471:LEU:HD23	5:L:472:GLN:H	1.84	0.41
5:L:582:VAL:HG21	5:L:587:ILE:HD11	2.03	0.41
1:M:281:LEU:HD23	1:M:282:VAL:HA	2.02	0.41
1:G:58:GLU:OE1	1:G:170:ARG:HB3	2.20	0.41
1:H:44:ARG:HD3	1:H:185:TYR:HE1	1.86	0.41
1:H:88:LEU:HD21	1:H:115:ILE:CD1	2.50	0.41
2:I:98:VAL:CG2	2:I:124:MET:HE3	2.42	0.41
2:I:156:PHE:CD2	2:I:177:ILE:HD12	2.55	0.41
2:I:198:ILE:HG12	2:I:369:MET:HE1	2.01	0.41
3:J:259:ARG:HG3	8:P:31:DG:H21	1.82	0.41
3:J:278:ARG:HH21	5:L:407:GLU:CG	2.33	0.41
3:J:840:LEU:HB2	3:J:869:CYS:SG	2.60	0.41
3:J:1022:PRO:HB2	3:J:1023:HIS:CD2	2.55	0.41
3:J:1081:VAL:HG23	3:J:1082:ASP:O	2.19	0.41
5:L:491:GLU:C	5:L:494:ILE:HG22	2.45	0.41
5:L:511:ILE:HD12	5:L:511:ILE:HA	1.87	0.41
7:O:56:DC:P	7:O:56:DC:H3'	2.61	0.41
8:P:16:DA:H2''	8:P:17:DA:C8	2.55	0.41
1:G:89:ALA:HB3	1:G:124:VAL:CG1	2.50	0.41
2:I:241:LEU:HG	2:I:246:LEU:CD1	2.50	0.41
2:I:519:ASN:ND2	2:I:796:LEU:HD23	2.34	0.41
2:I:990:ASP:C	2:I:994:ARG:HH12	2.28	0.41
2:I:1048:LYS:HE3	2:I:1048:LYS:HB2	1.73	0.41
3:J:582:ILE:HG22	3:J:620:PHE:HE1	1.85	0.41
3:J:641:ILE:HD12	3:J:644:MET:CE	2.42	0.41
3:J:782:GLY:HA2	6:N:11:VAL:HG23	2.02	0.41
3:J:1032:SER:HB3	3:J:1116:SER:HA	2.03	0.41
5:L:134:VAL:CG2	5:L:269:LEU:HD11	2.51	0.41
5:L:148:TYR:OH	5:L:218:ARG:HG3	2.21	0.41
5:L:492:ASP:HA	5:L:495:ARG:CD	2.50	0.41
6:N:7:GLU:O	6:N:11:VAL:HG13	2.21	0.41
6:N:23:ILE:O	6:N:26:LYS:HB2	2.20	0.41
8:P:67:DT:H2''	8:P:68:DG:H8	1.84	0.41
2:I:24:VAL:O	2:I:24:VAL:HG13	2.20	0.41
2:I:232:ILE:HD12	2:I:325:LEU:CD1	2.51	0.41
2:I:618:GLN:HG2	2:I:619:ALA:N	2.36	0.41
2:I:870:ILE:CG2	2:I:931:VAL:HG11	2.48	0.41
2:I:1141:LEU:HD23	2:I:1173:ALA:CB	2.51	0.41
2:I:1240:ASP:OD1	3:J:445:LYS:NZ	2.38	0.41
2:I:1277:ALA:HB3	3:J:434:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:421:VAL:CG2	3:J:439:PRO:HG3	2.50	0.41
3:J:643:ASP:HB3	3:J:720:ASN:HD21	1.84	0.41
3:J:650:LYS:NZ	3:J:760:THR:O	2.54	0.41
3:J:707:ILE:O	3:J:714:GLU:N	2.31	0.41
3:J:803:VAL:HA	3:J:1313:SER:CB	2.50	0.41
3:J:871:LEU:O	3:J:874:GLU:HB2	2.21	0.41
3:J:923:ILE:HG21	3:J:1145:PHE:HE2	1.86	0.41
3:J:1179:PRO:HD3	3:J:1184:ASP:HB3	2.02	0.41
5:L:227:GLN:HB3	5:L:252:LEU:HD13	2.03	0.41
5:L:277:MET:HB2	5:L:362:ASN:ND2	2.35	0.41
5:L:279:ARG:HH22	5:L:346:GLN:CD	2.29	0.41
6:N:37:CYS:SG	6:N:58:CYS:HB2	2.61	0.41
1:G:42:ALA:HB1	1:G:224:LEU:HD11	2.03	0.41
1:G:42:ALA:HB1	1:G:224:LEU:CD1	2.51	0.41
1:H:151:GLY:HA2	1:H:178:SER:OG	2.21	0.41
2:I:110:PRO:HD2	2:I:111:GLU:CD	2.46	0.41
2:I:145:ILE:CB	2:I:456:VAL:HG22	2.46	0.41
2:I:299:LYS:HE3	2:I:299:LYS:HB2	1.83	0.41
2:I:303:ASP:HB3	2:I:308:GLU:CG	2.50	0.41
2:I:373:GLY:O	5:L:91:ILE:HD13	2.20	0.41
2:I:511:LEU:HD23	2:I:511:LEU:HA	1.82	0.41
2:I:520:PRO:HG3	2:I:714:VAL:HG11	2.02	0.41
2:I:578:TYR:HB3	2:I:590:PRO:HG2	2.01	0.41
2:I:705:GLU:HB2	2:I:794:LEU:CB	2.43	0.41
2:I:796:LEU:N	2:I:1231:TYR:OH	2.52	0.41
2:I:818:VAL:HG12	2:I:819:SER:O	2.21	0.41
2:I:877:VAL:HG11	2:I:883:LEU:CD2	2.50	0.41
2:I:1290:MET:SD	2:I:1294:LYS:HE3	2.61	0.41
3:J:58:CYS:CB	3:J:61:ILE:HD12	2.51	0.41
3:J:66:LYS:HD2	3:J:69:GLU:OE1	2.20	0.41
3:J:480:ALA:O	3:J:485:MET:N	2.54	0.41
3:J:516:ASP:OD1	3:J:516:ASP:N	2.45	0.41
3:J:636:GLY:O	3:J:638:SER:N	2.54	0.41
3:J:648:GLU:O	3:J:648:GLU:HG2	2.21	0.41
3:J:672:LEU:HD23	6:N:48:ARG:CA	2.51	0.41
3:J:840:LEU:HD12	3:J:865:HIS:HA	2.02	0.41
3:J:981:GLU:OE2	3:J:983:LYS:HE2	2.20	0.41
3:J:1040:MET:HG2	3:J:1076:PRO:HB2	2.03	0.41
3:J:1046:ILE:CA	3:J:1062:LEU:HG	2.51	0.41
3:J:1145:PHE:HD1	3:J:1145:PHE:HA	1.75	0.41
3:J:1164:SER:O	3:J:1175:LEU:HD12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1181:ASP:OD1	3:J:1181:ASP:N	2.53	0.41
3:J:1194:ARG:HD2	3:J:1194:ARG:HA	1.86	0.41
4:K:30:MET:HE1	4:K:49:ILE:CB	2.41	0.41
4:K:62:GLN:O	4:K:66:VAL:HG23	2.20	0.41
5:L:316:PHE:CE1	5:L:330:LEU:HD23	2.55	0.41
5:L:344:LEU:O	5:L:347:ILE:HB	2.20	0.41
5:L:547:VAL:HG11	5:L:598:LEU:HD11	2.03	0.41
5:L:611:LEU:HD23	5:L:611:LEU:HA	1.96	0.41
7:O:63:DT:H3'	7:O:63:DT:P	2.61	0.41
8:P:33:DA:H8	8:P:33:DA:H5''	1.86	0.41
1:G:82:LEU:HB3	1:G:173:VAL:HG12	2.03	0.41
2:I:78:PRO:HG3	2:I:129:LEU:HD12	2.03	0.41
2:I:238:GLN:CA	2:I:285:ILE:O	2.67	0.41
2:I:243:PRO:HG2	2:I:278:GLU:CG	2.50	0.41
2:I:720:ARG:NH2	2:I:749:ASP:OD2	2.54	0.41
2:I:985:GLU:O	2:I:989:LEU:HD13	2.21	0.41
3:J:347:VAL:HG12	3:J:348:ASP:O	2.21	0.41
3:J:449:LEU:HD12	3:J:449:LEU:HA	1.91	0.41
3:J:499:ILE:HD12	3:J:499:ILE:HA	1.91	0.41
3:J:759:ILE:HG23	3:J:771:GLN:CB	2.51	0.41
3:J:822:MET:HE3	3:J:842:ARG:NH1	2.36	0.41
3:J:1015:GLU:O	3:J:1017:VAL:HG23	2.21	0.41
3:J:1038:THR:O	3:J:1076:PRO:HA	2.21	0.41
3:J:1062:LEU:HB3	3:J:1066:GLU:HG2	2.03	0.41
3:J:1151:LYS:HD3	3:J:1151:LYS:HA	1.64	0.41
3:J:1173:ARG:HH12	3:J:1192:LYS:HB2	1.85	0.41
3:J:1237:VAL:HG11	3:J:1253:ILE:HD13	2.03	0.41
5:L:465:ARG:HB3	5:L:465:ARG:NH1	2.36	0.41
1:G:61:ILE:CD1	1:G:78:ILE:HD12	2.51	0.40
2:I:35:PHE:O	2:I:39:ILE:HG22	2.20	0.40
2:I:375:PRO:HD3	5:L:103:ARG:CG	2.50	0.40
2:I:510:GLN:OE1	2:I:534:GLY:HA2	2.21	0.40
2:I:532:ALA:C	2:I:533:LEU:HD23	2.46	0.40
2:I:817:LEU:HD11	2:I:1080:ASN:ND2	2.35	0.40
2:I:898:GLU:CG	5:L:544:THR:HG21	2.51	0.40
2:I:1116:HIS:CE1	3:J:641:ILE:HG22	2.56	0.40
2:I:1328:LYS:HA	2:I:1328:LYS:HD3	1.82	0.40
3:J:178:ALA:H	3:J:179:LYS:NZ	2.19	0.40
3:J:451:PRO:HD2	3:J:625:MET:SD	2.61	0.40
3:J:452:LEU:HD13	3:J:500:ILE:HG23	2.02	0.40
3:J:677:GLU:HG2	6:N:52:PHE:CZ	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:756:GLU:O	3:J:758:PRO:HD3	2.21	0.40
3:J:1068:THR:HG23	3:J:1071:GLY:H	1.86	0.40
3:J:1348:LYS:O	3:J:1352:ILE:HG13	2.21	0.40
5:L:91:ILE:HD13	5:L:103:ARG:NE	2.36	0.40
5:L:577:GLY:O	5:L:581:ASP:HA	2.21	0.40
8:P:53:DT:H6	8:P:53:DT:H2'	1.69	0.40
1:H:31:LEU:O	1:H:198:LEU:HD12	2.21	0.40
2:I:203:LYS:O	2:I:204:LEU:HG	2.21	0.40
2:I:468:LEU:O	2:I:471:VAL:HG12	2.21	0.40
2:I:685:MET:HE2	2:I:1073:LYS:HG3	2.03	0.40
2:I:1133:LYS:HB2	2:I:1133:LYS:HE3	1.87	0.40
3:J:142:GLU:O	3:J:142:GLU:HG2	2.20	0.40
3:J:964:LYS:HB2	3:J:964:LYS:HE2	1.87	0.40
3:J:1027:VAL:O	3:J:1121:LEU:HD13	2.21	0.40
3:J:1048:ARG:CZ	3:J:1059:LEU:HD12	2.51	0.40
4:K:15:ASN:C	4:K:17:PHE:H	2.28	0.40
4:K:71:GLU:HA	4:K:74:GLU:HG2	2.02	0.40
5:L:348:GLU:HA	5:L:355:ILE:HD11	2.02	0.40
5:L:547:VAL:CG1	5:L:598:LEU:HD11	2.51	0.40
5:L:573:LEU:HA	5:L:576:VAL:HB	2.02	0.40
6:N:28:ASN:HD21	6:N:54:GLY:CA	2.34	0.40
2:I:101:ARG:HA	2:I:119:GLU:HA	2.02	0.40
3:J:79:LYS:HB2	5:L:569:THR:HB	2.02	0.40
3:J:215:LYS:O	3:J:218:THR:HG22	2.21	0.40
3:J:259:ARG:HD2	3:J:259:ARG:HA	1.88	0.40
3:J:582:ILE:HG23	3:J:623:GLN:CB	2.51	0.40
3:J:639:VAL:O	3:J:639:VAL:HG13	2.21	0.40
3:J:848:VAL:O	3:J:856:ILE:HA	2.22	0.40
3:J:1049:GLN:HB2	3:J:1060:VAL:HB	2.02	0.40
3:J:1060:VAL:CG2	3:J:1106:ILE:HG23	2.48	0.40
3:J:1164:SER:HB2	3:J:1200:GLU:OE2	2.21	0.40
3:J:1361:THR:CG2	4:K:21:LEU:HG	2.51	0.40
5:L:148:TYR:C	5:L:161:LEU:HD11	2.46	0.40
1:G:135:ASP:O	1:G:138:ALA:HB3	2.22	0.40
2:I:84:GLU:OE2	2:I:88:ARG:HB2	2.22	0.40
2:I:245:ARG:HD2	2:I:337:PHE:CE2	2.57	0.40
2:I:727:VAL:HG12	2:I:728:ASP:N	2.37	0.40
2:I:810:TYR:CE2	2:I:1078:LYS:HD2	2.57	0.40
3:J:391:ALA:CB	3:J:397:ALA:HB2	2.52	0.40
3:J:527:LEU:HD21	3:J:536:LEU:HD23	2.04	0.40
3:J:689:ALA:O	3:J:693:VAL:HG23	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:766:GLY:O	3:J:767:LEU:HD12	2.22	0.40
3:J:903:LEU:HD21	3:J:1249:ASN:ND2	2.37	0.40
3:J:986:ASP:OD2	3:J:990:ARG:HG2	2.21	0.40
3:J:1022:PRO:HG2	3:J:1023:HIS:HD2	1.86	0.40
3:J:1271:SER:H	3:J:1299:GLY:CA	2.29	0.40
5:L:305:LEU:HD22	5:L:315:TRP:HA	2.02	0.40
5:L:426:LYS:CB	7:O:52:DA:H5'	2.51	0.40
5:L:426:LYS:CD	7:O:52:DA:H5'	2.43	0.40
5:L:463:LEU:HD13	5:L:494:ILE:CD1	2.50	0.40
1:M:262:LEU:HD23	1:M:302:GLU:CB	2.47	0.40
1:M:321:TRP:HA	1:M:322:PRO:O	2.21	0.40
8:P:12:DG:H2''	8:P:13:DG:C8	2.56	0.40
1:G:70:THR:O	1:G:70:THR:HG23	2.22	0.40
1:G:162:GLU:O	1:G:163:GLU:HG2	2.21	0.40
1:H:74:VAL:HA	1:H:132:HIS:O	2.20	0.40
2:I:53:PHE:O	2:I:57:PHE:HB2	2.22	0.40
2:I:233:ARG:HE	2:I:238:GLN:NE2	2.19	0.40
2:I:348:SER:O	2:I:352:ARG:HG2	2.20	0.40
2:I:856:ASN:O	2:I:857:VAL:HG13	2.22	0.40
2:I:870:ILE:HG22	2:I:871:VAL:H	1.86	0.40
2:I:878:THR:HG22	2:I:879:GLY:H	1.84	0.40
2:I:960:LEU:HD12	2:I:960:LEU:HA	1.84	0.40
2:I:1211:ARG:HE	2:I:1220:GLN:HE22	1.68	0.40
2:I:1290:MET:HG3	2:I:1290:MET:O	2.22	0.40
3:J:73:GLY:C	3:J:76:LYS:HE3	2.47	0.40
3:J:123:ARG:NH2	3:J:1334:GLU:HG2	2.36	0.40
3:J:409:TRP:CZ3	3:J:412:LEU:HD13	2.56	0.40
3:J:583:VAL:HA	3:J:620:PHE:CE1	2.56	0.40
3:J:670:SER:O	3:J:672:LEU:HD12	2.22	0.40
3:J:827:GLU:OE1	3:J:827:GLU:HA	2.22	0.40
3:J:952:VAL:HG22	3:J:1015:GLU:HB3	2.03	0.40
3:J:1046:ILE:HD12	3:J:1059:LEU:HB3	2.03	0.40
3:J:1184:ASP:OD1	3:J:1184:ASP:N	2.54	0.40
3:J:1203:ARG:C	3:J:1203:ARG:HD2	2.47	0.40
3:J:1242:ARG:HD2	3:J:1242:ARG:HA	1.83	0.40
3:J:1317:GLU:HA	3:J:1317:GLU:OE1	2.22	0.40
3:J:1323:ALA:HB2	3:J:1331:VAL:CG1	2.51	0.40
5:L:390:ILE:O	5:L:393:LYS:HB2	2.21	0.40
5:L:392:LYS:HE2	5:L:393:LYS:NZ	2.37	0.40
1:M:271:LYS:HE2	1:M:271:LYS:HB2	1.86	0.40
8:P:41:DT:H2''	8:P:42:DT:OP2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	G	227/329 (69%)	195 (86%)	32 (14%)	0	100	100
1	H	215/329 (65%)	188 (87%)	26 (12%)	1 (0%)	24	56
1	M	71/329 (22%)	63 (89%)	8 (11%)	0	100	100
2	I	1339/1342 (100%)	1177 (88%)	158 (12%)	4 (0%)	36	65
3	J	1339/1430 (94%)	1187 (89%)	152 (11%)	0	100	100
4	K	77/91 (85%)	69 (90%)	8 (10%)	0	100	100
5	L	467/616 (76%)	422 (90%)	45 (10%)	0	100	100
6	N	70/72 (97%)	62 (89%)	6 (9%)	2 (3%)	3	26
All	All	3805/4538 (84%)	3363 (88%)	435 (11%)	7 (0%)	44	72

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	I	546	GLU
2	I	974	ARG
6	N	29	ALA
2	I	443	ASP
6	N	30	HIS
1	H	94	GLY
2	I	199	ASP

5.3.2 Protein sidechains [i](#)

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	G	193/286 (68%)	191 (99%)	2 (1%)	68	74
1	H	184/286 (64%)	182 (99%)	2 (1%)	65	73
1	M	65/286 (23%)	65 (100%)	0	100	100
2	I	1155/1157 (100%)	1149 (100%)	6 (0%)	81	80
3	J	1127/1189 (95%)	1124 (100%)	3 (0%)	86	83
4	K	67/75 (89%)	67 (100%)	0	100	100
5	L	421/543 (78%)	421 (100%)	0	100	100
6	N	61/61 (100%)	61 (100%)	0	100	100
All	All	3273/3883 (84%)	3260 (100%)	13 (0%)	81	81

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	118	ASP
1	G	177	TYR
1	H	46	ILE
1	H	83	LEU
2	I	57	PHE
2	I	199	ASP
2	I	516	ASP
2	I	705	GLU
2	I	750	ILE
2	I	1233	LEU
3	J	316	ILE
3	J	1031	VAL
3	J	1132	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	23	HIS
1	H	93	GLN
2	I	65	ASN
2	I	69	GLN
2	I	139	ASN
2	I	165	HIS

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Mol	Chain	Res	Type
2	I	314	ASN
2	I	526	HIS
2	I	551	HIS
2	I	618	GLN
2	I	649	GLN
2	I	761	GLN
2	I	766	ASN
2	I	799	ASN
2	I	824	GLN
2	I	832	HIS
2	I	932	GLN
2	I	1080	ASN
2	I	1116	HIS
2	I	1135	GLN
2	I	1220	GLN
2	I	1264	GLN
2	I	1268	GLN
3	J	335	GLN
3	J	341	ASN
3	J	489	ASN
3	J	560	ASN
3	J	680	ASN
3	J	720	ASN
3	J	777	HIS
3	J	861	ASN
3	J	875	ASN
3	J	910	ASN
3	J	951	GLN
3	J	954	ASN
3	J	1023	HIS
3	J	1227	HIS
3	J	1249	ASN
4	K	75	GLN
5	L	227	GLN
5	L	246	GLN
5	L	265	GLN
5	L	271	ASN
5	L	472	GLN
6	N	28	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 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
9	1N7	J	1504	-	30,30,46	5.20	15 (50%)	47,48,72	2.42	18 (38%)
9	1N7	I	1401	-	30,30,46	4.94	14 (46%)	47,48,72	2.22	14 (29%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	1N7	J	1504	-	-	0/7/72/92	0/4/4/4
9	1N7	I	1401	-	-	2/7/72/92	0/4/4/4

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	J	1504	1N7	C3-C19	19.11	1.84	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	I	1401	1N7	C3-C19	17.77	1.82	1.53
9	J	1504	1N7	C3-C4	12.46	1.73	1.53
9	I	1401	1N7	C3-C4	11.27	1.71	1.53
9	I	1401	1N7	C5-C4	-9.04	1.40	1.54
9	J	1504	1N7	C5-C4	-8.62	1.41	1.54
9	I	1401	1N7	C2-C19	-7.83	1.42	1.56
9	J	1504	1N7	C2-C19	-7.59	1.42	1.56
9	I	1401	1N7	C8-C7	5.79	1.69	1.54
9	J	1504	1N7	C8-C7	5.65	1.69	1.54
9	J	1504	1N7	C5-C9	4.61	1.63	1.55
9	I	1401	1N7	O4-C4	-4.07	1.36	1.43
9	J	1504	1N7	O4-C4	-4.05	1.36	1.43
9	J	1504	1N7	C2-C15	3.59	1.61	1.55
9	I	1401	1N7	C5-C9	3.55	1.61	1.55
9	I	1401	1N7	C7-C6	3.46	1.61	1.54
9	J	1504	1N7	C7-C6	3.45	1.61	1.54
9	I	1401	1N7	C5-C6	-3.41	1.49	1.55
9	I	1401	1N7	C18-C6	-3.39	1.47	1.53
9	J	1504	1N7	C14-C15	-3.30	1.48	1.53
9	J	1504	1N7	C10-C5	3.00	1.59	1.54
9	I	1401	1N7	C14-C15	-2.90	1.49	1.53
9	J	1504	1N7	C1-C2	2.87	1.59	1.54
9	I	1401	1N7	C2-C15	2.86	1.59	1.55
9	J	1504	1N7	C18-C6	-2.75	1.48	1.53
9	I	1401	1N7	O2-C13	-2.49	1.36	1.43
9	J	1504	1N7	C5-C6	-2.48	1.51	1.55
9	I	1401	1N7	C1-C2	2.47	1.58	1.54
9	J	1504	1N7	O2-C13	-2.36	1.36	1.43

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	J	1504	1N7	C9-C5-C6	5.93	106.06	100.11
9	J	1504	1N7	C9-C5-C4	-5.55	112.67	117.67
9	I	1401	1N7	C7-C6-C18	-5.00	111.49	118.36
9	I	1401	1N7	C19-C3-C4	-4.97	107.80	114.29
9	I	1401	1N7	C9-C5-C4	-4.62	113.51	117.67
9	I	1401	1N7	C3-C19-C18	-4.42	104.36	110.89
9	J	1504	1N7	C14-C13-C12	-4.40	105.24	110.62
9	J	1504	1N7	C1-C12-C13	-4.12	105.03	110.48
9	J	1504	1N7	C7-C6-C5	3.96	107.38	103.54
9	I	1401	1N7	C2-C19-C18	3.90	116.18	111.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	J	1504	1N7	C7-C6-C18	-3.89	113.02	118.36
9	I	1401	1N7	C5-C6-C18	3.79	119.51	114.72
9	J	1504	1N7	C16-C17-C18	-3.54	107.63	111.50
9	I	1401	1N7	C6-C5-C4	3.49	110.60	107.42
9	J	1504	1N7	C8-C9-C20	-3.45	106.96	112.18
9	J	1504	1N7	C19-C18-C17	-3.41	107.56	111.86
9	I	1401	1N7	C19-C18-C17	-3.31	107.69	111.86
9	I	1401	1N7	C16-C15-C2	-3.30	109.15	112.66
9	J	1504	1N7	C21-C20-C22	-3.20	105.39	110.34
9	J	1504	1N7	C2-C19-C18	3.13	115.33	111.84
9	I	1401	1N7	C8-C9-C20	-3.09	107.50	112.18
9	J	1504	1N7	C6-C18-C17	3.07	115.93	111.85
9	J	1504	1N7	C10-C5-C4	-3.05	106.00	109.06
9	I	1401	1N7	C21-C20-C22	-2.99	105.70	110.34
9	I	1401	1N7	C14-C13-C12	-2.99	106.97	110.62
9	J	1504	1N7	C15-C14-C13	-2.71	108.62	112.71
9	J	1504	1N7	C10-C5-C6	2.43	115.02	111.20
9	I	1401	1N7	C11-C2-C15	-2.37	106.47	110.44
9	J	1504	1N7	C8-C9-C5	2.33	105.80	103.54
9	J	1504	1N7	C16-C15-C2	-2.18	110.34	112.66
9	I	1401	1N7	C8-C7-C6	-2.15	100.93	105.14
9	J	1504	1N7	C5-C6-C18	2.03	117.29	114.72

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	I	1401	1N7	C9-C20-C22-C23
9	I	1401	1N7	C21-C20-C22-C23

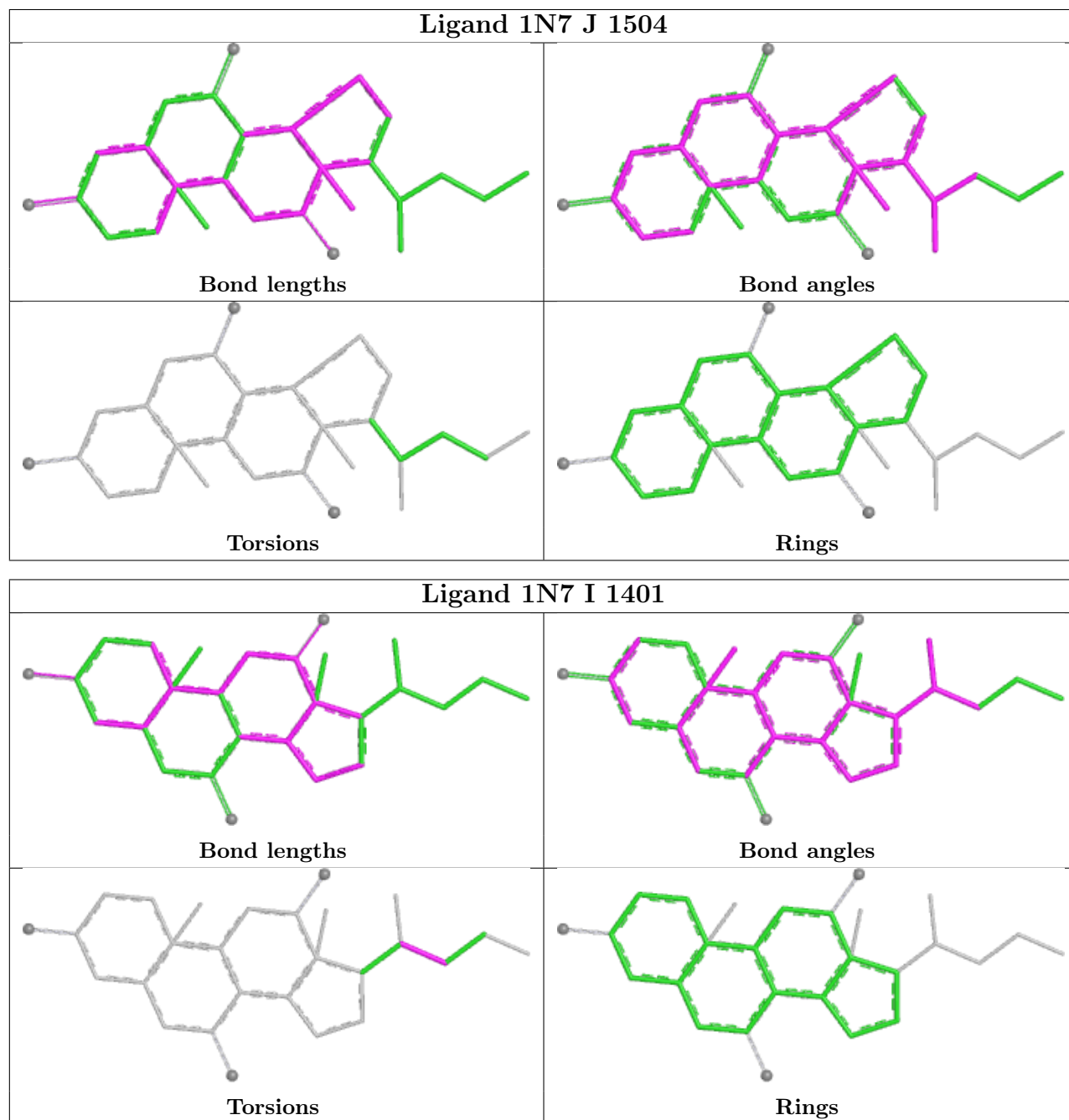
There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	J	1504	1N7	5	0
9	I	1401	1N7	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

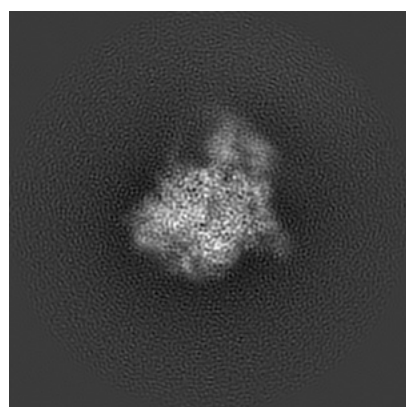
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20466. These allow visual inspection of the internal detail of the map and identification of artifacts.

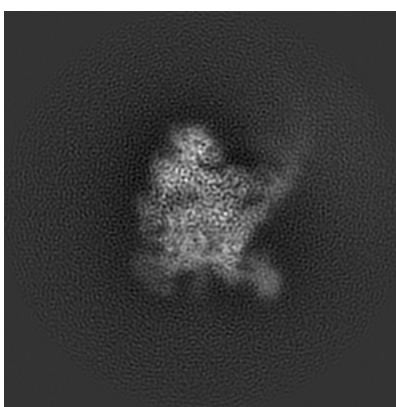
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

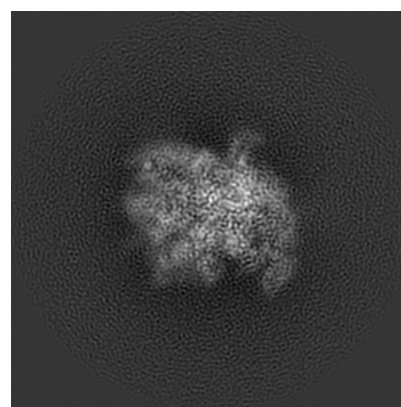
6.1.1 Primary map



X



Y

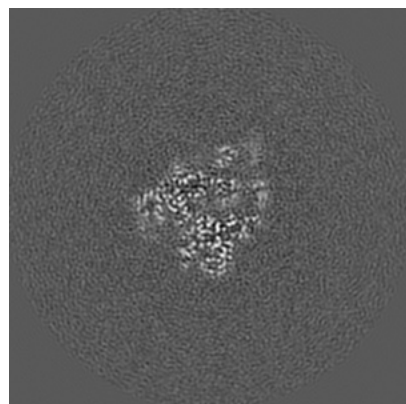


Z

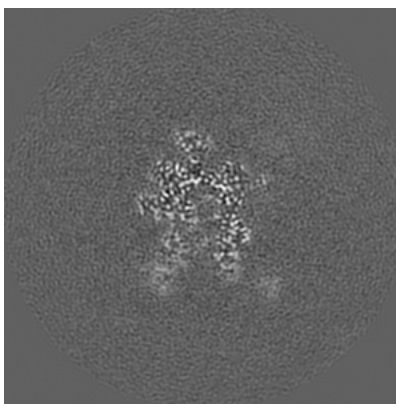
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

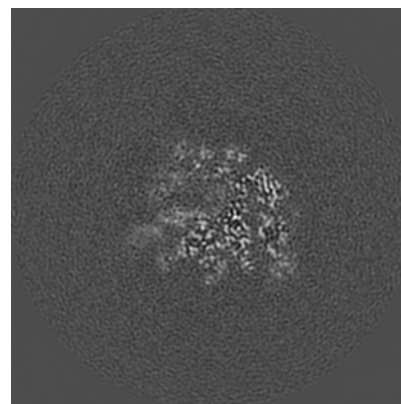
6.2.1 Primary map



X Index: 128



Y Index: 128

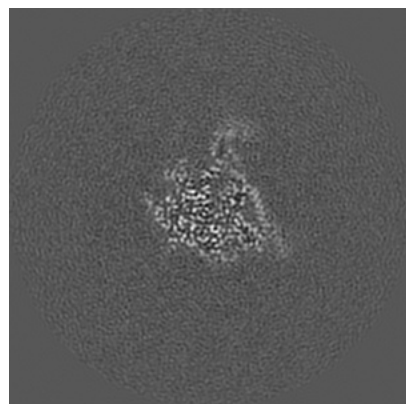


Z Index: 128

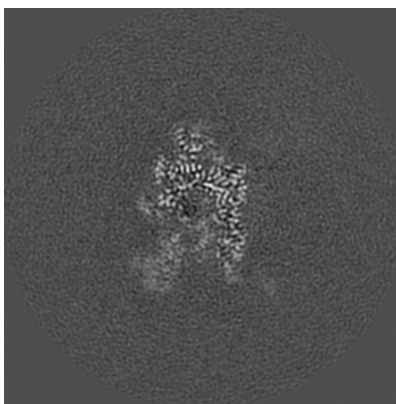
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

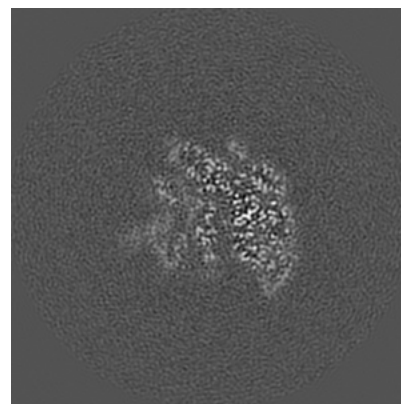
6.3.1 Primary map



X Index: 147



Y Index: 125

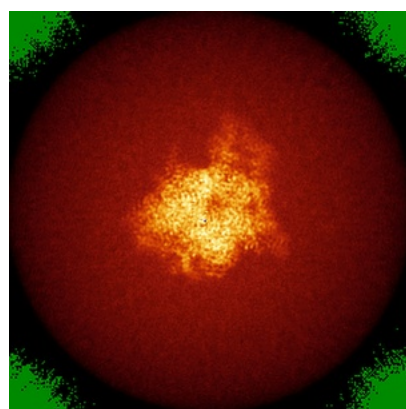


Z Index: 121

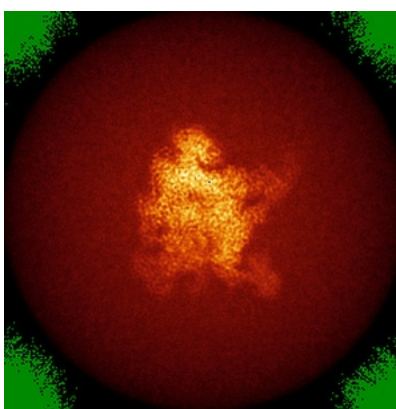
The images above show the largest variance slices of the map in three orthogonal directions.

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

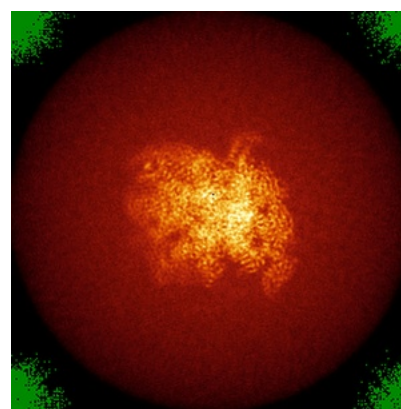
6.4.1 Primary map



X



Y

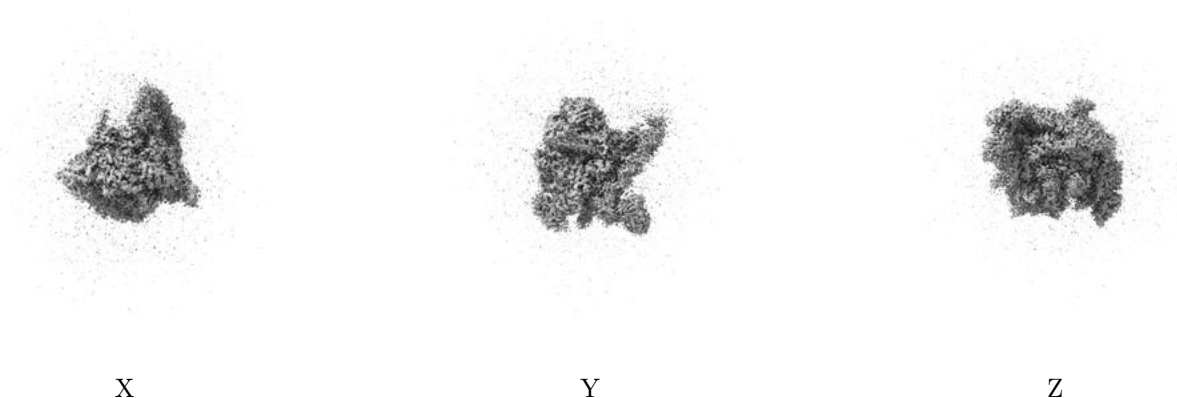


Z

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 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

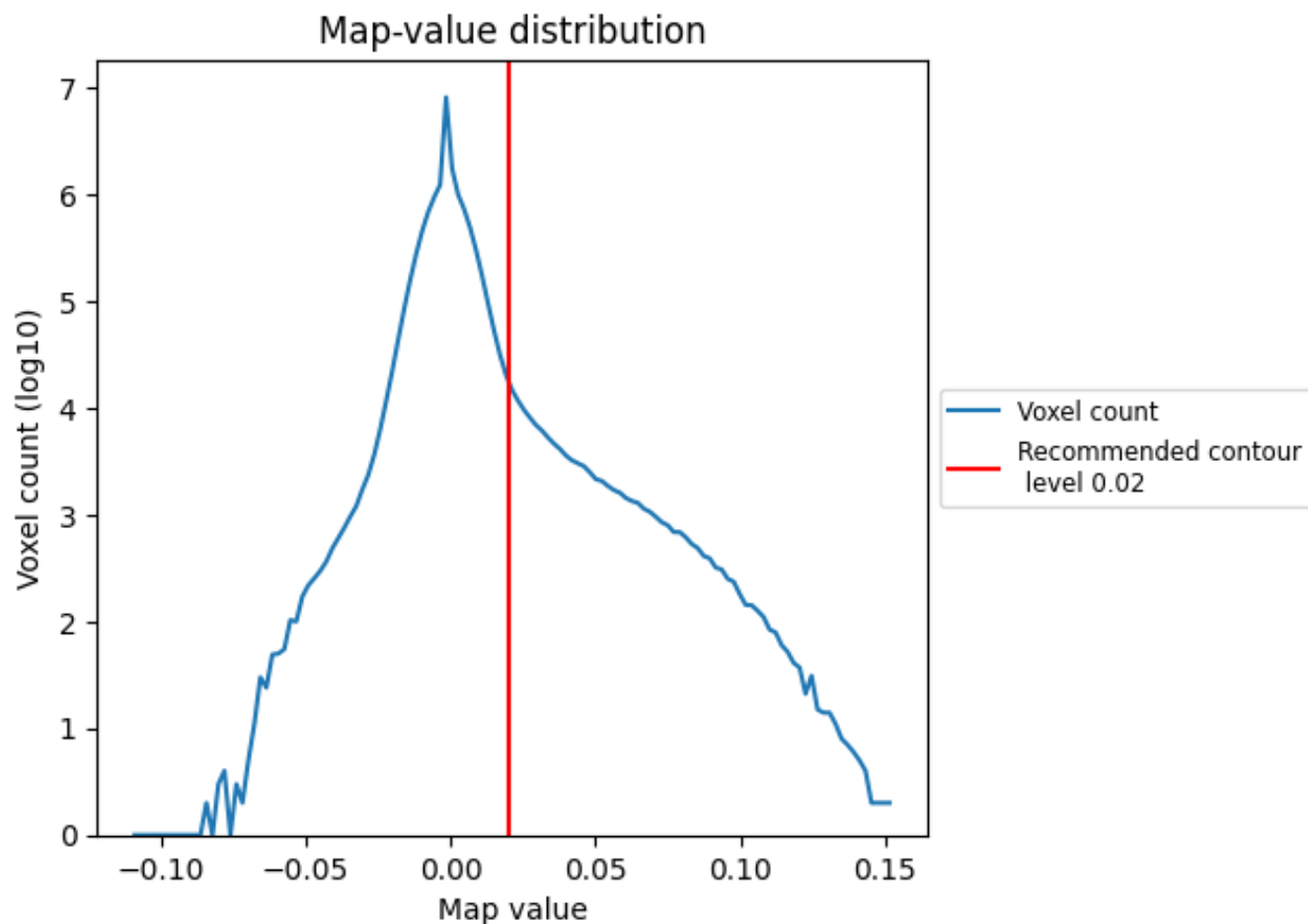
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

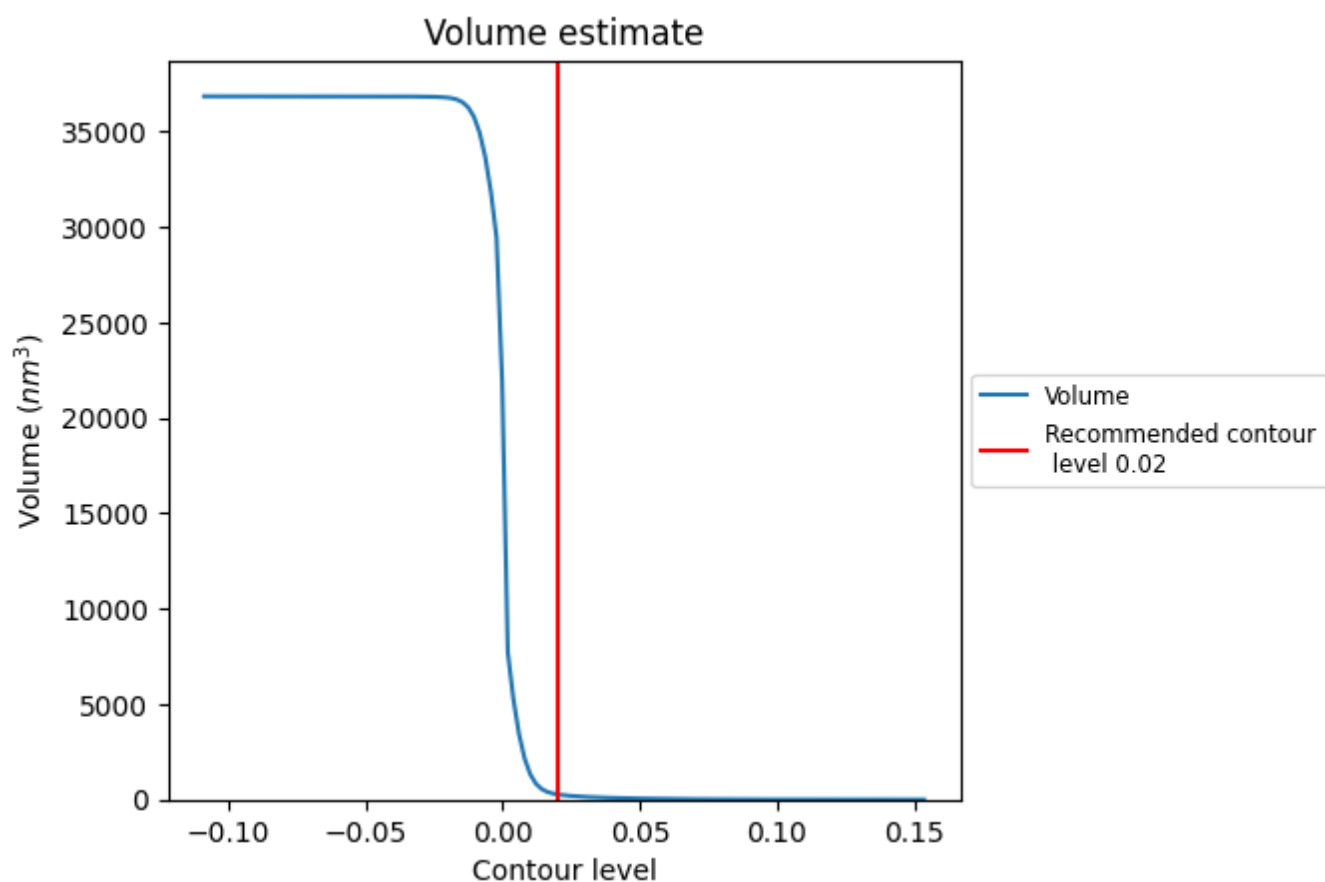
This section contains the results of statistical analysis of the map.

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.

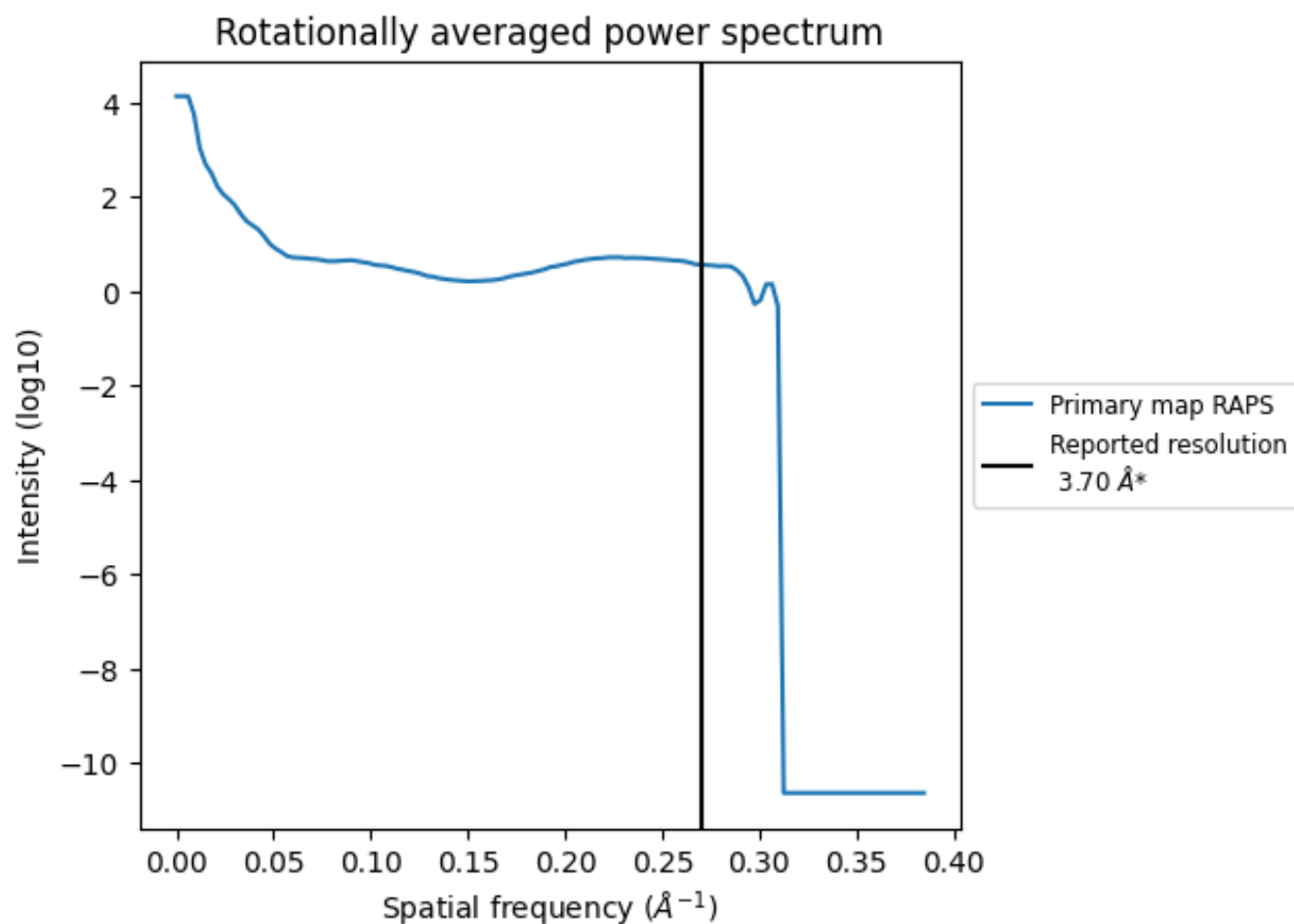
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 270 nm^3 ; this corresponds to an approximate mass of 244 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 ⓘ

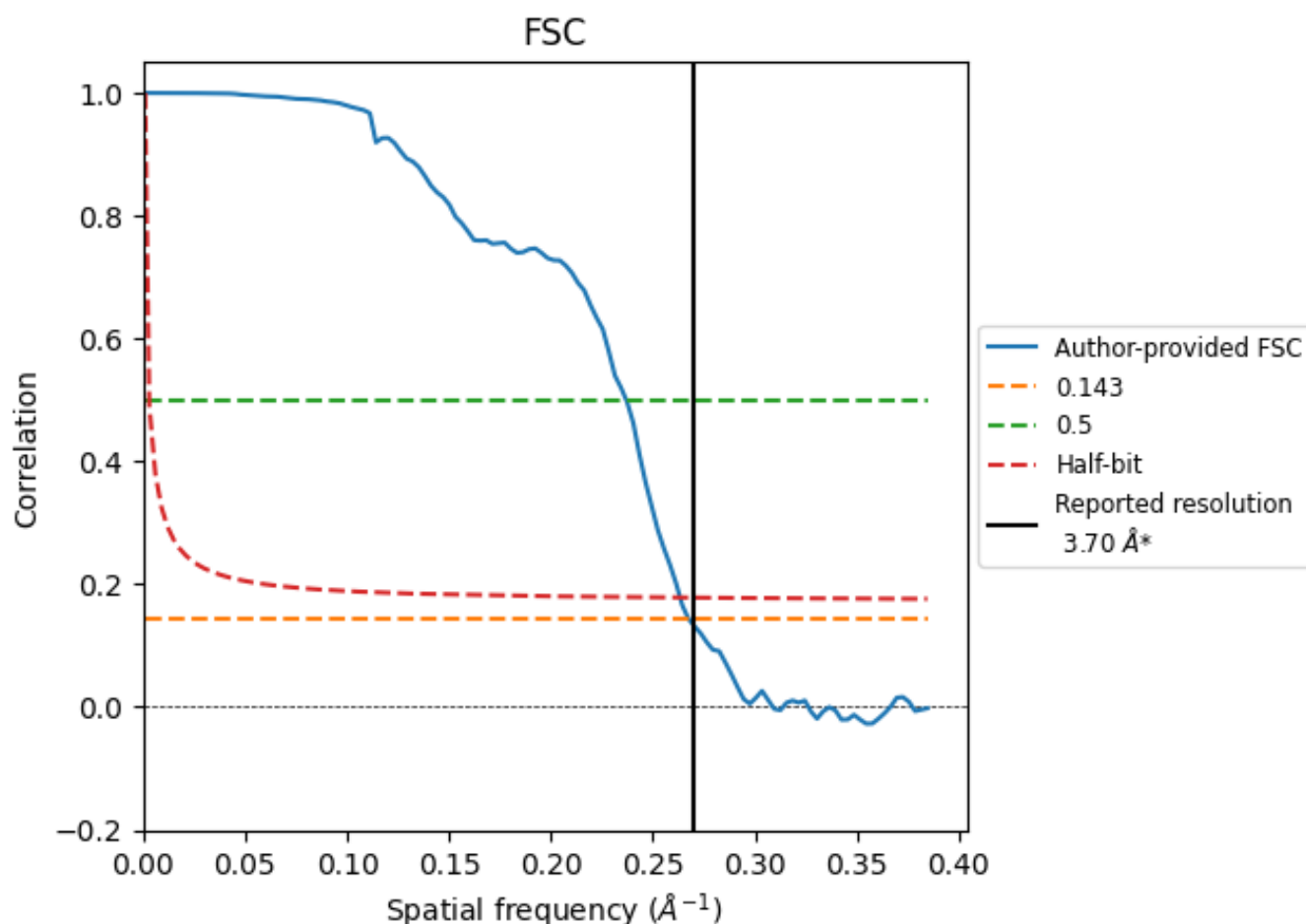


*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

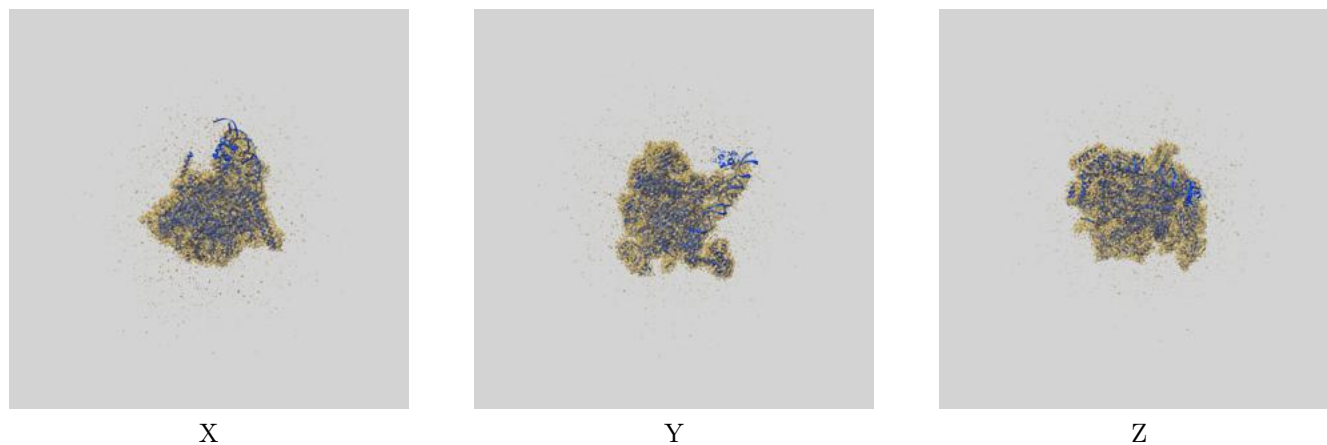
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	3.74	4.22	3.80
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

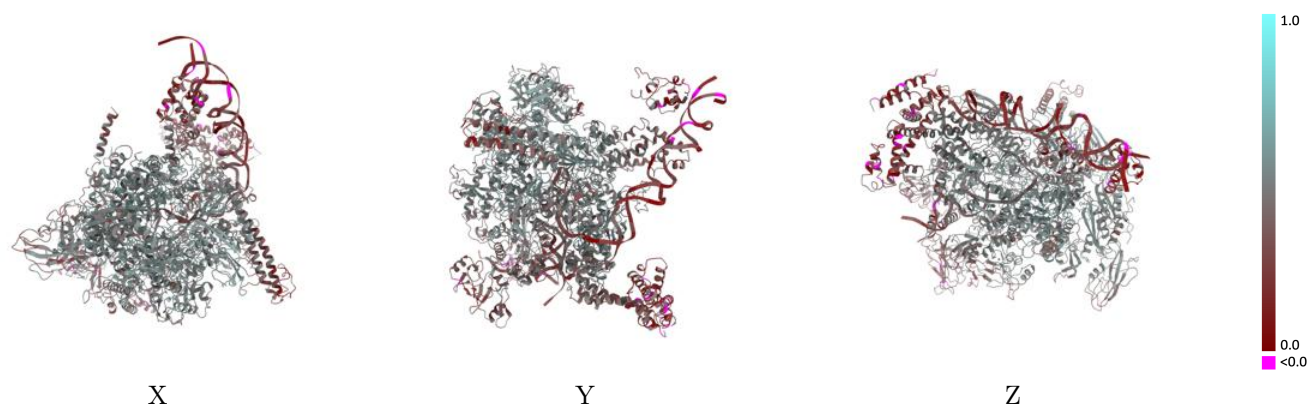
This section contains information regarding the fit between EMDB map EMD-20466 and PDB model 6PSW. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



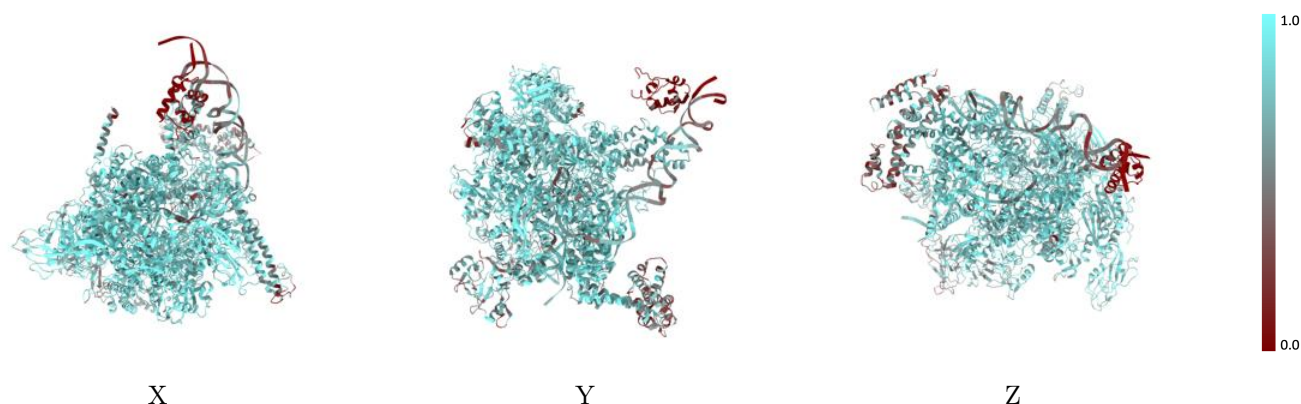
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



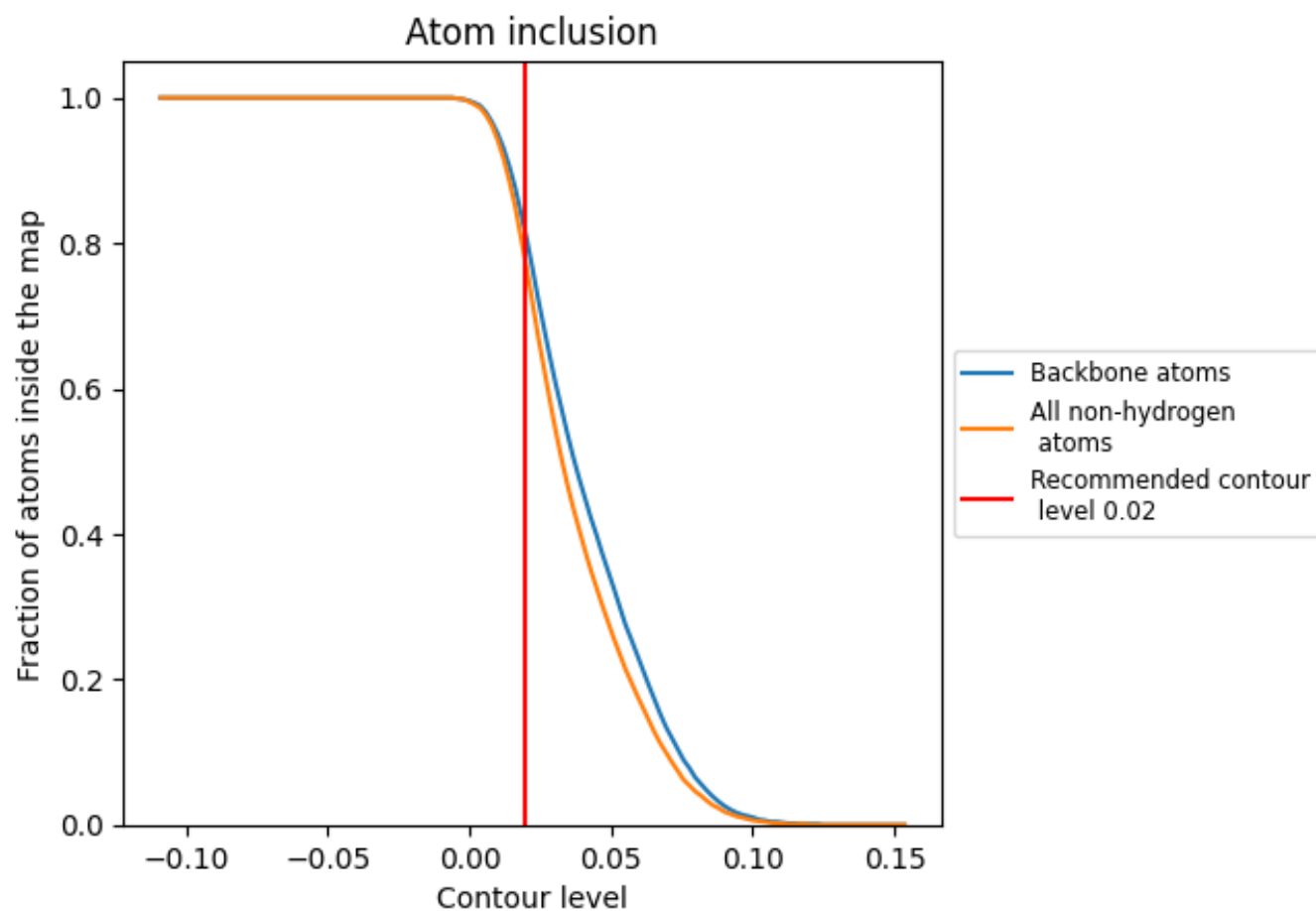
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 77% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7700	0.4380
G	0.8590	0.5010
H	0.8260	0.4660
I	0.8270	0.4750
J	0.8220	0.4710
K	0.7380	0.4650
L	0.6770	0.3560
M	0.0460	0.2530
N	0.6890	0.3990
O	0.6260	0.2570
P	0.5650	0.2460

1.0

0.0

<0.0