



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 08:19 AM UTC

PDB ID : 6RI7 / pdb_00006ri7
EMDB ID : EMD-4885
Title : Cryo-EM structure of E. coli RNA polymerase elongation complex bound to GreB transcription factor
Authors : Abdelkareem, M.; Saint-Andre, C.; Takacs, M.; Papai, G.; Crucifix, C.; Guo, X.; Ortiz, J.; Weixlbaumer, A.
Deposited on : 2019-04-23
Resolution : 3.90 Å (reported)
Based on initial model : 6ALH

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

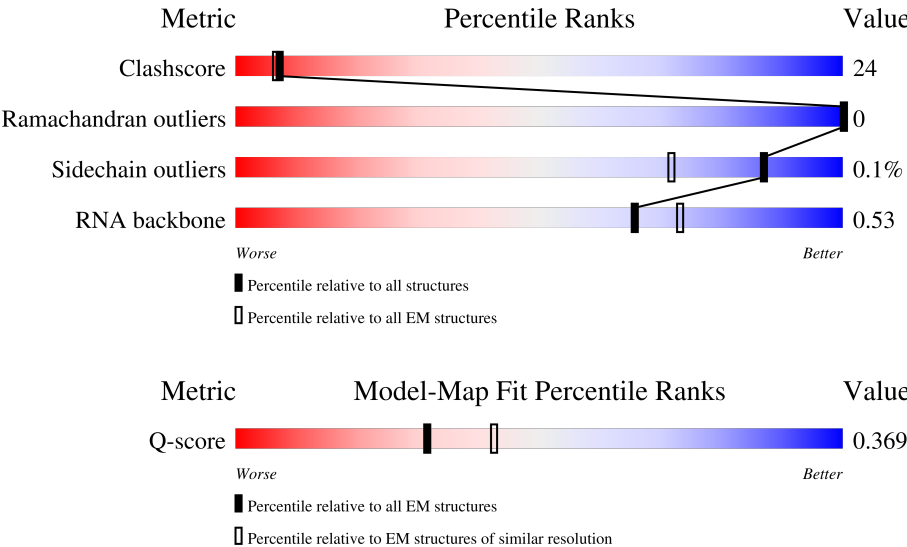
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	N	39	
2	T	39	
3	F	158	

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Mol	Chain	Length	Quality of chain
3	G	158	65% 94% 5%
4	A	329	44% 25% 31%
4	B	329	41% 28% 30%
5	C	1342	5% 52% 46%
6	D	1407	53% 44%
7	E	91	49% 31% 20%
8	R	14	7% 43% 21% 29%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 28461 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	22	Total	C	N	O	P	0	0
			454	215	88	129	22		

- Molecule 2 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	T	32	Total	C	N	O	P	0	0
			650	310	116	192	32		

- Molecule 3 is a protein called Transcription elongation factor GreB.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	156	Total	C	N	O	S	0	0
			1292	821	225	242	4		
3	G	156	Total	C	N	O		0	0
			771	459	156	156			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	228	Total	C	N	O	S	0	0
			1768	1102	312	348	6		
4	B	229	Total	C	N	O	S	0	0
			1772	1104	313	349	6		

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	1319	Total	C	N	O	S	0	0
			10407	6530	1814	2020	43		

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	1358	Total	C	N	O	S	0	0
			10545	6620	1883	1992	50		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	73	Total	C	N	O	S	0	0
			582	355	111	115	1		

- Molecule 8 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	R	10	Total	C	N	O	P	0	0
			217	96	39	72	10		

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
9	D	2	Total	Zn	0
			2	2	

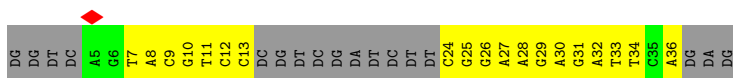
- Molecule 10 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

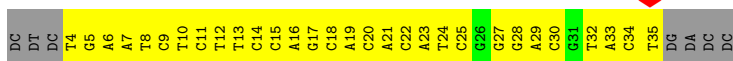
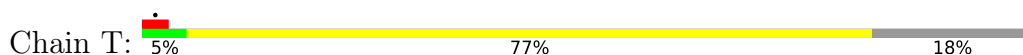
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

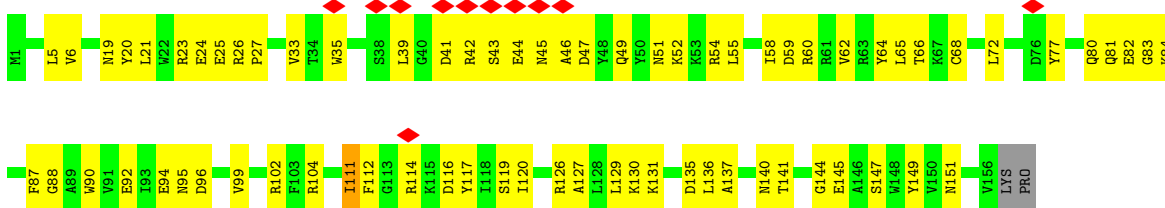
- Molecule 1: Non-template DNA



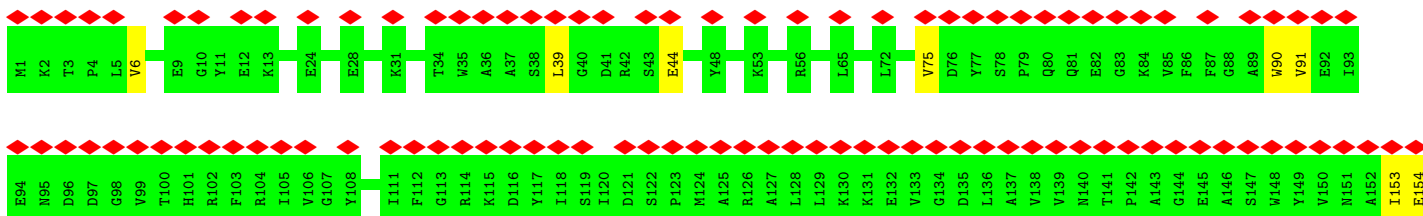
- Molecule 2: Template DNA



- Molecule 3: Transcription elongation factor GreB

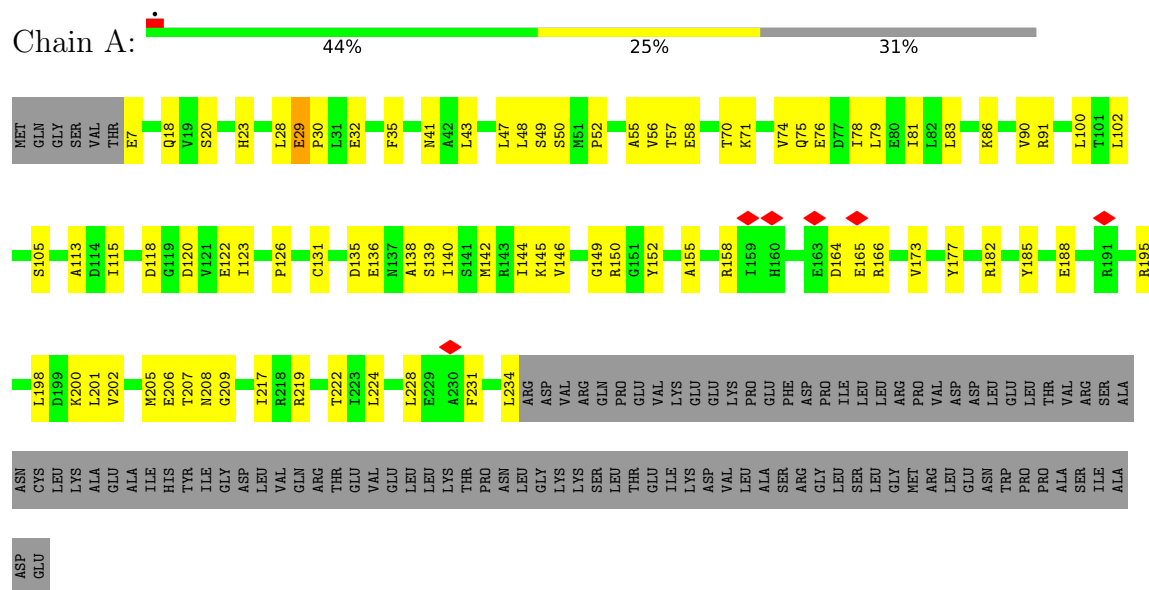


- Molecule 3: Transcription elongation factor GreB

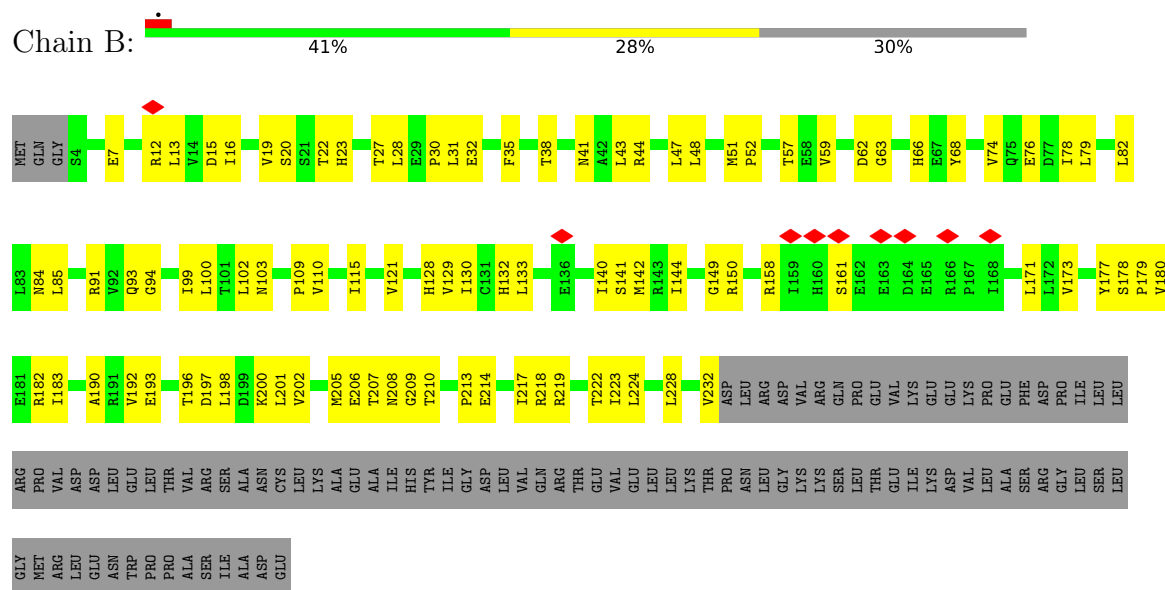




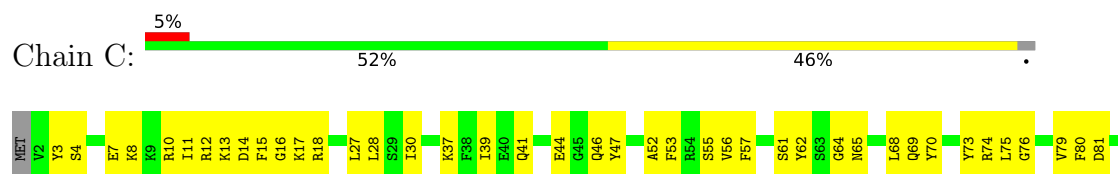
• Molecule 4: DNA-directed RNA polymerase subunit alpha



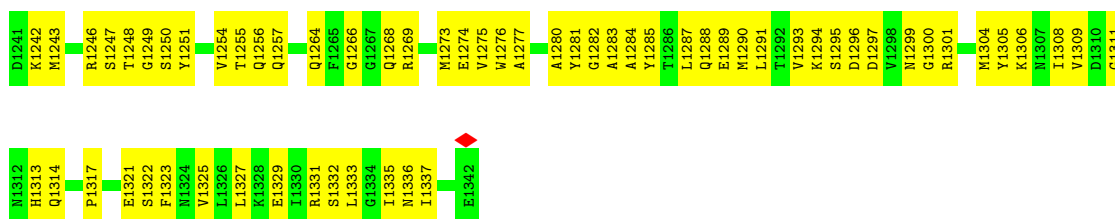
• Molecule 4: DNA-directed RNA polymerase subunit alpha



• Molecule 5: DNA-directed RNA polymerase subunit beta

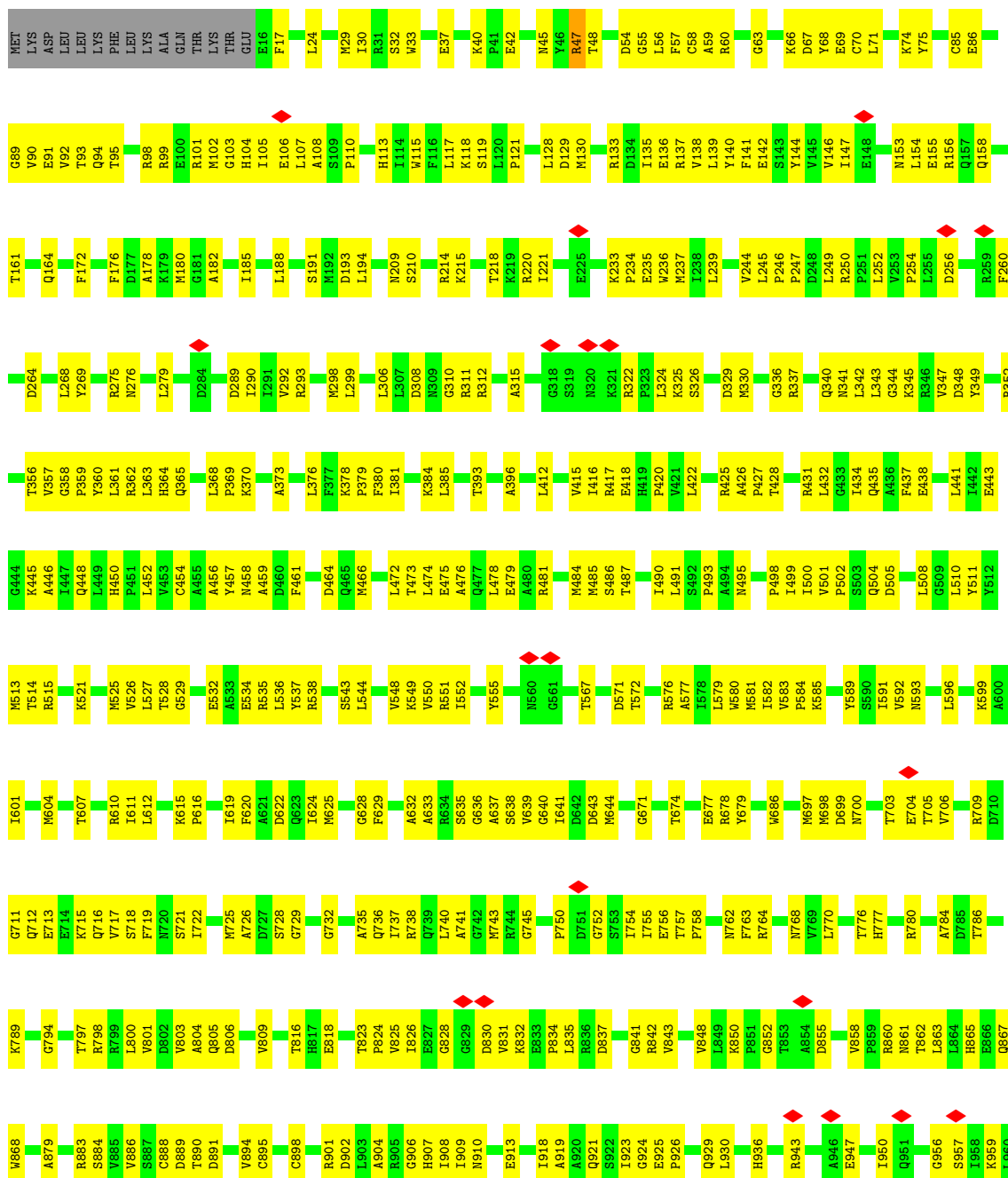


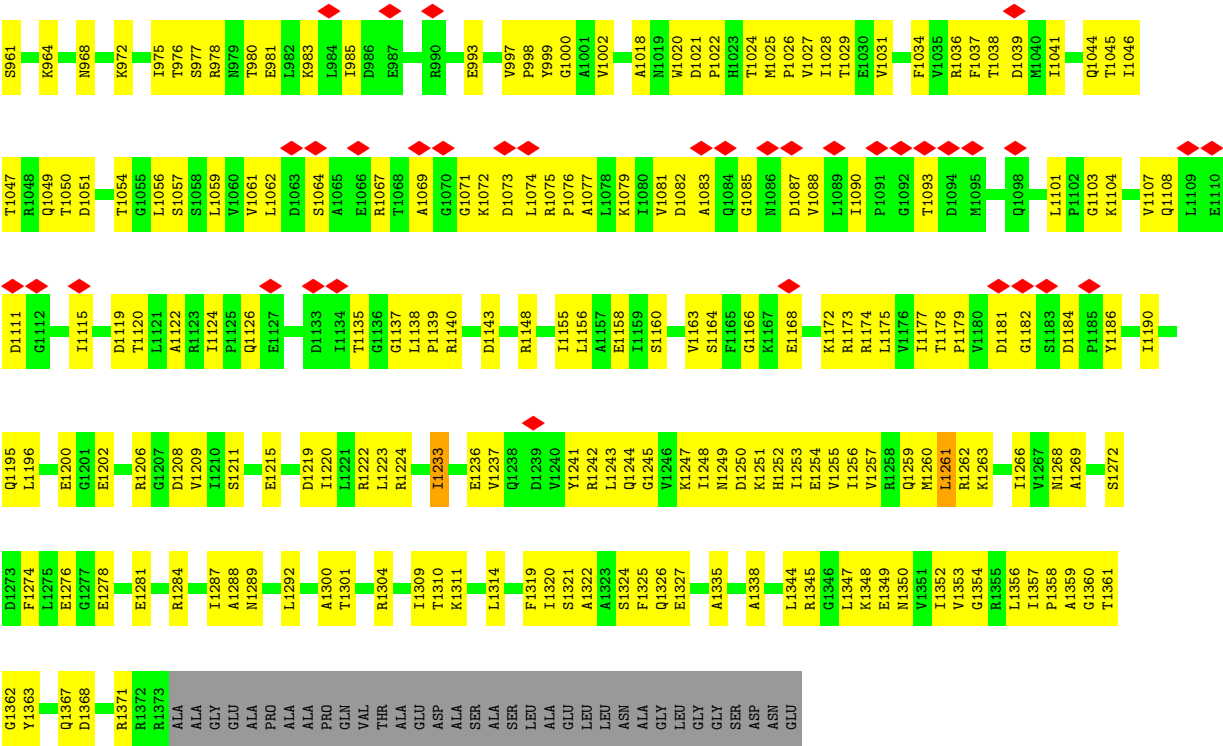
Q1157	R1069	R986	ALA	R839	M885	L806	E523	S421	L319	V242	G162	E84
D1166	H1070	W997	SER	S840	Q886	S807	I524	D424	D320	R245	K163	C85
L1172	G1071	L1000	ASP	R841	Q887	E611	K527	I425	L321	L246	T164	I87
A1173	K1072	G1001	V913	D842	Q888	V615	R529	D427	L322	R247	S166	R88
L1176	K1073	L1002	K914	T843	A689	Q618	R529	V428	A323	G248	S167	T91
R1177	G1074	L1001	D915	K844	V690	A619	I530	M429	K324		N173	T92
K1178	V1075	L1002	S916	L845	T892	A619	P535		L325		A174	S93
G1179	I1076	T1003	L918		L893	N620	A543	L448	S326		R175	A94
N1180	I1077	G1004	R919	E848	K697	S621	G544	G449	F253		L176	P95
A1183	K1078	E1005	P921	E849	P698	D624	F545	N450	D254		L177	L96
T1184	N1079	E1006	T851	T851	L699	E825	E546	R451	G329		K99	R97
F1187	P1080	K1007	N922	A852	T702	E826	V547	R452	H330		L184	V98
G1188	I1082	Q1008	G923	D853	T702	G627	R547	R454	K331		L185	K99
A1190	E1083	Q1009	V924			D632	D549	S455	A257		F186	L100
K1191	D1084	M1009	T927	E858		L633	D549	V456			E187	R101
P1195	V1084	Q1010	T928	G858		R637	D549	M459			L188	Y105
K1196	D1094	L1011	T929	E859		F645	D549	L468			K265	E106
E1197	I1096	E1012	T930	L862		R647	D549	V471			N192	R107
L1198	P1100	A1015	D930			Q649	D549	L475			L194	E108
K1199	G1102	Q1016	L931	D866		D651	D549	V475			F195	A109
L1204	P1109	Q1017	Q932	E867		L644	D549	R478			V196	V114
I1209	P1109	E1020	Q932	E876		F645	D549	L484			R202	I117
R1210	P1109	K1022	D959	T877		R647	D549	D485			K203	K118
G1215	P1109	E1026	L964	T878		Q649	D549	T486			L204	E119
R1216	P1109	K1027	L967	D881		D654	D549	Q490			A206	Q120
I1217	P1109	K1032		I882		V655	D549	D491			G125	E121
G1218	P1109	K1035		K886		S856	D549	M494			L210	E126
E1219	P1109	L1036		V887		T857	D549	A495			R211	I127
F1221	P1109	T1037		T888		S662	D549	K496			Y215	P128
E1222	P1109	Q1038		K890		V663	D549	P497			T216	T131
R1223	P1109	G1039		GLY		G664	D549	I498			T217	D132
P1224	P1109	D1040		GLU		A665	D549	F505			L221	M133
T1226	P1109	A1043		GLU		S666	D549	F506			D222	I138
V1227	P1109	V1046		GLU		G667	D549	G507			F223	M139
G1228	P1109	L1047		GLN		L667	D549	A399			D300	R143
Y1229	P1109	K1048		LEU		I668	D549	V400			I302	V144
M1230	P1109	L1049		THR		P669	D549	G401			D303	I145
Y1231	P1109	V1050		PRO		E672	D549	M403			E304	V146
M1232	P1109	K1051		GLU		D674	D549	K404			E231	Q148
L1233	P1109	V1052		LEU		D675	D549	F405			I232	S147
K1234	P1109	R1058		ARG		A676	D549	N406			R333	L149
L1238	P1109	P1062		ALA		G678	D549	L409			G307	H150
V1239	P1109	G1063		ILE		M881	D549	L410			E308	V155
D1240	P1109	M1066		ALA		N684	D549	R411			L309	D158
		G1068		PHE			D549	P520			A313	
				GLY			D549	L521			M315	
				GLU			D549	S522			E316	
				LYS			D549				L317	
							D549				S318	



• Molecule 6: DNA-directed RNA polymerase subunit beta'

Chain D: 53% 44%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	121680	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 ($e^-/\text{\AA}^2$)	59	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	2.535	Depositor
Minimum map value	-1.180	Depositor
Average map value	0.014	Depositor
Map value standard deviation	0.107	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	299.232, 299.232, 299.232	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.039, 1.039, 1.039	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, 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	N	0.43	0/509	0.69	1/781 (0.1%)
2	T	0.51	0/727	0.52	0/1118
3	F	0.29	0/1319	0.46	0/1780
3	G	0.14	0/770	0.29	0/1071
4	A	0.50	0/1790	0.56	0/2426
4	B	0.41	0/1794	0.56	0/2432
5	C	0.48	0/10573	0.57	0/14265
6	D	0.47	0/10706	0.60	0/14456
7	E	0.44	0/584	0.59	0/786
8	R	0.47	0/242	0.39	0/376
All	All	0.46	0/29014	0.57	1/39491 (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
4	A	0	1
5	C	0	1
6	D	0	1
All	All	0	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	34	DT	C2'-C3'-O3'	-8.81	98.29	111.50

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	29	GLU	Peptide
5	C	1295	SER	Peptide
6	D	47	ARG	Peptide

5.2 Too-close contacts [i](#)

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	N	454	0	248	22	0
2	T	650	0	361	61	0
3	F	1292	0	1281	63	0
3	G	771	0	348	5	0
4	A	1768	0	1793	66	0
4	B	1772	0	1799	86	0
5	C	10407	0	10420	547	0
6	D	10545	0	10760	553	0
7	E	582	0	593	32	0
8	R	217	0	107	15	0
9	D	2	0	0	0	0
10	D	1	0	0	0	0
All	All	28461	0	27710	1317	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 24.

All (1317) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:12:DC:O2	2:T:28:DG:N2	1.96	0.98
5:C:888:THR:O	5:C:913:VAL:HA	1.64	0.97
1:N:10:DG:N2	2:T:30:DC:O2	2.00	0.92
1:N:10:DG:N1	2:T:30:DC:N3	2.17	0.91
4:A:7:GLU:HB3	4:B:150:ARG:HH12	1.34	0.90
4:A:207:THR:HG22	4:A:209:GLY:H	1.37	0.90
4:B:59:VAL:O	4:B:171:LEU:HB2	1.72	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:515:MET:HE3	5:C:517:GLN:HB2	1.54	0.89
5:C:101:ARG:HE	5:C:118:LYS:HD3	1.39	0.86
5:C:985:GLU:O	5:C:989:LEU:HB2	1.76	0.86
6:D:824:PRO:HD3	6:D:835:LEU:HD12	1.57	0.84
1:N:13:DC:O2	2:T:27:DG:N2	2.11	0.83
4:A:56:VAL:HA	4:A:146:VAL:HG22	1.61	0.82
6:D:591:ILE:HG23	6:D:592:VAL:HG13	1.59	0.82
5:C:133:ASN:O	5:C:527:LYS:NZ	2.11	0.82
6:D:1027:VAL:HB	6:D:1122:ALA:H	1.45	0.82
6:D:1350:ASN:HD22	6:D:1358:PRO:HD3	1.43	0.81
5:C:1246:ARG:HH21	5:C:1249:GLY:H	1.28	0.80
6:D:129:ASP:OD2	6:D:220:ARG:NH1	2.14	0.80
6:D:555:TYR:HE2	6:D:585:LYS:HD2	1.47	0.80
6:D:393:THR:HG23	6:D:396:ALA:H	1.47	0.79
6:D:1166:GLY:HA3	6:D:1174:ARG:HD2	1.65	0.79
6:D:144:TYR:OH	6:D:293:ARG:NH2	2.15	0.78
5:C:1246:ARG:NH2	5:C:1250:SER:O	2.17	0.78
5:C:17:LYS:N	5:C:1188:ASP:OD2	2.15	0.78
6:D:425:ARG:NH1	6:D:458:ASN:O	2.16	0.78
5:C:741:MET:SD	5:C:974:ARG:NH1	2.56	0.78
6:D:245:LEU:O	6:D:250:ARG:NH1	2.17	0.78
5:C:12:ARG:HD3	5:C:1183:ALA:HB2	1.66	0.78
6:D:959:LYS:HB3	6:D:983:LYS:HB2	1.66	0.78
5:C:131:THR:HG22	5:C:133:ASN:H	1.45	0.78
6:D:741:ALA:O	6:D:762:ASN:ND2	2.17	0.77
4:A:166:ARG:NH2	5:C:876:GLU:OE1	2.17	0.77
1:N:29:DG:N2	2:T:11:DC:O2	2.16	0.77
6:D:709:ARG:NH2	6:D:712:GLN:OE1	2.17	0.77
6:D:308:ASP:OD2	6:D:311:ARG:NE	2.18	0.76
5:C:69:GLN:HE21	5:C:101:ARG:HD2	1.50	0.76
6:D:1241:TYR:O	6:D:1245:GLY:N	2.19	0.76
5:C:1314:GLN:HA	7:E:28:ARG:HH22	1.51	0.76
6:D:113:HIS:CE1	6:D:115:TRP:HB2	2.20	0.76
5:C:591:TYR:OH	5:C:637:ARG:NH2	2.18	0.76
5:C:230:PHE:HB2	5:C:333:ILE:HB	1.68	0.75
1:N:32:DA:H2"	1:N:33:DT:H71	1.67	0.75
4:B:23:HIS:ND1	4:B:206:GLU:OE2	2.19	0.75
5:C:490:GLN:HA	5:C:493:ILE:HG22	1.68	0.75
5:C:1311:GLY:O	7:E:31:GLN:NE2	2.19	0.75
5:C:992:LEU:HD13	5:C:996:ARG:HB2	1.68	0.75
6:D:1172:LYS:HA	6:D:1190:ILE:O	1.85	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:961:SER:HB2	6:D:981:GLU:HB3	1.69	0.75
6:D:883:ARG:NH2	6:D:898:CYS:SG	2.59	0.74
5:C:143:ARG:NH2	5:C:512:SER:O	2.21	0.74
4:A:74:VAL:HG22	4:A:76:GLU:H	1.51	0.74
6:D:1061:VAL:O	6:D:1104:LYS:N	2.21	0.74
4:B:74:VAL:HG12	4:B:76:GLU:H	1.51	0.74
4:B:93:GLN:HG3	4:B:94:GLY:H	1.52	0.74
4:A:29:GLU:HG3	4:A:30:PRO:HD3	1.69	0.73
3:F:52:LYS:NZ	6:D:1244:GLN:OE1	2.21	0.73
5:C:747:GLY:O	5:C:974:ARG:NH2	2.20	0.73
5:C:1287:LEU:HD22	6:D:1357:ILE:HD11	1.70	0.73
6:D:490:ILE:HG13	6:D:491:LEU:HG	1.70	0.73
6:D:67:ASP:OD1	6:D:95:THR:N	2.22	0.73
5:C:12:ARG:NH2	5:C:793:GLU:OE1	2.16	0.73
5:C:549:ASP:OD1	5:C:550:VAL:N	2.21	0.72
4:B:103:ASN:HA	4:B:140:ILE:O	1.88	0.72
4:B:182:ARG:NH1	6:D:534:GLU:OE1	2.22	0.72
1:N:29:DG:H2'	1:N:30:DA:C8	2.25	0.72
5:C:143:ARG:NH2	5:C:507:GLY:O	2.21	0.72
5:C:557:ARG:NH2	5:C:607:SER:O	2.22	0.72
5:C:1142:ARG:NH2	5:C:1166:ASP:OD1	2.22	0.72
5:C:672:GLU:N	5:C:672:GLU:OE1	2.22	0.72
6:D:343:LEU:HD21	6:D:1348:LYS:HG3	1.72	0.71
5:C:1297:ASP:CG	5:C:1300:GLY:H	1.98	0.71
2:T:9:DC:H2'	2:T:10:DT:H71	1.73	0.71
5:C:915:ASP:OD2	5:C:919:ARG:NH2	2.23	0.71
4:B:182:ARG:HD2	6:D:581:MET:HE1	1.72	0.71
5:C:811:ASN:HA	5:C:815:SER:HB2	1.73	0.70
6:D:357:VAL:HG22	6:D:461:PHE:CE2	2.26	0.70
3:F:44:GLU:OE1	5:C:678:ARG:NH2	2.20	0.70
6:D:604:MET:HE1	6:D:620:PHE:HZ	1.56	0.70
6:D:1049:GLN:O	6:D:1057:SER:HA	1.91	0.70
5:C:318:SER:OG	5:C:320:ASP:OD1	2.08	0.70
5:C:453:ILE:HD12	5:C:587:LEU:HD21	1.74	0.70
5:C:1122:LYS:NZ	5:C:1229:TYR:OH	2.23	0.70
8:R:7:G:H2'	8:R:8:A:H8	1.56	0.70
4:B:22:THR:OG1	4:B:207:THR:N	2.25	0.69
5:C:590:PRO:HB2	5:C:655:VAL:HG21	1.73	0.69
2:T:7:DA:H2'	2:T:8:DT:C6	2.28	0.69
6:D:1069:ALA:HA	6:D:1072:LYS:HE2	1.74	0.69
6:D:584:PRO:HD3	6:D:620:PHE:CD1	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:915:ASP:OD1	5:C:917:SER:N	2.24	0.69
5:C:797:GLY:N	5:C:1231:TYR:OH	2.25	0.69
5:C:1118:GLY:O	5:C:1121:ALA:N	2.26	0.69
6:D:491:LEU:HB2	6:D:904:ALA:HA	1.73	0.69
2:T:18:DC:H2'	2:T:19:DA:C8	2.28	0.68
4:B:208:ASN:OD1	4:B:209:GLY:N	2.26	0.68
6:D:515:ARG:NH2	6:D:718:SER:O	2.26	0.68
6:D:591:ILE:HD11	6:D:604:MET:HA	1.73	0.68
6:D:528:THR:N	6:D:532:GLU:OE2	2.26	0.68
7:E:15:ASN:HD22	7:E:18:ASP:CG	2.01	0.68
5:C:839:VAL:HG12	5:C:1049:ILE:HA	1.76	0.68
6:D:529:GLY:O	6:D:532:GLU:HG2	1.93	0.68
2:T:22:DC:H2'	2:T:23:DA:H8	1.59	0.68
4:A:7:GLU:HB3	4:B:150:ARG:NH1	2.08	0.68
6:D:357:VAL:HG22	6:D:461:PHE:HE2	1.59	0.68
6:D:1350:ASN:O	6:D:1354:GLY:N	2.26	0.68
4:A:28:LEU:HD22	4:A:201:LEU:HD23	1.74	0.68
5:C:1223:ARG:NH2	6:D:719:PHE:O	2.27	0.68
4:A:100:LEU:HD23	4:A:115:ILE:HG21	1.77	0.67
6:D:841:GLY:HA2	6:D:901:ARG:HD3	1.76	0.67
4:A:102:LEU:HD12	4:A:115:ILE:HG12	1.76	0.67
5:C:10:ARG:NH1	5:C:697:LYS:HD3	2.10	0.67
3:F:42:ARG:HB2	3:F:45:ASN:HB2	1.75	0.67
5:C:288:PRO:HG2	5:C:291:TYR:HB2	1.77	0.67
5:C:211:ARG:NH2	5:C:217:THR:OG1	2.23	0.67
6:D:37:GLU:OE2	6:D:106:GLU:N	2.23	0.67
1:N:24:DC:N3	2:T:16:DA:N1	2.42	0.67
4:B:23:HIS:HA	4:B:206:GLU:HG2	1.77	0.67
5:C:302:ILE:HG22	5:C:309:LEU:HA	1.75	0.66
6:D:576:ARG:HD3	6:D:593:ASN:HA	1.76	0.66
6:D:93:THR:HG22	6:D:94:GLN:H	1.60	0.66
5:C:551:HIS:H	5:C:554:HIS:CE1	2.13	0.66
5:C:148:GLN:NE2	5:C:535:PRO:O	2.22	0.66
5:C:1223:ARG:NH2	6:D:721:SER:OG	2.29	0.66
4:B:192:VAL:HG12	4:B:193:GLU:H	1.60	0.66
2:T:18:DC:H2'	2:T:19:DA:H8	1.60	0.66
6:D:1143:ASP:OD1	6:D:1148:ARG:NH1	2.27	0.66
5:C:3:TYR:OH	5:C:1157:GLN:OE1	2.13	0.66
5:C:1274:GLU:N	5:C:1274:GLU:OE1	2.29	0.66
5:C:1329:GLU:O	5:C:1332:SER:OG	2.07	0.66
6:D:91:GLU:OE1	6:D:101:ARG:NH2	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:1360:GLY:O	6:D:1363:TYR:N	2.29	0.66
5:C:544:GLY:O	5:C:548:ARG:NH1	2.29	0.66
6:D:883:ARG:NH2	6:D:895:CYS:SG	2.69	0.66
5:C:559:CYS:SG	5:C:562:GLU:N	2.64	0.65
5:C:985:GLU:O	5:C:989:LEU:CB	2.43	0.65
6:D:555:TYR:CE2	6:D:585:LYS:HD2	2.30	0.65
5:C:1083:GLU:CD	5:C:1083:GLU:H	2.03	0.65
6:D:674:THR:N	6:D:677:GLU:OE2	2.21	0.65
1:N:10:DG:H2'	1:N:11:DT:C6	2.31	0.65
5:C:618:GLN:NE2	6:D:770:LEU:H	1.95	0.65
6:D:1038:THR:OG1	6:D:1079:LYS:N	2.29	0.65
5:C:812:PHE:CD2	5:C:813:GLU:HG2	2.32	0.65
6:D:678:ARG:NH1	6:D:756:GLU:OE1	2.30	0.65
6:D:936:HIS:N	6:D:1135:THR:O	2.27	0.65
4:A:140:ILE:HD12	4:A:142:MET:HE3	1.79	0.65
4:B:79:LEU:HA	4:B:82:LEU:HD12	1.79	0.65
5:C:411:ARG:NH2	5:C:427:ASP:OD2	2.25	0.65
5:C:582:ASN:OD1	5:C:583:GLU:N	2.29	0.65
6:D:610:ARG:HG3	6:D:611:ILE:HG13	1.79	0.65
4:A:18:GLN:NE2	4:A:20:SER:O	2.30	0.65
4:A:57:THR:HG22	4:A:58:GLU:HG3	1.78	0.65
5:C:97:ARG:HB3	5:C:121:GLU:HB2	1.79	0.65
5:C:611:GLU:OE2	5:C:637:ARG:NH2	2.30	0.65
5:C:1106:ARG:O	5:C:1108:ASN:N	2.29	0.65
3:F:33:VAL:HG12	3:F:51:ASN:HB3	1.78	0.65
5:C:255:ILE:HB	5:C:263:VAL:HB	1.79	0.65
5:C:204:LEU:HD13	5:C:208:ILE:HD13	1.79	0.64
5:C:1254:VAL:HG13	5:C:1255:THR:H	1.62	0.64
6:D:843:VAL:HG22	6:D:863:LEU:HA	1.78	0.64
6:D:1155:ILE:N	6:D:1211:SER:OG	2.28	0.64
8:R:7:G:H2'	8:R:8:A:C8	2.33	0.64
4:A:75:GLN:HG3	4:A:76:GLU:HG3	1.79	0.64
5:C:81:ASP:O	5:C:85:CYS:HB2	1.98	0.64
6:D:322:ARG:NH1	8:R:8:A:O2'	2.27	0.64
6:D:527:LEU:HB2	6:D:550:VAL:HG12	1.79	0.64
4:B:100:LEU:HD21	4:B:121:VAL:HG11	1.79	0.64
6:D:113:HIS:HD2	6:D:239:LEU:HD11	1.62	0.64
6:D:1249:ASN:OD1	6:D:1250:ASP:N	2.31	0.64
5:C:810:TYR:CE2	5:C:1078:LYS:HD3	2.33	0.64
5:C:821:ARG:NH1	5:C:824:GLN:OE1	2.30	0.64
5:C:915:ASP:OD1	5:C:916:SER:N	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:155:GLU:HB2	6:D:158:GLN:HB2	1.80	0.64
5:C:95:PRO:HA	5:C:126:GLU:HG2	1.80	0.63
5:C:1290:MET:HA	5:C:1294:LYS:HD2	1.80	0.63
6:D:718:SER:OG	6:D:719:PHE:N	2.29	0.63
5:C:882:ILE:HG13	5:C:919:ARG:HG2	1.79	0.63
3:F:42:ARG:NH2	3:F:44:GLU:OE2	2.31	0.63
5:C:1094:VAL:HG22	5:C:1095:ASP:H	1.61	0.63
3:F:21:LEU:HD23	3:F:58:ILE:HG13	1.79	0.63
5:C:818:VAL:HG21	5:C:1066:MET:HE1	1.79	0.63
6:D:1173:ARG:HG3	6:D:1174:ARG:H	1.60	0.63
5:C:1083:GLU:OE1	5:C:1083:GLU:N	2.26	0.63
4:B:35:PHE:HA	4:B:38:THR:HG22	1.79	0.63
5:C:1291:LEU:HD22	6:D:345:LYS:HE3	1.81	0.63
6:D:491:LEU:HD23	6:D:498:PRO:HA	1.80	0.63
6:D:1061:VAL:HG12	6:D:1103:GLY:HA2	1.81	0.63
5:C:933:VAL:HG22	5:C:1050:VAL:HG22	1.80	0.63
5:C:1072:ASN:ND2	5:C:1111:GLN:OE1	2.31	0.63
5:C:1275:VAL:HG13	5:C:1287:LEU:HD11	1.81	0.63
6:D:888:CYS:SG	6:D:890:THR:OG1	2.50	0.63
1:N:7:DT:H2"	1:N:8:DA:N7	2.13	0.63
5:C:842:ASP:HB2	5:C:1047:LEU:HD21	1.80	0.63
6:D:425:ARG:HG2	6:D:426:ALA:H	1.63	0.63
5:C:866:ASP:OD1	5:C:869:GLY:N	2.32	0.62
6:D:56:LEU:HB3	6:D:250:ARG:HH21	1.64	0.62
4:B:214:GLU:OE2	4:B:218:ARG:NE	2.32	0.62
5:C:685:MET:SD	5:C:1073:LYS:HG2	2.39	0.62
5:C:1257:GLN:HE22	6:D:341:ASN:HB3	1.64	0.62
5:C:339:ASN:OD1	5:C:340:ASP:N	2.29	0.62
5:C:509:SER:HB3	5:C:512:SER:H	1.64	0.62
5:C:785:ASP:OD2	5:C:791:LEU:N	2.33	0.62
5:C:1214:ASP:O	5:C:1218:GLY:N	2.28	0.62
4:B:27:THR:HG22	4:B:202:VAL:HG22	1.80	0.62
6:D:156:ARG:NH2	6:D:191:SER:OG	2.32	0.62
6:D:1158:GLU:HG3	6:D:1186:TYR:CZ	2.34	0.62
4:A:182:ARG:HB3	4:A:206:GLU:HB3	1.82	0.62
4:B:205:MET:HE3	4:B:213:PRO:HB3	1.81	0.62
5:C:406:ASN:HB3	5:C:411:ARG:HB2	1.82	0.62
5:C:766:ASN:OD1	5:C:767:GLN:N	2.32	0.62
5:C:1276:TRP:CZ2	6:D:801:VAL:HG21	2.34	0.62
6:D:527:LEU:HD21	6:D:536:LEU:HD12	1.81	0.62
5:C:211:ARG:HH22	5:C:217:THR:HG1	1.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:560:PRO:HB2	6:D:776:THR:HG21	1.80	0.62
6:D:269:TYR:HE1	6:D:306:LEU:HD11	1.65	0.62
6:D:638:SER:OG	6:D:639:VAL:N	2.30	0.62
4:B:205:MET:HE1	4:B:217:ILE:HG13	1.81	0.62
3:F:52:LYS:HA	3:F:55:LEU:HD12	1.81	0.62
5:C:65:ASN:O	5:C:105:TYR:N	2.33	0.62
3:G:6:VAL:O	3:G:75:VAL:N	2.30	0.62
4:B:19:VAL:HB	4:B:23:HIS:HB3	1.80	0.61
5:C:1073:LYS:NZ	8:R:14:G:OP1	2.27	0.61
3:F:129:LEU:HG	3:F:130:LYS:HG3	1.80	0.61
5:C:506:PHE:O	5:C:512:SER:OG	2.15	0.61
5:C:1192:GLU:OE2	6:D:764:ARG:NE	2.22	0.61
6:D:834:PRO:HG2	6:D:837:ASP:HB2	1.83	0.61
5:C:144:VAL:HG23	5:C:515:MET:HB2	1.82	0.61
2:T:5:DG:OP2	2:T:5:DG:H2'	2.01	0.61
5:C:596:ASP:OD1	5:C:597:GLY:N	2.33	0.61
5:C:739:ASP:OD1	5:C:740:GLU:N	2.31	0.61
6:D:956:GLY:HA3	6:D:985:ILE:O	2.00	0.61
5:C:380:ALA:HB2	3:G:39:LEU:HA	1.82	0.61
6:D:362:ARG:O	6:D:364:HIS:N	2.33	0.61
6:D:1036:ARG:HE	6:D:1081:VAL:HG11	1.65	0.61
6:D:1268:ASN:N	6:D:1301:THR:OG1	2.34	0.61
2:T:14:DC:OP1	6:D:311:ARG:NH1	2.25	0.61
5:C:1306:LYS:O	5:C:1309:VAL:HG22	2.00	0.61
6:D:901:ARG:HH21	6:D:906:GLY:HA2	1.64	0.61
6:D:964:LYS:HB3	6:D:977:SER:HB3	1.83	0.61
6:D:29:MET:O	6:D:32:SER:OG	2.18	0.61
6:D:1027:VAL:HG21	6:D:1122:ALA:HB3	1.80	0.61
5:C:922:ASN:OD1	5:C:923:GLY:N	2.33	0.61
5:C:983:GLY:HA3	5:C:1002:LEU:HA	1.83	0.61
8:R:10:G:H2'	8:R:11:U:H6	1.65	0.61
4:B:28:LEU:HD12	4:B:201:LEU:HD23	1.83	0.61
5:C:320:ASP:OD1	5:C:321:LEU:N	2.34	0.61
6:D:825:VAL:HG23	6:D:832:LYS:HB2	1.82	0.61
2:T:8:DT:OP2	2:T:8:DT:H6	1.83	0.60
4:A:231:PHE:CE1	4:B:28:LEU:HD11	2.36	0.60
5:C:10:ARG:NH1	5:C:790:ASP:OD2	2.30	0.60
5:C:759:SER:HB3	5:C:763:THR:O	2.00	0.60
5:C:101:ARG:HA	5:C:118:LYS:HG2	1.83	0.60
5:C:678:ARG:NH1	5:C:681:MET:SD	2.74	0.60
6:D:800:LEU:O	6:D:803:VAL:HG12	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:R:10:G:H2'	8:R:11:U:C6	2.36	0.60
5:C:88:ARG:NE	5:C:1040:ASP:OD2	2.27	0.60
6:D:55:GLY:H	6:D:58:CYS:HB2	1.66	0.60
6:D:1077:ALA:HA	6:D:1101:LEU:HG	1.82	0.60
5:C:207:THR:HA	5:C:210:LEU:HD12	1.83	0.60
5:C:253:PHE:HA	5:C:265:LYS:HG3	1.83	0.60
6:D:218:THR:HA	6:D:221:ILE:HG22	1.82	0.60
6:D:510:LEU:HD22	6:D:601:ILE:HD12	1.84	0.60
6:D:950:ILE:HG13	6:D:1020:TRP:CH2	2.36	0.60
5:C:619:ALA:N	5:C:654:ASP:OD2	2.34	0.60
6:D:85:CYS:HB3	6:D:90:VAL:H	1.65	0.60
6:D:431:ARG:HD3	6:D:493:PRO:HG3	1.83	0.60
6:D:58:CYS:SG	6:D:60:ARG:HG2	2.41	0.60
6:D:514:THR:HG21	6:D:596:LEU:HD12	1.84	0.60
7:E:26:ARG:HG3	7:E:30:MET:HE2	1.83	0.60
5:C:914:LYS:HG2	5:C:915:ASP:H	1.67	0.60
6:D:632:ALA:O	6:D:635:SER:OG	2.16	0.60
4:B:183:ILE:HG22	4:B:205:MET:HG3	1.83	0.60
5:C:1273:MET:HG2	5:C:1276:TRP:CZ3	2.36	0.60
6:D:119:SER:OG	6:D:121:PRO:O	2.19	0.60
4:B:44:ARG:CZ	6:D:538:ARG:HD2	2.30	0.60
5:C:806:PRO:HA	5:C:811:ASN:HD21	1.67	0.60
5:C:866:ASP:OD1	5:C:870:ILE:N	2.28	0.60
3:F:120:ILE:O	3:F:126:ARG:NH1	2.34	0.59
6:D:37:GLU:HB2	6:D:104:HIS:NE2	2.17	0.59
6:D:848:VAL:HB	6:D:858:VAL:HG22	1.83	0.59
5:C:814:ASP:OD2	5:C:1106:ARG:NH2	2.35	0.59
6:D:59:ALA:HA	6:D:63:GLY:H	1.68	0.59
6:D:1311:LYS:O	6:D:1314:LEU:N	2.35	0.59
6:D:1350:ASN:HA	6:D:1353:VAL:HG12	1.84	0.59
3:F:90:TRP:CD2	3:F:104:ARG:HB2	2.38	0.59
3:F:95:ASN:OD1	3:F:96:ASP:N	2.35	0.59
4:B:32:GLU:HB3	4:B:35:PHE:CD2	2.38	0.59
4:B:196:THR:HG23	6:D:443:GLU:HG3	1.83	0.59
5:C:128:PRO:HG2	5:C:506:PHE:CD2	2.37	0.59
5:C:528:ARG:NH2	5:C:576:SER:O	2.35	0.59
6:D:842:ARG:NH1	6:D:1254:GLU:OE2	2.36	0.59
4:A:28:LEU:HB2	4:A:201:LEU:HB3	1.84	0.59
3:F:136:LEU:HG	3:F:149:TYR:CE1	2.38	0.59
5:C:580:GLN:NE2	5:C:605:TYR:OH	2.36	0.59
6:D:362:ARG:O	6:D:365:GLN:HG2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:74:ARG:HH21	5:C:121:GLU:CD	2.10	0.59
6:D:431:ARG:N	6:D:921:GLN:OE1	2.35	0.59
6:D:947:GLU:O	6:D:1020:TRP:NE1	2.35	0.59
5:C:825:GLU:OE1	5:C:827:ARG:NH1	2.36	0.58
5:C:851:THR:HG23	5:C:853:ASP:H	1.68	0.58
6:D:235:GLU:OE1	6:D:235:GLU:N	2.34	0.58
6:D:425:ARG:HG2	6:D:426:ALA:N	2.17	0.58
6:D:426:ALA:O	6:D:428:THR:N	2.36	0.58
6:D:1079:LYS:NZ	6:D:1087:ASP:OD1	2.26	0.58
7:E:15:ASN:ND2	7:E:18:ASP:H	2.01	0.58
5:C:1313:HIS:CD2	7:E:31:GLN:HE22	2.20	0.58
6:D:641:ILE:HD11	6:D:764:ARG:HG3	1.85	0.58
2:T:20:DC:O3'	6:D:352:ARG:NH2	2.35	0.58
4:A:78:ILE:HA	4:A:81:ILE:HD12	1.84	0.58
5:C:339:ASN:HB3	5:C:343:HIS:H	1.68	0.58
5:C:514:PHE:CE2	5:C:760:ASN:HB3	2.39	0.58
6:D:1160:SER:HB2	6:D:1206:ARG:H	1.68	0.58
4:A:43:LEU:HD13	4:A:217:ILE:HD11	1.85	0.58
5:C:594:VAL:HG11	5:C:650:VAL:HG23	1.84	0.58
6:D:45:ASN:ND2	6:D:48:THR:OG1	2.30	0.58
6:D:755:ILE:HG22	6:D:757:THR:H	1.68	0.58
6:D:70:CYS:SG	6:D:71:LEU:N	2.76	0.58
6:D:185:ILE:HA	6:D:188:LEU:HD12	1.84	0.58
5:C:145:ILE:HB	5:C:456:VAL:HG22	1.85	0.58
5:C:271:ALA:HA	5:C:274:ILE:HD12	1.85	0.58
5:C:688:GLN:NE2	8:R:12:G:O3'	2.35	0.58
5:C:176:ILE:HD11	5:C:428:VAL:HG21	1.86	0.58
5:C:1018:TYR:O	5:C:1022:LYS:HG2	2.04	0.58
6:D:709:ARG:HH12	6:D:713:GLU:H	1.51	0.58
6:D:1335:ALA:O	6:D:1338:ALA:N	2.36	0.58
7:E:58:LEU:HD12	7:E:59:ILE:HG12	1.85	0.58
5:C:718:ALA:HB2	5:C:783:LEU:HD11	1.86	0.58
6:D:368:LEU:HD22	6:D:373:ALA:HB2	1.86	0.58
6:D:475:GLU:OE2	7:E:28:ARG:NE	2.37	0.58
6:D:85:CYS:SG	6:D:86:GLU:N	2.76	0.57
6:D:435:GLN:OE1	6:D:486:SER:OG	2.19	0.57
6:D:842:ARG:HH21	6:D:1251:LYS:HG3	1.69	0.57
7:E:46:THR:HA	7:E:49:ILE:HD12	1.86	0.57
5:C:1297:ASP:OD1	5:C:1299:ASN:N	2.37	0.57
5:C:735:LYS:HA	5:C:748:ILE:HG22	1.86	0.57
6:D:1368:ASP:OD1	6:D:1371:ARG:NH2	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:19:VAL:HG12	4:B:20:SER:H	1.69	0.57
6:D:1281:GLU:HG3	6:D:1284:ARG:H	1.68	0.57
5:C:11:ILE:HG23	5:C:1149:TYR:OH	2.04	0.57
6:D:902:ASP:HB2	6:D:909:ILE:HD13	1.86	0.57
2:T:32:DT:H2"	2:T:33:DA:C5	2.38	0.57
5:C:805:MET:HE1	5:C:1221:PHE:CZ	2.40	0.57
5:C:1308:ILE:HD12	6:D:380:PHE:HE1	1.70	0.57
6:D:805:GLN:CD	6:D:1348:LYS:HB2	2.30	0.57
6:D:950:ILE:HG13	6:D:1020:TRP:HH2	1.69	0.57
5:C:859:GLU:HA	5:C:862:LEU:HB2	1.86	0.57
5:C:1296:ASP:CG	5:C:1322:SER:H	2.12	0.57
6:D:1024:THR:HG23	6:D:1124:ILE:H	1.70	0.57
5:C:521:LEU:HD12	5:C:794:LEU:HD21	1.86	0.57
5:C:732:ILE:HD11	5:C:769:PRO:HB3	1.85	0.57
6:D:113:HIS:HE1	6:D:115:TRP:HB2	1.65	0.57
2:T:14:DC:H2"	2:T:15:DC:OP2	2.05	0.56
4:B:84:ASN:HD21	6:D:551:ARG:HH22	1.51	0.56
5:C:68:LEU:HD11	5:C:100:LEU:HB3	1.86	0.56
5:C:325:LEU:O	5:C:328:SER:OG	2.19	0.56
5:C:404:LYS:NZ	5:C:449:GLY:O	2.31	0.56
6:D:644:MET:SD	6:D:740:LEU:HD23	2.45	0.56
2:T:19:DA:OP1	5:C:1269:ARG:NE	2.35	0.56
5:C:468:LEU:HA	5:C:471:VAL:HG12	1.87	0.56
5:C:1103:VAL:HG22	5:C:1111:GLN:HE21	1.69	0.56
6:D:310:GLY:HA2	6:D:315:ALA:HB2	1.86	0.56
6:D:1082:ASP:OD1	6:D:1085:GLY:N	2.37	0.56
7:E:25:ARG:NH2	7:E:68:GLU:OE1	2.38	0.56
3:F:77:TYR:OH	3:F:80:GLN:HB3	2.05	0.56
4:A:91:ARG:HB3	4:A:122:GLU:HB3	1.87	0.56
4:B:59:VAL:HG22	4:B:144:ILE:HA	1.85	0.56
5:C:1077:SER:OG	5:C:1078:LYS:N	2.37	0.56
5:C:1234:LYS:HE2	5:C:1238:LEU:HD11	1.86	0.56
6:D:209:ASN:HA	6:D:214:ARG:HH21	1.69	0.56
6:D:786:THR:HA	6:D:789:LYS:HE2	1.87	0.56
5:C:675:ASP:OD2	5:C:677:ASN:N	2.31	0.56
2:T:18:DC:H4'	5:C:1273:MET:HE2	1.88	0.56
4:A:105:SER:HB3	4:A:139:SER:HB2	1.88	0.56
6:D:373:ALA:O	6:D:376:LEU:N	2.38	0.56
6:D:961:SER:O	6:D:980:THR:HA	2.04	0.56
5:C:1239:VAL:O	5:C:1242:LYS:N	2.38	0.56
7:E:31:GLN:HB2	7:E:46:THR:HG21	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:562:GLU:OE1	5:C:662:SER:OG	2.22	0.56
5:C:931:VAL:HG22	5:C:1052:VAL:HG22	1.87	0.56
3:F:135:ASP:OD1	3:F:136:LEU:N	2.36	0.56
4:A:135:ASP:OD1	4:A:136:GLU:N	2.38	0.56
5:C:1331:ARG:HG2	6:D:102:MET:HE1	1.87	0.56
6:D:830:ASP:OD1	6:D:831:VAL:N	2.38	0.56
5:C:97:ARG:HD3	5:C:123:TYR:HB3	1.87	0.56
5:C:1209:GLN:HA	5:C:1225:VAL:O	2.05	0.56
5:C:1282:GLY:HA3	7:E:17:PHE:CZ	2.41	0.56
6:D:604:MET:HE1	6:D:620:PHE:CZ	2.41	0.56
6:D:1269:ALA:O	6:D:1272:SER:OG	2.14	0.56
5:C:921:PRO:O	5:C:924:VAL:HG22	2.06	0.55
6:D:1045:THR:HG22	6:D:1067:ARG:HD3	1.88	0.55
3:F:68:CYS:HA	3:F:72:LEU:HD13	1.89	0.55
4:B:44:ARG:HG3	4:B:183:ILE:HD11	1.88	0.55
5:C:818:VAL:HG22	5:C:1096:ILE:HG12	1.88	0.55
6:D:842:ARG:HH21	6:D:1251:LYS:CG	2.19	0.55
7:E:26:ARG:NE	7:E:53:GLU:OE1	2.37	0.55
2:T:19:DA:H5''	5:C:1269:ARG:HD3	1.88	0.55
4:B:15:ASP:OD1	4:B:16:ILE:N	2.39	0.55
5:C:667:LEU:HA	5:C:702:THR:HG21	1.88	0.55
6:D:615:LYS:HB2	6:D:616:PRO:HD3	1.88	0.55
2:T:22:DC:H2'	2:T:23:DA:C8	2.39	0.55
6:D:425:ARG:HD2	6:D:459:ALA:HB2	1.88	0.55
5:C:786:GLY:N	5:C:789:THR:OG1	2.40	0.55
5:C:256:GLU:HA	5:C:261:VAL:HA	1.89	0.55
5:C:387:ASN:HD21	5:C:394:ARG:HH11	1.53	0.55
5:C:498:ILE:HD12	5:C:498:ILE:H	1.72	0.55
5:C:1176:LEU:O	5:C:1179:GLY:N	2.22	0.55
6:D:722:ILE:HA	6:D:725:MET:HE3	1.88	0.55
6:D:1069:ALA:HA	6:D:1072:LYS:HB2	1.87	0.55
5:C:850:ILE:HG13	5:C:1048:LYS:HD3	1.88	0.55
5:C:1149:TYR:CE1	5:C:1180:MET:HE3	2.42	0.55
6:D:37:GLU:HB2	6:D:104:HIS:CE1	2.42	0.55
6:D:384:LYS:HG3	6:D:415:VAL:HG12	1.88	0.55
6:D:798:ARG:O	6:D:801:VAL:HG22	2.07	0.55
2:T:7:DA:H8	2:T:7:DA:OP2	1.89	0.55
5:C:300:ASP:OD1	5:C:313:ALA:N	2.38	0.54
5:C:402:ARG:HH21	5:C:417:SER:C	2.14	0.54
5:C:657:THR:OG1	5:C:1187:PHE:HB2	2.08	0.54
5:C:698:PRO:HG3	5:C:1231:TYR:CZ	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:1246:ARG:NH2	5:C:1249:GLY:H	2.00	0.54
6:D:289:ASP:HA	6:D:292:VAL:HG22	1.88	0.54
3:F:60:ARG:NH1	6:D:752:GLY:O	2.41	0.54
5:C:128:PRO:HG2	5:C:506:PHE:HD2	1.72	0.54
5:C:718:ALA:HA	5:C:751:TYR:CE2	2.42	0.54
5:C:1062:PRO:HB3	5:C:1077:SER:O	2.07	0.54
6:D:349:TYR:HE1	6:D:379:PRO:HG2	1.72	0.54
6:D:526:VAL:C	6:D:527:LEU:HD12	2.31	0.54
5:C:295:LYS:HB2	5:C:317:LEU:HD12	1.90	0.54
5:C:810:TYR:CD1	6:D:359:PRO:HD2	2.43	0.54
5:C:1071:GLY:O	5:C:1073:LYS:N	2.40	0.54
6:D:464:ASP:OD1	8:R:14:G:O2'	2.23	0.54
6:D:549:LYS:HG2	6:D:571:ASP:OD1	2.07	0.54
6:D:1168:GLU:HA	6:D:1173:ARG:HB2	1.89	0.54
6:D:1219:ASP:HA	6:D:1222:ARG:HG2	1.89	0.54
5:C:620:ASN:HD21	6:D:768:ASN:HB2	1.71	0.54
5:C:759:SER:HG	5:C:763:THR:H	1.54	0.54
6:D:513:MET:HE3	6:D:579:LEU:HB2	1.88	0.54
5:C:79:VAL:HG23	5:C:80:PHE:CD2	2.43	0.54
5:C:98:VAL:HG21	5:C:124:MET:HE3	1.88	0.54
5:C:302:ILE:HD13	5:C:307:GLY:HA2	1.90	0.54
5:C:69:GLN:NE2	5:C:101:ARG:HD2	2.19	0.54
5:C:155:VAL:HA	5:C:175:ARG:O	2.08	0.54
6:D:1025:MET:HB3	6:D:1124:ILE:HD12	1.89	0.54
6:D:1350:ASN:ND2	6:D:1358:PRO:HD3	2.19	0.54
4:B:62:ASP:OD1	4:B:63:GLY:N	2.41	0.54
5:C:519:ASN:HD22	5:C:689:ALA:HB3	1.72	0.54
5:C:964:LEU:HD12	5:C:967:LEU:HD23	1.90	0.54
6:D:342:LEU:HD23	6:D:1352:ILE:HG23	1.89	0.54
5:C:13:LYS:HB2	5:C:1149:TYR:CE1	2.42	0.54
6:D:794:GLY:O	6:D:797:THR:OG1	2.24	0.54
2:T:5:DG:OP2	2:T:5:DG:H8	1.91	0.54
6:D:269:TYR:CE1	6:D:306:LEU:HD11	2.42	0.54
2:T:23:DA:H2'	2:T:24:DT:C6	2.43	0.53
4:B:109:PRO:HA	4:B:132:HIS:CD2	2.43	0.53
5:C:1129:ASN:OD1	5:C:1177:ARG:NH2	2.41	0.53
6:D:107:LEU:HD23	6:D:276:ASN:ND2	2.23	0.53
5:C:690:VAL:HG12	5:C:1234:LYS:O	2.08	0.53
5:C:1225:VAL:HB	6:D:638:SER:HB2	1.90	0.53
5:C:590:PRO:HG3	5:C:605:TYR:HE1	1.73	0.53
5:C:605:TYR:C	5:C:606:LEU:HD12	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:838:CYS:HB2	5:C:918:LEU:HD22	1.90	0.53
6:D:1164:SER:HA	6:D:1200:GLU:HG2	1.90	0.53
8:R:12:G:H2'	8:R:13:U:H6	1.73	0.53
5:C:1212:LEU:HD13	5:C:1225:VAL:HG22	1.89	0.53
5:C:1247:SER:OG	5:C:1248:THR:N	2.41	0.53
6:D:1322:ALA:O	6:D:1325:PHE:N	2.36	0.53
5:C:93:SER:HA	5:C:128:PRO:HA	1.90	0.53
5:C:672:GLU:HG2	5:C:673:HIS:N	2.23	0.53
3:F:6:VAL:HG21	3:F:72:LEU:HB3	1.91	0.53
3:F:20:TYR:HD2	3:F:21:LEU:HD12	1.72	0.53
4:B:47:LEU:HD23	4:B:183:ILE:HD13	1.91	0.53
6:D:1208:ASP:OD1	6:D:1209:VAL:N	2.41	0.53
3:F:92:GLU:HG2	3:F:102:ARG:HB2	1.91	0.53
5:C:1276:TRP:CE2	6:D:801:VAL:HG21	2.42	0.53
3:G:91:VAL:HA	3:G:153:ILE:HA	1.90	0.53
5:C:210:LEU:HD11	5:C:429:MET:HE1	1.89	0.53
5:C:632:ASP:O	5:C:647:ARG:N	2.42	0.53
2:T:20:DC:H4'	6:D:352:ARG:HH22	1.73	0.53
5:C:61:SER:OG	5:C:64:GLY:N	2.41	0.53
5:C:339:ASN:ND2	5:C:342:ASP:H	2.07	0.53
5:C:550:VAL:HG23	5:C:554:HIS:ND1	2.24	0.53
6:D:425:ARG:HG2	6:D:427:PRO:HD2	1.90	0.53
6:D:709:ARG:NH1	6:D:713:GLU:H	2.06	0.53
6:D:968:ASN:OD1	6:D:972:LYS:N	2.41	0.53
1:N:27:DA:P	6:D:1148:ARG:HE	2.32	0.53
4:A:55:ALA:O	4:A:146:VAL:HG13	2.08	0.53
5:C:987:GLU:HG2	5:C:991:LYS:HE3	1.91	0.53
5:C:1211:ARG:C	5:C:1212:LEU:HD12	2.33	0.53
8:R:6:C:H2'	8:R:7:G:C8	2.43	0.53
5:C:18:ARG:HH21	5:C:620:ASN:C	2.17	0.52
6:D:341:ASN:C	6:D:342:LEU:HD12	2.34	0.52
6:D:473:THR:HG23	6:D:476:ALA:H	1.72	0.52
1:N:10:DG:O6	2:T:30:DC:N4	2.30	0.52
5:C:494:ASN:O	5:C:497:PRO:HD2	2.09	0.52
5:C:1122:LYS:HG2	5:C:1229:TYR:CZ	2.44	0.52
5:C:1173:ALA:O	5:C:1176:LEU:N	2.41	0.52
5:C:1192:GLU:HA	5:C:1195:ILE:HD12	1.91	0.52
3:F:47:ASP:H	6:D:736:GLN:HE21	1.57	0.52
3:F:82:GLU:HG2	3:F:83:GLY:H	1.74	0.52
5:C:189:ASP:O	5:C:192:ASP:N	2.39	0.52
5:C:705:GLU:H	5:C:705:GLU:CD	2.17	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:1255:THR:O	5:C:1257:GLN:N	2.42	0.52
5:C:1336:ASN:OD1	5:C:1337:ILE:N	2.42	0.52
6:D:45:ASN:C	6:D:47:ARG:H	2.18	0.52
6:D:943:ARG:O	6:D:947:GLU:HG2	2.09	0.52
1:N:25:DG:H2'	1:N:26:DG:C8	2.44	0.52
4:B:84:ASN:ND2	6:D:551:ARG:HH22	2.08	0.52
4:B:219:ARG:O	4:B:223:ILE:HG12	2.09	0.52
5:C:10:ARG:NH1	5:C:791:LEU:HD12	2.24	0.52
6:D:37:GLU:CD	6:D:106:GLU:H	2.16	0.52
6:D:511:TYR:HE2	6:D:515:ARG:HH11	1.56	0.52
6:D:1252:HIS:O	6:D:1255:VAL:HG12	2.09	0.52
2:T:6:DA:H2''	2:T:7:DA:C8	2.44	0.52
5:C:759:SER:OG	5:C:762:ASN:N	2.43	0.52
6:D:552:ILE:O	6:D:567:THR:OG1	2.16	0.52
3:F:64:TYR:HD2	3:F:65:LEU:HD12	1.74	0.52
5:C:387:ASN:HD21	5:C:394:ARG:NH1	2.07	0.52
5:C:878:THR:N	5:C:881:ASP:OD2	2.43	0.52
6:D:264:ASP:OD2	6:D:325:LYS:N	2.33	0.52
6:D:481:ARG:HA	6:D:485:MET:HE3	1.92	0.52
6:D:577:ALA:O	6:D:580:TRP:N	2.42	0.52
6:D:741:ALA:C	6:D:762:ASN:HD22	2.15	0.52
6:D:865:HIS:CD2	6:D:867:GLN:H	2.27	0.52
6:D:1233:ILE:O	6:D:1237:VAL:HG12	2.09	0.52
6:D:141:PHE:HD1	6:D:180:MET:HE2	1.75	0.52
6:D:495:ASN:HD22	6:D:1247:LYS:HB2	1.75	0.52
2:T:34:DC:H2'	2:T:35:DT:C6	2.45	0.52
6:D:956:GLY:CA	6:D:985:ILE:O	2.58	0.52
6:D:1263:LYS:HA	6:D:1281:GLU:HA	1.90	0.52
7:E:8:ASP:HB2	7:E:55:GLU:CD	2.35	0.52
3:F:59:ASP:HA	3:F:62:VAL:HG12	1.91	0.52
4:A:195:ARG:HE	4:A:198:LEU:HD11	1.75	0.52
5:C:1284:ALA:HB3	6:D:1361:THR:HB	1.91	0.52
6:D:420:PRO:HA	6:D:437:PHE:O	2.10	0.52
6:D:1029:THR:N	6:D:1119:ASP:O	2.40	0.52
3:F:43:SER:O	3:F:49:GLN:NE2	2.42	0.51
6:D:361:LEU:HA	6:D:365:GLN:HE21	1.74	0.51
6:D:452:LEU:HG	6:D:625:MET:CE	2.40	0.51
2:T:20:DC:H2'	2:T:21:DA:C8	2.45	0.51
6:D:193:ASP:OD1	6:D:194:LEU:N	2.43	0.51
6:D:888:CYS:SG	6:D:889:ASP:N	2.83	0.51
3:F:119:SER:OG	3:F:120:ILE:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:796:LEU:N	5:C:1231:TYR:OH	2.43	0.51
5:C:1325:VAL:HG13	6:D:249:LEU:HD13	1.91	0.51
2:T:10:DT:OP2	2:T:10:DT:H2'	2.11	0.51
2:T:20:DC:C3'	6:D:352:ARG:HH22	2.24	0.51
4:A:150:ARG:NH1	4:B:7:GLU:O	2.27	0.51
4:A:231:PHE:HE2	4:B:43:LEU:HD21	1.76	0.51
4:B:110:VAL:HG12	4:B:130:ILE:HD12	1.91	0.51
5:C:560:PRO:O	6:D:780:ARG:NH2	2.44	0.51
5:C:702:THR:C	5:C:1183:ALA:HB1	2.36	0.51
6:D:349:TYR:CD2	6:D:472:LEU:HD11	2.46	0.51
3:F:35:TRP:HB3	6:D:599:LYS:NZ	2.25	0.51
4:A:79:LEU:HD21	5:C:693:LEU:HD11	1.93	0.51
5:C:558:VAL:HG11	5:C:573:ASN:HB3	1.92	0.51
5:C:1280:ALA:HB1	6:D:918:ILE:HG22	1.92	0.51
6:D:110:PRO:HB2	6:D:182:ALA:HB1	1.92	0.51
6:D:513:MET:HE1	6:D:579:LEU:HD13	1.92	0.51
6:D:607:THR:HA	6:D:610:ARG:HG2	1.91	0.51
6:D:921:GLN:O	6:D:924:GLY:N	2.43	0.51
6:D:1107:VAL:HG22	6:D:1122:ALA:HB2	1.92	0.51
2:T:25:DC:OP1	5:C:139:ASN:ND2	2.43	0.51
5:C:133:ASN:CG	5:C:713:GLY:HA3	2.36	0.51
5:C:702:THR:N	5:C:705:GLU:OE2	2.33	0.51
5:C:1116:HIS:CE1	6:D:641:ILE:HG22	2.46	0.51
5:C:1239:VAL:HG13	5:C:1240:ASP:N	2.25	0.51
6:D:57:PHE:HB3	6:D:98:ARG:HH12	1.74	0.51
6:D:1036:ARG:NE	6:D:1081:VAL:HG11	2.26	0.51
3:F:84:LYS:HD3	3:F:130:LYS:HG2	1.92	0.51
4:B:190:ALA:HB2	4:B:200:LYS:HB2	1.92	0.51
5:C:257:ALA:HB1	5:C:282:VAL:HG11	1.93	0.51
5:C:960:LEU:HB3	5:C:1025:PHE:CE1	2.46	0.51
5:C:1002:LEU:HD22	5:C:1008:GLN:HB2	1.93	0.51
7:E:17:PHE:O	7:E:20:VAL:N	2.44	0.51
5:C:177:ILE:HG12	5:C:183:TRP:CD1	2.46	0.51
5:C:389:PHE:HB2	5:C:390:PHE:CE2	2.46	0.51
5:C:1002:LEU:HD21	5:C:1007:LYS:HB2	1.93	0.51
2:T:5:DG:H2''	2:T:6:DA:N7	2.26	0.51
4:A:58:GLU:HB2	4:A:145:LYS:HB3	1.92	0.51
5:C:1058:ARG:HE	5:C:1240:ASP:CG	2.19	0.51
6:D:640:GLY:O	6:D:643:ASP:HB2	2.10	0.51
5:C:633:LEU:HA	5:C:645:PHE:O	2.11	0.50
5:C:804:PHE:HB3	5:C:1100:PRO:HG3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:1232:MET:C	5:C:1233:LEU:HD12	2.35	0.50
6:D:1140:ARG:HH21	6:D:1236:GLU:CD	2.18	0.50
4:A:149:GLY:HA3	4:A:177:TYR:CZ	2.46	0.50
5:C:1256:GLN:NE2	6:D:99:ARG:HH22	2.09	0.50
6:D:537:TYR:CE1	6:D:544:LEU:HD13	2.46	0.50
2:T:6:DA:H2"	2:T:7:DA:H8	1.75	0.50
4:B:41:ASN:ND2	5:C:1216:ARG:O	2.43	0.50
6:D:147:ILE:HG12	6:D:178:ALA:HA	1.93	0.50
6:D:555:TYR:HD2	6:D:585:LYS:HB3	1.76	0.50
6:D:572:THR:OG1	6:D:576:ARG:HD2	2.12	0.50
6:D:743:MET:HG3	6:D:745:GLY:H	1.76	0.50
5:C:1043:ALA:O	5:C:1046:VAL:HG12	2.12	0.50
5:C:101:ARG:HH21	5:C:118:LYS:NZ	2.10	0.50
5:C:1256:GLN:HE21	6:D:99:ARG:HH22	1.57	0.50
6:D:252:LEU:HD11	6:D:260:PHE:HB3	1.93	0.50
6:D:709:ARG:NH1	6:D:712:GLN:H	2.09	0.50
6:D:709:ARG:CZ	6:D:712:GLN:H	2.24	0.50
6:D:726:ALA:O	6:D:729:GLY:N	2.35	0.50
2:T:13:DT:C4	2:T:14:DC:N4	2.80	0.50
3:F:87:PHE:CD1	3:F:120:ILE:HD12	2.47	0.50
4:A:231:PHE:CE2	4:B:43:LEU:HD21	2.46	0.50
5:C:84:GLU:HA	5:C:87:ILE:HD12	1.93	0.50
5:C:809:GLY:O	5:C:811:ASN:N	2.44	0.50
6:D:826:ILE:HG22	6:D:828:GLY:H	1.76	0.50
4:A:23:HIS:HB2	4:A:205:MET:O	2.12	0.50
5:C:914:LYS:HG2	5:C:915:ASP:N	2.27	0.50
5:C:1109:ILE:HG12	6:D:644:MET:HE1	1.94	0.50
5:C:1239:VAL:HG13	5:C:1240:ASP:H	1.77	0.50
6:D:93:THR:HG22	6:D:94:GLN:N	2.25	0.50
6:D:349:TYR:CE2	6:D:472:LEU:HD11	2.46	0.50
6:D:1242:ARG:O	6:D:1245:GLY:N	2.44	0.50
7:E:9:ALA:N	7:E:55:GLU:OE2	2.42	0.50
5:C:715:THR:OG1	5:C:784:ALA:O	2.28	0.50
5:C:1035:LYS:O	5:C:1038:GLN:HG2	2.11	0.50
6:D:188:LEU:O	6:D:191:SER:OG	2.24	0.50
5:C:41:GLN:NE2	5:C:73:TYR:O	2.45	0.49
5:C:88:ARG:HA	5:C:934:PHE:CZ	2.46	0.49
5:C:724:VAL:HB	5:C:775:GLU:H	1.77	0.49
5:C:1082:ILE:H	5:C:1082:ILE:HD12	1.75	0.49
5:C:1220:GLN:HG2	5:C:1221:PHE:O	2.11	0.49
6:D:233:LYS:O	6:D:236:TRP:HB2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:826:ILE:HG22	6:D:828:GLY:N	2.27	0.49
6:D:1051:ASP:HB3	6:D:1054:THR:OG1	2.11	0.49
5:C:11:ILE:HG22	5:C:1172:LEU:HD11	1.93	0.49
5:C:870:ILE:HD13	5:C:944:ARG:HD3	1.93	0.49
5:C:1323:PHE:CZ	5:C:1327:LEU:HD11	2.47	0.49
6:D:1050:THR:HA	6:D:1057:SER:HA	1.94	0.49
6:D:1155:ILE:C	6:D:1156:LEU:HD12	2.38	0.49
6:D:1309:ILE:HG13	6:D:1310:THR:N	2.26	0.49
3:F:47:ASP:N	6:D:736:GLN:HE21	2.10	0.49
4:B:102:LEU:HD13	4:B:115:ILE:HA	1.94	0.49
5:C:699:LEU:HG	5:C:799:ASN:HD22	1.78	0.49
5:C:747:GLY:C	5:C:974:ARG:HH21	2.17	0.49
5:C:798:GLN:OE1	5:C:827:ARG:HB2	2.12	0.49
5:C:886:LYS:HG2	5:C:916:SER:HB2	1.94	0.49
6:D:74:LYS:HG2	6:D:75:TYR:CD1	2.48	0.49
6:D:416:ILE:O	6:D:418:GLU:N	2.46	0.49
6:D:705:THR:OG1	6:D:718:SER:HA	2.12	0.49
6:D:735:ALA:O	6:D:738:ARG:HB3	2.13	0.49
6:D:1269:ALA:HB1	6:D:1272:SER:HB2	1.93	0.49
4:B:219:ARG:O	4:B:222:THR:OG1	2.28	0.49
5:C:1254:VAL:HG13	5:C:1255:THR:N	2.26	0.49
5:C:1283:ALA:HA	6:D:479:GLU:OE1	2.11	0.49
6:D:919:ALA:HA	6:D:1252:HIS:ND1	2.27	0.49
6:D:1061:VAL:O	6:D:1104:LYS:CA	2.59	0.49
6:D:1357:ILE:O	6:D:1362:GLY:HA3	2.12	0.49
4:A:71:LYS:HE2	4:A:140:ILE:HG22	1.93	0.49
5:C:98:VAL:O	5:C:121:GLU:HA	2.12	0.49
5:C:742:TYR:HB3	5:C:743:PRO:HD2	1.94	0.49
5:C:1288:GLN:NE2	5:C:1317:PRO:HB3	2.28	0.49
6:D:95:THR:O	6:D:98:ARG:HB3	2.11	0.49
6:D:113:HIS:CD2	6:D:239:LEU:HD11	2.44	0.49
6:D:1178:THR:HA	6:D:1184:ASP:HB3	1.93	0.49
3:F:95:ASN:HB3	3:F:99:VAL:H	1.78	0.49
5:C:12:ARG:HH21	5:C:793:GLU:CD	2.15	0.49
5:C:215:TYR:HE2	5:C:426:ILE:HD11	1.77	0.49
6:D:957:SER:HB3	6:D:985:ILE:HB	1.94	0.49
6:D:1046:ILE:HD12	6:D:1059:LEU:HD22	1.94	0.49
3:F:25:GLU:OE2	3:F:54:ARG:NH2	2.46	0.49
5:C:678:ARG:HG3	5:C:1106:ARG:HB3	1.94	0.49
5:C:821:ARG:O	5:C:824:GLN:HB2	2.13	0.49
6:D:1026:PRO:HB2	6:D:1028:ILE:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:205:PRO:O	5:C:208:ILE:HG22	2.13	0.49
5:C:742:TYR:H	5:C:746:ALA:HB2	1.78	0.49
5:C:1069:ARG:NH2	5:C:1114:GLU:OE2	2.39	0.49
5:C:1105:SER:HA	6:D:736:GLN:OE1	2.13	0.49
6:D:140:TYR:OH	6:D:312:ARG:HG2	2.12	0.49
6:D:1138:LEU:HB3	6:D:1139:PRO:HD3	1.94	0.49
6:D:1266:ILE:HB	6:D:1276:GLU:O	2.12	0.49
3:G:90:TRP:N	3:G:154:GLU:O	2.46	0.49
5:C:10:ARG:HH11	5:C:697:LYS:HD3	1.77	0.49
5:C:624:ASP:O	5:C:626:GLU:N	2.46	0.49
5:C:997:TRP:CD1	5:C:1000:LEU:HD21	2.48	0.49
4:B:15:ASP:HB3	4:B:27:THR:OG1	2.13	0.49
5:C:223:LEU:HD21	5:C:426:ILE:HG23	1.94	0.49
5:C:1124:ILE:HG21	5:C:1180:MET:SD	2.53	0.49
5:C:1285:TYR:HD2	6:D:475:GLU:HB3	1.76	0.49
6:D:485:MET:O	6:D:487:THR:N	2.46	0.49
6:D:501:VAL:HG22	6:D:502:PRO:O	2.13	0.49
6:D:580:TRP:CZ3	6:D:589:TYR:HA	2.47	0.49
6:D:1163:VAL:HG12	6:D:1202:GLU:O	2.12	0.49
6:D:1272:SER:HB3	6:D:1274:PHE:HD2	1.76	0.49
5:C:915:ASP:CG	5:C:917:SER:H	2.20	0.48
6:D:153:ASN:C	6:D:154:LEU:HD12	2.38	0.48
6:D:254:PRO:HA	6:D:260:PHE:CD1	2.48	0.48
6:D:336:GLY:O	6:D:340:GLN:CB	2.61	0.48
6:D:432:LEU:O	6:D:434:ILE:N	2.45	0.48
6:D:750:PRO:HD3	6:D:777:HIS:CD2	2.48	0.48
6:D:968:ASN:ND2	6:D:972:LYS:HB2	2.28	0.48
2:T:29:DA:H2"	2:T:30:DC:C6	2.48	0.48
3:F:51:ASN:O	3:F:55:LEU:HG	2.13	0.48
5:C:18:ARG:HE	5:C:620:ASN:HA	1.78	0.48
5:C:148:GLN:OE1	5:C:454:ARG:NH1	2.46	0.48
5:C:594:VAL:HG12	5:C:595:THR:O	2.13	0.48
5:C:747:GLY:HA2	5:C:974:ARG:HE	1.78	0.48
5:C:1264:GLN:O	5:C:1266:GLY:N	2.45	0.48
6:D:1126:GLN:HE21	6:D:1195:GLN:HE21	1.59	0.48
3:F:141:THR:N	3:F:144:GLY:O	2.46	0.48
5:C:569:ILE:C	5:C:571:LEU:H	2.20	0.48
5:C:810:TYR:CE1	6:D:359:PRO:HD2	2.48	0.48
4:A:49:SER:OG	4:A:50:SER:N	2.46	0.48
5:C:232:ILE:HG12	5:C:237:LEU:HG	1.96	0.48
5:C:1314:GLN:HB2	7:E:28:ARG:HH12	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:725:MET:O	6:D:728:SER:OG	2.31	0.48
6:D:1284:ARG:O	6:D:1287:ILE:HG13	2.13	0.48
6:D:1349:GLU:OE1	6:D:1349:GLU:N	2.37	0.48
6:D:1357:ILE:HG22	6:D:1359:ALA:H	1.77	0.48
5:C:39:ILE:HD11	5:C:75:LEU:HD22	1.94	0.48
6:D:103:GLY:C	6:D:244:VAL:HG22	2.37	0.48
6:D:805:GLN:O	6:D:1347:LEU:HB2	2.13	0.48
1:N:36:DA:H2	2:T:4:DT:H3	1.60	0.48
5:C:30:ILE:HD12	5:C:30:ILE:H	1.79	0.48
5:C:575:LEU:HD23	5:C:576:SER:O	2.14	0.48
5:C:870:ILE:HB	5:C:944:ARG:HD3	1.96	0.48
5:C:886:LYS:O	5:C:916:SER:N	2.40	0.48
5:C:1293:VAL:HG11	5:C:1304:MET:HG2	1.96	0.48
6:D:805:GLN:OE1	6:D:1348:LYS:HB2	2.13	0.48
5:C:459:MET:HB3	5:C:505:PHE:CZ	2.49	0.48
5:C:848:GLU:HG2	5:C:889:PRO:HD3	1.96	0.48
5:C:1211:ARG:O	5:C:1212:LEU:HD12	2.14	0.48
6:D:369:PRO:HG3	6:D:446:ALA:O	2.14	0.48
6:D:1172:LYS:HA	6:D:1190:ILE:C	2.37	0.48
1:N:9:DC:C2	1:N:10:DG:C8	3.02	0.48
4:B:158:ARG:HA	4:B:161:SER:OG	2.13	0.48
6:D:495:ASN:ND2	6:D:1247:LYS:O	2.47	0.48
6:D:611:ILE:HG22	6:D:612:LEU:HD12	1.94	0.48
6:D:865:HIS:CE1	6:D:868:TRP:HD1	2.31	0.48
5:C:662:SER:O	5:C:666:SER:N	2.30	0.48
6:D:823:THR:HG22	6:D:879:ALA:HB2	1.95	0.48
6:D:850:LYS:HG2	6:D:852:GLY:H	1.79	0.48
3:F:24:GLU:C	3:F:27:PRO:HD2	2.39	0.47
3:F:26:ARG:NH2	6:D:1243:LEU:O	2.46	0.47
5:C:195:PHE:CD1	5:C:203:LYS:HG2	2.49	0.47
5:C:688:GLN:HE22	8:R:13:U:H5'	1.78	0.47
6:D:136:GLU:O	6:D:139:LEU:N	2.47	0.47
6:D:336:GLY:O	6:D:340:GLN:HB3	2.14	0.47
6:D:555:TYR:HB2	6:D:585:LYS:O	2.14	0.47
6:D:1056:LEU:HD13	6:D:1108:GLN:HE22	1.79	0.47
5:C:240:GLU:C	5:C:241:LEU:HD12	2.38	0.47
5:C:673:HIS:ND1	6:D:763:PHE:O	2.45	0.47
6:D:130:MET:HB3	6:D:135:ILE:HD11	1.95	0.47
6:D:709:ARG:HG3	6:D:711:GLY:H	1.78	0.47
6:D:1158:GLU:HG3	6:D:1186:TYR:CE2	2.49	0.47
6:D:1357:ILE:C	6:D:1359:ALA:H	2.21	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:319:LEU:HA	5:C:322:LEU:HD12	1.96	0.47
5:C:1067:ALA:HB2	5:C:1073:LYS:HA	1.96	0.47
5:C:1118:GLY:O	5:C:1119:MET:C	2.57	0.47
5:C:1331:ARG:HG3	6:D:33:TRP:CH2	2.50	0.47
6:D:907:HIS:ND1	6:D:908:ILE:O	2.46	0.47
6:D:1029:THR:HG23	6:D:1119:ASP:O	2.14	0.47
4:A:152:TYR:CE1	5:C:824:GLN:HG2	2.49	0.47
4:B:47:LEU:HD23	4:B:183:ILE:HG21	1.96	0.47
5:C:52:ALA:O	5:C:55:SER:OG	2.22	0.47
5:C:530:ILE:HB	5:C:573:ASN:O	2.14	0.47
5:C:873:ILE:HG13	5:C:944:ARG:HH22	1.80	0.47
5:C:1285:TYR:CD2	6:D:475:GLU:HB3	2.49	0.47
5:C:1289:GLU:OE2	6:D:472:LEU:HB2	2.15	0.47
6:D:68:TYR:OH	6:D:94:GLN:HG3	2.14	0.47
6:D:450:HIS:HE1	6:D:452:LEU:HG	1.80	0.47
6:D:860:ARG:HG3	6:D:861:ASN:CG	2.40	0.47
1:N:24:DC:N3	2:T:16:DA:C2	2.83	0.47
4:B:192:VAL:HG12	4:B:193:GLU:N	2.26	0.47
5:C:519:ASN:O	5:C:522:SER:N	2.47	0.47
5:C:558:VAL:CG1	5:C:573:ASN:HB3	2.44	0.47
5:C:599:VAL:H	5:C:627:GLY:CA	2.28	0.47
5:C:805:MET:HE1	5:C:1221:PHE:CE2	2.50	0.47
5:C:1333:LEU:C	5:C:1335:ILE:H	2.23	0.47
8:R:9:U:H2'	8:R:10:G:H8	1.79	0.47
8:R:12:G:H2'	8:R:13:U:C6	2.49	0.47
4:A:57:THR:HG23	4:A:158:ARG:NH1	2.29	0.47
4:A:208:ASN:OD1	4:A:209:GLY:N	2.48	0.47
5:C:1103:VAL:HB	5:C:1104:PRO:HD3	1.96	0.47
6:D:40:LYS:HB3	6:D:42:GLU:OE1	2.14	0.47
6:D:611:ILE:C	6:D:612:LEU:HD12	2.40	0.47
6:D:628:GLY:O	6:D:629:PHE:C	2.57	0.47
1:N:29:DG:N2	2:T:11:DC:C2	2.83	0.47
3:F:140:ASN:HA	3:F:145:GLU:HA	1.97	0.47
5:C:257:ALA:HB3	5:C:262:TYR:CE2	2.50	0.47
6:D:45:ASN:ND2	6:D:48:THR:H	2.13	0.47
6:D:215:LYS:O	6:D:218:THR:HG22	2.14	0.47
6:D:347:VAL:HG12	6:D:348:ASP:O	2.14	0.47
6:D:1090:ILE:HB	6:D:1093:THR:OG1	2.15	0.47
6:D:1181:ASP:OD1	6:D:1182:GLY:N	2.47	0.47
6:D:1261:LEU:HD12	6:D:1304:ARG:HH21	1.79	0.47
7:E:54:ILE:HD13	7:E:59:ILE:HB	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:144:ILE:HG22	4:A:146:VAL:HG23	1.97	0.47
5:C:355:PRO:HG2	5:C:356:THR:HG23	1.97	0.47
5:C:421:SER:OG	5:C:424:ASP:N	2.40	0.47
6:D:983:LYS:HA	6:D:993:GLU:O	2.14	0.47
7:E:10:VAL:HG21	7:E:16:ARG:HH11	1.80	0.47
7:E:54:ILE:O	7:E:57:GLY:N	2.42	0.47
5:C:15:PHE:CG	5:C:1190:ALA:HB2	2.49	0.47
5:C:102:LEU:HD23	5:C:117:ILE:HD11	1.97	0.47
5:C:591:TYR:HD2	5:C:606:LEU:HD13	1.80	0.47
5:C:684:ASN:OD1	5:C:687:ARG:NH2	2.48	0.47
5:C:845:LEU:HD21	5:C:890:LYS:HA	1.97	0.47
5:C:960:LEU:O	5:C:963:GLU:HB2	2.14	0.47
3:F:26:ARG:NH1	3:F:55:LEU:HD22	2.30	0.47
4:B:59:VAL:HG21	4:B:85:LEU:HD13	1.96	0.47
5:C:1116:HIS:HE1	6:D:641:ILE:H	1.63	0.47
5:C:1214:ASP:HB3	5:C:1217:THR:OG1	2.14	0.47
6:D:30:ILE:O	6:D:33:TRP:HB2	2.16	0.47
6:D:85:CYS:C	6:D:89:GLY:HA2	2.39	0.47
4:A:135:ASP:HB3	4:A:138:ALA:HB3	1.96	0.46
6:D:816:THR:HB	6:D:818:GLU:OE1	2.15	0.46
3:F:77:TYR:HE2	3:F:81:GLN:H	1.63	0.46
4:B:78:ILE:O	4:B:82:LEU:HG	2.16	0.46
5:C:620:ASN:HD21	6:D:768:ASN:CB	2.28	0.46
5:C:1296:ASP:OD1	5:C:1321:GLU:HB3	2.14	0.46
6:D:1041:ILE:HG22	6:D:1044:GLN:HB2	1.97	0.46
6:D:805:GLN:OE1	6:D:1348:LYS:HE3	2.16	0.46
6:D:818:GLU:OE1	6:D:818:GLU:N	2.48	0.46
6:D:1073:ASP:HA	6:D:1075:ARG:HH12	1.80	0.46
1:N:24:DC:H42	2:T:16:DA:H61	1.63	0.46
4:A:152:TYR:CE1	5:C:824:GLN:HA	2.50	0.46
5:C:13:LYS:HD3	5:C:14:ASP:N	2.29	0.46
5:C:471:VAL:O	5:C:475:VAL:HG23	2.16	0.46
5:C:615:VAL:HG21	5:C:645:PHE:HD2	1.80	0.46
6:D:275:ARG:HG2	6:D:299:LEU:HA	1.98	0.46
6:D:508:LEU:HD21	6:D:637:ALA:HB3	1.97	0.46
5:C:1305:TYR:O	5:C:1309:VAL:HG13	2.16	0.46
6:D:1047:THR:HB	6:D:1062:LEU:HD11	1.98	0.46
2:T:5:DG:H2''	2:T:6:DA:C8	2.50	0.46
2:T:21:DA:H2'	2:T:22:DC:C6	2.51	0.46
4:A:188:GLU:OE2	4:A:200:LYS:HD2	2.15	0.46
4:B:180:VAL:HA	4:B:207:THR:HA	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:702:THR:HA	5:C:1184:THR:H	1.80	0.46
5:C:803:ALA:CB	5:C:1227:VAL:HG12	2.46	0.46
5:C:812:PHE:HD2	5:C:813:GLU:HG2	1.80	0.46
5:C:1246:ARG:HH21	5:C:1249:GLY:N	2.04	0.46
6:D:135:ILE:O	6:D:138:VAL:HB	2.16	0.46
6:D:136:GLU:OE2	6:D:312:ARG:NH2	2.45	0.46
5:C:206:ALA:O	5:C:209:ILE:HG22	2.16	0.46
5:C:669:PRO:HG3	5:C:1069:ARG:NH2	2.30	0.46
5:C:1032:LYS:HE2	5:C:1036:ILE:HD11	1.97	0.46
5:C:1288:GLN:HG3	6:D:1356:LEU:HD23	1.98	0.46
6:D:330:MET:O	6:D:337:ARG:HG2	2.15	0.46
6:D:521:LYS:O	6:D:543:SER:N	2.35	0.46
6:D:1143:ASP:OD1	6:D:1148:ARG:HD2	2.15	0.46
4:A:113:ALA:HB2	4:A:126:PRO:HB3	1.98	0.46
5:C:448:LEU:HD11	5:C:554:HIS:HA	1.98	0.46
5:C:590:PRO:HG3	5:C:605:TYR:CE1	2.51	0.46
5:C:639:LYS:O	5:C:641:GLU:HG2	2.15	0.46
5:C:1151:LEU:HD21	5:C:1198:LEU:HD13	1.97	0.46
5:C:1281:TYR:CZ	6:D:431:ARG:HG2	2.51	0.46
6:D:290:ILE:HD12	6:D:290:ILE:H	1.79	0.46
3:F:26:ARG:HB3	3:F:27:PRO:HD3	1.97	0.46
3:F:111:ILE:O	3:F:112:PHE:CD1	2.69	0.46
4:B:79:LEU:O	4:B:82:LEU:HB2	2.16	0.46
5:C:726:TYR:CE2	5:C:728:ASP:HB2	2.51	0.46
5:C:1119:MET:HG3	5:C:1204:LEU:HD13	1.97	0.46
6:D:697:MET:HG3	6:D:698:MET:N	2.29	0.46
6:D:804:ALA:C	6:D:806:ASP:H	2.23	0.46
4:A:155:ALA:O	4:A:158:ARG:N	2.49	0.46
6:D:146:VAL:HB	6:D:156:ARG:O	2.15	0.46
6:D:709:ARG:CG	6:D:711:GLY:H	2.29	0.46
6:D:805:GLN:HG2	6:D:1347:LEU:HB2	1.98	0.46
1:N:30:DA:H2''	1:N:31:DG:C8	2.51	0.45
3:F:87:PHE:CG	3:F:88:GLY:N	2.83	0.45
4:A:83:LEU:O	4:A:86:LYS:HB3	2.16	0.45
4:B:179:PRO:O	4:B:208:ASN:N	2.32	0.45
5:C:70:TYR:HA	5:C:100:LEU:HD23	1.98	0.45
5:C:204:LEU:HB3	5:C:208:ILE:HG21	1.96	0.45
5:C:615:VAL:HG13	5:C:650:VAL:HA	1.98	0.45
6:D:709:ARG:NH1	6:D:713:GLU:O	2.49	0.45
6:D:901:ARG:NH2	6:D:906:GLY:HA2	2.30	0.45
2:T:20:DC:C4'	6:D:352:ARG:HH22	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:141:THR:HG22	6:D:671:GLY:HA3	1.98	0.45
5:C:1063:GLY:H	5:C:1076:ILE:HG23	1.81	0.45
6:D:1363:TYR:OH	6:D:1367:GLN:NE2	2.49	0.45
3:F:94:GLU:OE2	3:F:151:ASN:ND2	2.49	0.45
4:A:32:GLU:HB2	4:A:35:PHE:CD2	2.51	0.45
5:C:148:GLN:OE1	5:C:459:MET:HE1	2.16	0.45
5:C:202:ARG:HH21	5:C:369:MET:HA	1.81	0.45
6:D:865:HIS:CE1	6:D:868:TRP:CD1	3.05	0.45
6:D:1064:SER:O	6:D:1072:LYS:NZ	2.29	0.45
4:A:47:LEU:HD23	4:A:47:LEU:HA	1.77	0.45
4:B:149:GLY:HA3	4:B:177:TYR:CZ	2.51	0.45
5:C:242:VAL:O	5:C:245:ARG:HB2	2.16	0.45
5:C:559:CYS:SG	5:C:561:ILE:N	2.77	0.45
5:C:886:LYS:NZ	5:C:916:SER:HB3	2.30	0.45
6:D:1039:ASP:HB3	6:D:1077:ALA:HB3	1.98	0.45
5:C:409:LEU:HD23	5:C:409:LEU:HA	1.80	0.45
5:C:1277:ALA:O	5:C:1280:ALA:N	2.50	0.45
6:D:526:VAL:HG12	6:D:549:LYS:HB2	1.99	0.45
6:D:537:TYR:CE1	6:D:544:LEU:HB2	2.52	0.45
4:B:47:LEU:HD11	4:B:180:VAL:HG11	1.99	0.45
4:B:51:MET:O	4:B:150:ARG:HA	2.17	0.45
5:C:223:LEU:HD11	5:C:426:ILE:HG21	1.98	0.45
6:D:90:VAL:HG12	6:D:91:GLU:O	2.16	0.45
6:D:137:ARG:HG2	6:D:142:GLU:OE2	2.16	0.45
6:D:432:LEU:HD22	6:D:435:GLN:HE21	1.82	0.45
6:D:454:CYS:O	6:D:457:TYR:N	2.50	0.45
6:D:1039:ASP:O	6:D:1076:PRO:HA	2.17	0.45
6:D:1251:LYS:O	6:D:1254:GLU:HB2	2.17	0.45
2:T:15:DC:H5'	2:T:15:DC:C6	2.52	0.45
5:C:162:GLY:O	5:C:164:THR:N	2.49	0.45
5:C:175:ARG:HG2	5:C:185:ASP:CG	2.42	0.45
5:C:818:VAL:CG2	5:C:1066:MET:HE1	2.45	0.45
5:C:929:ILE:HG13	5:C:930:ASP:N	2.30	0.45
5:C:1081:PRO:HB2	5:C:1083:GLU:OE1	2.17	0.45
6:D:128:LEU:HD13	6:D:128:LEU:O	2.16	0.45
6:D:1326:GLN:O	6:D:1327:GLU:HB3	2.17	0.45
3:F:46:ALA:HA	3:F:49:GLN:HB2	1.98	0.45
3:F:90:TRP:CE2	3:F:104:ARG:HB2	2.51	0.45
5:C:1308:ILE:HD12	6:D:380:PHE:CE1	2.52	0.45
6:D:341:ASN:O	6:D:345:LYS:HE2	2.16	0.45
6:D:918:ILE:HG13	6:D:919:ALA:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:29:DA:P	5:C:496:LYS:HZ3	2.40	0.45
4:B:102:LEU:HB3	4:B:142:MET:SD	2.57	0.45
5:C:37:LYS:HD2	5:C:47:TYR:CE1	2.52	0.45
5:C:232:ILE:HB	5:C:331:LYS:HA	1.99	0.45
5:C:580:GLN:HB2	5:C:588:GLU:HG3	1.98	0.45
5:C:1069:ARG:CZ	5:C:1231:TYR:HD2	2.30	0.45
5:C:1094:VAL:HG22	5:C:1095:ASP:N	2.31	0.45
5:C:1101:LEU:HD12	6:D:505:ASP:OD1	2.17	0.45
6:D:1036:ARG:HA	6:D:1111:ASP:OD1	2.16	0.45
6:D:1163:VAL:HG22	6:D:1164:SER:H	1.82	0.45
6:D:1173:ARG:HG3	6:D:1174:ARG:N	2.31	0.45
4:A:48:LEU:HD23	4:A:48:LEU:HA	1.76	0.45
5:C:344:GLY:HA3	5:C:346:TYR:CE2	2.52	0.45
5:C:1149:TYR:CD1	5:C:1180:MET:HE3	2.52	0.45
5:C:1304:MET:HE3	5:C:1308:ILE:HD11	1.98	0.45
6:D:59:ALA:HB1	6:D:90:VAL:HG11	1.98	0.45
6:D:362:ARG:N	6:D:365:GLN:HE21	2.14	0.45
6:D:850:LYS:HB3	6:D:855:ASP:HB2	1.98	0.45
6:D:1036:ARG:HG3	6:D:1081:VAL:HG21	1.99	0.45
6:D:1215:GLU:OE2	6:D:1224:ARG:NH1	2.50	0.45
7:E:21:LEU:HD23	7:E:21:LEU:HA	1.81	0.45
2:T:14:DC:C2	2:T:15:DC:C4	3.05	0.44
2:T:17:DG:H2'	2:T:18:DC:C6	2.52	0.44
4:A:57:THR:O	4:A:173:VAL:HG22	2.17	0.44
5:C:521:LEU:HD13	5:C:796:LEU:HD21	1.98	0.44
5:C:633:LEU:HD13	5:C:644:LEU:HD23	1.99	0.44
6:D:74:LYS:HG2	6:D:75:TYR:CE1	2.52	0.44
6:D:358:GLY:N	6:D:359:PRO:HD3	2.32	0.44
6:D:1028:ILE:HA	6:D:1120:THR:HA	1.99	0.44
6:D:1034:PHE:CD2	6:D:1083:ALA:HA	2.51	0.44
2:T:27:DG:H2''	2:T:28:DG:O5'	2.16	0.44
4:B:30:PRO:C	4:B:31:LEU:HD12	2.43	0.44
5:C:236:LYS:HB3	5:C:286:GLU:HG3	1.99	0.44
5:C:599:VAL:H	5:C:627:GLY:HA3	1.82	0.44
6:D:103:GLY:O	6:D:244:VAL:N	2.42	0.44
6:D:890:THR:HG22	6:D:891:ASP:N	2.33	0.44
4:B:133:LEU:HD21	4:B:140:ILE:HG12	1.99	0.44
5:C:303:ASP:O	5:C:307:GLY:N	2.50	0.44
5:C:516:ASP:O	5:C:518:ASN:N	2.44	0.44
5:C:832:HIS:HE1	5:C:1238:LEU:HD22	1.82	0.44
6:D:17:PHE:HZ	6:D:1353:VAL:HG21	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:268:LEU:HD23	6:D:268:LEU:HA	1.81	0.44
6:D:356:THR:OG1	6:D:357:VAL:N	2.51	0.44
6:D:438:GLU:OE2	6:D:481:ARG:NH2	2.36	0.44
6:D:452:LEU:HD13	6:D:500:ILE:HG22	1.99	0.44
6:D:475:GLU:HG3	7:E:24:ALA:HB1	1.99	0.44
6:D:947:GLU:C	6:D:1022:PRO:HB3	2.43	0.44
6:D:1237:VAL:CG1	6:D:1253:ILE:HD13	2.47	0.44
5:C:225:PHE:HE2	5:C:347:ILE:HB	1.83	0.44
5:C:619:ALA:O	5:C:621:SER:N	2.50	0.44
5:C:817:LEU:HD11	5:C:1080:ASN:HD22	1.82	0.44
6:D:210:SER:O	6:D:214:ARG:HG3	2.18	0.44
6:D:356:THR:HG23	6:D:448:GLN:HG2	1.99	0.44
6:D:583:VAL:HA	6:D:620:PHE:HE1	1.81	0.44
3:F:116:ASP:OD1	3:F:116:ASP:N	2.51	0.44
5:C:582:ASN:HB3	5:C:586:PHE:H	1.80	0.44
5:C:632:ASP:HA	5:C:647:ARG:HB2	2.00	0.44
5:C:1015:ALA:O	5:C:1018:TYR:HB3	2.18	0.44
5:C:1268:GLN:NE2	6:D:352:ARG:HB2	2.32	0.44
6:D:161:THR:HG22	6:D:164:GLN:CD	2.42	0.44
6:D:926:PRO:HG2	6:D:1248:ILE:HD11	1.99	0.44
6:D:1347:LEU:O	6:D:1348:LYS:C	2.61	0.44
3:F:39:LEU:HD13	3:F:41:ASP:OD2	2.17	0.44
5:C:76:GLY:O	5:C:95:PRO:HD2	2.18	0.44
5:C:808:ASN:H	6:D:633:ALA:HB2	1.83	0.44
6:D:102:MET:HG2	6:D:246:PRO:HG3	2.00	0.44
6:D:108:ALA:HB3	6:D:279:LEU:HD22	2.00	0.44
6:D:275:ARG:CZ	6:D:298:MET:HB3	2.48	0.44
6:D:909:ILE:HD11	6:D:913:GLU:HB3	1.99	0.44
4:B:103:ASN:OD1	4:B:141:SER:HA	2.17	0.44
5:C:217:THR:O	5:C:221:LEU:HG	2.17	0.44
5:C:1024:GLU:O	5:C:1027:LYS:HG2	2.18	0.44
6:D:68:TYR:HA	6:D:92:VAL:CG2	2.47	0.44
6:D:1347:LEU:HG	6:D:1357:ILE:HG23	1.99	0.44
5:C:232:ILE:HA	5:C:237:LEU:HG	1.99	0.44
5:C:448:LEU:HD23	5:C:451:ARG:HD2	1.98	0.44
6:D:245:LEU:HD12	6:D:246:PRO:HD2	1.98	0.44
6:D:352:ARG:HG3	6:D:466:MET:O	2.18	0.44
6:D:700:ASN:O	6:D:704:GLU:HB2	2.18	0.44
6:D:976:THR:O	6:D:999:TYR:HE1	2.01	0.44
7:E:4:VAL:HG13	7:E:5:THR:HG23	1.99	0.44
4:B:228:LEU:HA	4:B:228:LEU:HD23	1.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:546:GLU:OE1	5:C:546:GLU:N	2.43	0.44
5:C:944:ARG:NE	5:C:948:ILE:HD11	2.33	0.44
5:C:1066:MET:HE2	5:C:1076:ILE:HB	2.00	0.44
5:C:1250:SER:OG	5:C:1251:TYR:N	2.51	0.44
5:C:1297:ASP:O	5:C:1301:ARG:HB2	2.17	0.44
6:D:85:CYS:O	6:D:89:GLY:HA2	2.18	0.44
6:D:363:LEU:N	6:D:622:ASP:OD2	2.44	0.44
2:T:17:DG:H2'	2:T:18:DC:H6	1.83	0.43
5:C:452:ARG:HG3	5:C:585:GLY:O	2.18	0.43
5:C:521:LEU:O	5:C:524:ILE:HG22	2.17	0.43
5:C:691:PRO:HA	5:C:788:SER:OG	2.18	0.43
5:C:708:VAL:HG11	5:C:794:LEU:HD22	1.98	0.43
5:C:964:LEU:HD22	5:C:1025:PHE:CG	2.53	0.43
5:C:993:PRO:HG2	5:C:996:ARG:HG2	1.99	0.43
6:D:37:GLU:HG3	6:D:105:ILE:HA	2.00	0.43
6:D:185:ILE:O	6:D:188:LEU:HB2	2.17	0.43
6:D:635:SER:OG	6:D:636:GLY:N	2.50	0.43
5:C:27:LEU:O	5:C:528:ARG:NH1	2.52	0.43
5:C:106:GLU:HA	5:C:114:VAL:HG23	1.99	0.43
5:C:210:LEU:HD21	5:C:429:MET:SD	2.58	0.43
5:C:277:LEU:O	5:C:281:ASP:N	2.48	0.43
6:D:450:HIS:CE1	6:D:452:LEU:H	2.36	0.43
6:D:577:ALA:O	6:D:580:TRP:HB3	2.19	0.43
6:D:975:ILE:H	6:D:1000:GLY:HA2	1.84	0.43
6:D:1067:ARG:NH1	6:D:1072:LYS:O	2.50	0.43
6:D:1360:GLY:O	6:D:1361:THR:C	2.61	0.43
2:T:10:DT:H4'	2:T:11:DC:OP1	2.18	0.43
2:T:15:DC:H1'	2:T:16:DA:H5'	2.00	0.43
5:C:263:VAL:HG22	5:C:273:HIS:CE1	2.54	0.43
5:C:1066:MET:HE3	5:C:1066:MET:HB2	1.88	0.43
6:D:431:ARG:CD	6:D:493:PRO:HG3	2.47	0.43
6:D:640:GLY:N	6:D:643:ASP:OD2	2.44	0.43
6:D:1025:MET:HB3	6:D:1124:ILE:HB	2.00	0.43
6:D:1223:LEU:HD23	6:D:1223:LEU:HA	1.83	0.43
3:F:19:ASN:O	3:F:23:ARG:HB3	2.19	0.43
3:F:77:TYR:CZ	3:F:81:GLN:OE1	2.71	0.43
4:A:224:LEU:HD22	4:B:228:LEU:CD1	2.48	0.43
4:B:57:THR:O	4:B:173:VAL:HB	2.17	0.43
5:C:329:GLY:O	5:C:331:LYS:NZ	2.49	0.43
5:C:796:LEU:N	5:C:796:LEU:HD12	2.34	0.43
5:C:927:THR:HG22	5:C:928:VAL:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:252:LEU:HA	6:D:252:LEU:HD12	1.76	0.43
2:T:25:DC:P	5:C:139:ASN:HD22	2.42	0.43
4:A:118:ASP:C	4:A:120:ASP:H	2.26	0.43
4:B:224:LEU:HA	4:B:224:LEU:HD23	1.75	0.43
5:C:550:VAL:HG23	5:C:554:HIS:CG	2.53	0.43
5:C:697:LYS:HG3	5:C:697:LYS:O	2.19	0.43
5:C:1223:ARG:HH22	6:D:721:SER:N	2.17	0.43
5:C:1314:GLN:HA	7:E:28:ARG:NH2	2.28	0.43
2:T:13:DT:C5	2:T:14:DC:N4	2.86	0.43
3:F:112:PHE:C	3:F:114:ARG:H	2.27	0.43
3:F:112:PHE:O	3:F:117:TYR:HB3	2.19	0.43
4:A:224:LEU:HD23	4:A:228:LEU:HD13	2.01	0.43
5:C:81:ASP:O	5:C:85:CYS:CB	2.66	0.43
5:C:146:VAL:HG12	5:C:147:SER:N	2.34	0.43
6:D:133:ARG:O	6:D:137:ARG:HG3	2.18	0.43
6:D:358:GLY:O	6:D:360:TYR:N	2.46	0.43
6:D:1222:ARG:HG3	6:D:1223:LEU:HG	2.00	0.43
4:A:41:ASN:ND2	5:C:1218:GLY:HA3	2.34	0.43
4:A:185:TYR:HA	4:A:202:VAL:O	2.19	0.43
5:C:256:GLU:HB3	5:C:261:VAL:HG22	2.00	0.43
5:C:519:ASN:O	5:C:520:PRO:C	2.62	0.43
5:C:1130:ALA:O	5:C:1134:GLN:HG2	2.18	0.43
6:D:1261:LEU:HD12	6:D:1261:LEU:O	2.19	0.43
7:E:25:ARG:HH21	7:E:68:GLU:CD	2.26	0.43
5:C:832:HIS:CE1	5:C:1238:LEU:HD22	2.54	0.43
6:D:679:TYR:OH	6:D:754:ILE:O	2.14	0.43
6:D:842:ARG:HG2	6:D:843:VAL:H	1.84	0.43
6:D:1175:LEU:HD12	6:D:1175:LEU:HA	1.89	0.43
6:D:1319:PHE:CZ	6:D:1320:ILE:HG13	2.54	0.43
2:T:27:DG:H3'	2:T:27:DG:OP1	2.19	0.43
2:T:29:DA:H2''	2:T:30:DC:H6	1.83	0.43
5:C:145:ILE:HG22	5:C:146:VAL:O	2.19	0.43
5:C:217:THR:HG23	5:C:351:LEU:HD21	1.99	0.43
5:C:764:CYS:HB2	5:C:831:ILE:HG22	2.00	0.43
5:C:848:GLU:HG2	5:C:889:PRO:CD	2.49	0.43
6:D:264:ASP:CG	6:D:324:LEU:HB2	2.44	0.43
6:D:475:GLU:OE1	6:D:475:GLU:N	2.33	0.43
6:D:843:VAL:HG13	6:D:862:THR:O	2.18	0.43
4:B:19:VAL:HG21	4:B:23:HIS:HD2	1.83	0.43
5:C:1294:LYS:HB3	6:D:347:VAL:HG13	2.00	0.43
6:D:342:LEU:C	6:D:344:GLY:H	2.27	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:1156:LEU:HG	6:D:1209:VAL:HA	2.01	0.43
1:N:28:DA:H2"	1:N:29:DG:N7	2.34	0.42
5:C:91:THR:HG22	5:C:138:ILE:O	2.18	0.42
5:C:133:ASN:OD1	5:C:713:GLY:HA3	2.19	0.42
5:C:401:GLY:O	5:C:402:ARG:C	2.62	0.42
5:C:1101:LEU:HD21	6:D:508:LEU:HD22	2.01	0.42
6:D:370:LYS:NZ	6:D:443:GLU:OE2	2.29	0.42
6:D:432:LEU:HD13	6:D:456:ALA:HB1	2.00	0.42
6:D:909:ILE:HG13	6:D:910:ASN:O	2.18	0.42
6:D:980:THR:HB	6:D:997:VAL:HB	2.00	0.42
6:D:1029:THR:HG21	6:D:1115:ILE:HD13	2.00	0.42
6:D:1276:GLU:O	6:D:1278:GLU:N	2.52	0.42
1:N:24:DC:C4	1:N:25:DG:C6	3.07	0.42
4:B:19:VAL:HG12	4:B:20:SER:N	2.35	0.42
5:C:18:ARG:HG2	5:C:1188:ASP:OD1	2.19	0.42
5:C:453:ILE:CD1	5:C:587:LEU:HD21	2.46	0.42
5:C:569:ILE:HD12	6:D:784:ALA:HA	2.02	0.42
6:D:326:SER:H	6:D:329:ASP:HB2	1.84	0.42
6:D:499:ILE:HD12	6:D:499:ILE:HA	1.87	0.42
6:D:697:MET:HE1	6:D:737:ILE:O	2.20	0.42
2:T:14:DC:N3	2:T:15:DC:N4	2.67	0.42
4:A:195:ARG:HG2	4:A:198:LEU:HD13	2.00	0.42
5:C:745:GLU:OE1	5:C:1017:GLN:HG3	2.18	0.42
5:C:1002:LEU:HD23	5:C:1003:THR:N	2.34	0.42
5:C:1110:GLY:O	5:C:1111:GLN:C	2.62	0.42
5:C:1314:GLN:HG3	7:E:28:ARG:HH22	1.84	0.42
6:D:417:ARG:NH1	7:E:43:ASN:HB2	2.34	0.42
6:D:441:LEU:HD12	6:D:441:LEU:N	2.34	0.42
6:D:525:MET:O	6:D:548:VAL:HG23	2.20	0.42
6:D:716:GLN:HG3	6:D:717:VAL:O	2.19	0.42
2:T:20:DC:C4'	6:D:352:ARG:HH12	2.32	0.42
4:B:178:SER:HB2	4:B:180:VAL:HG22	2.01	0.42
5:C:816:ILE:HD12	5:C:1074:GLY:HA3	2.00	0.42
6:D:422:LEU:HD21	6:D:484:MET:HE1	2.01	0.42
6:D:432:LEU:HD22	6:D:435:GLN:NE2	2.35	0.42
6:D:1289:ASN:HA	6:D:1292:LEU:HB2	2.00	0.42
6:D:1348:LYS:O	6:D:1352:ILE:HG12	2.19	0.42
3:F:77:TYR:OH	3:F:81:GLN:OE1	2.35	0.42
3:F:77:TYR:CZ	3:F:80:GLN:HB3	2.53	0.42
4:B:12:ARG:HH11	4:B:13:LEU:HB3	1.84	0.42
5:C:421:SER:N	5:C:424:ASP:OD2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:468:LEU:HA	5:C:468:LEU:HD23	1.77	0.42
5:C:724:VAL:HA	5:C:734:ILE:HD12	2.00	0.42
5:C:1314:GLN:HG3	7:E:28:ARG:NH2	2.34	0.42
5:C:1333:LEU:HD13	6:D:115:TRP:CH2	2.55	0.42
6:D:24:LEU:HD23	6:D:24:LEU:HA	1.85	0.42
6:D:107:LEU:HA	6:D:276:ASN:HD21	1.84	0.42
6:D:478:LEU:HA	6:D:478:LEU:HD23	1.81	0.42
6:D:722:ILE:HA	6:D:725:MET:CE	2.50	0.42
6:D:1257:VAL:HA	6:D:1260:MET:SD	2.59	0.42
6:D:1259:GLN:HE22	6:D:1262:ARG:HD3	1.83	0.42
3:F:41:ASP:OD1	6:D:929:GLN:NE2	2.52	0.42
4:B:149:GLY:HA3	4:B:177:TYR:CE2	2.55	0.42
5:C:204:LEU:HA	5:C:204:LEU:HD23	1.81	0.42
5:C:514:PHE:CZ	5:C:760:ASN:HB3	2.54	0.42
5:C:830:THR:OG1	5:C:831:ILE:N	2.52	0.42
5:C:858:GLY:O	5:C:862:LEU:HG	2.19	0.42
5:C:1246:ARG:HE	5:C:1249:GLY:N	2.18	0.42
6:D:117:LEU:HD13	6:D:118:LYS:HG3	2.01	0.42
6:D:378:LYS:HA	6:D:381:ILE:HD12	2.02	0.42
6:D:697:MET:SD	6:D:738:ARG:HA	2.59	0.42
3:F:47:ASP:O	3:F:51:ASN:ND2	2.51	0.42
4:A:29:GLU:HG3	4:A:30:PRO:CD	2.44	0.42
5:C:803:ALA:HB2	5:C:1227:VAL:HG12	2.02	0.42
5:C:812:PHE:HA	6:D:505:ASP:OD2	2.19	0.42
5:C:888:THR:HG23	5:C:916:SER:OG	2.18	0.42
5:C:918:LEU:HA	5:C:918:LEU:HD12	1.83	0.42
5:C:1192:GLU:O	5:C:1196:LYS:HG2	2.20	0.42
5:C:1297:ASP:OD2	5:C:1300:GLY:N	2.41	0.42
6:D:234:PRO:O	6:D:237:MET:N	2.33	0.42
6:D:1002:VAL:O	6:D:1018:ALA:HA	2.20	0.42
6:D:1061:VAL:O	6:D:1104:LYS:HA	2.19	0.42
6:D:1256:ILE:O	6:D:1260:MET:HG3	2.20	0.42
4:A:164:ASP:OD1	4:A:165:GLU:N	2.49	0.42
4:B:99:ILE:C	4:B:100:LEU:HD12	2.45	0.42
5:C:150:HIS:CE1	5:C:454:ARG:HE	2.37	0.42
5:C:841:ARG:NH2	6:D:256:ASP:O	2.52	0.42
6:D:66:LYS:HE2	6:D:69:GLU:OE1	2.19	0.42
6:D:247:PRO:HA	6:D:250:ARG:CZ	2.49	0.42
8:R:9:U:H2'	8:R:10:G:C8	2.54	0.42
4:B:66:HIS:CD2	4:B:68:TYR:H	2.38	0.42
5:C:27:LEU:HA	5:C:27:LEU:HD23	1.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:149:LEU:HA	5:C:452:ARG:O	2.20	0.42
5:C:150:HIS:CE1	5:C:454:ARG:NE	2.87	0.42
5:C:689:ALA:HB2	5:C:1233:LEU:HD23	2.02	0.42
5:C:728:ASP:O	5:C:730:SER:N	2.53	0.42
6:D:54:ASP:N	6:D:58:CYS:SG	2.92	0.42
6:D:620:PHE:O	6:D:624:ILE:HG12	2.19	0.42
6:D:1256:ILE:HD12	6:D:1256:ILE:HG23	1.85	0.42
3:F:127:ALA:O	3:F:131:LYS:HE2	2.20	0.42
5:C:718:ALA:HA	5:C:751:TYR:HE2	1.83	0.42
5:C:742:TYR:HB2	5:C:746:ALA:HB2	2.02	0.42
5:C:809:GLY:HA3	6:D:629:PHE:CD2	2.55	0.42
5:C:1070:HIS:O	5:C:1108:ASN:ND2	2.53	0.42
5:C:1313:HIS:HB2	6:D:474:LEU:HB2	2.02	0.42
6:D:416:ILE:O	6:D:417:ARG:C	2.62	0.42
6:D:452:LEU:HG	6:D:625:MET:HE1	2.01	0.42
6:D:583:VAL:HA	6:D:620:PHE:CE1	2.54	0.42
4:A:7:GLU:OE1	4:B:150:ARG:NH2	2.53	0.41
5:C:57:PHE:HD2	5:C:70:TYR:HB2	1.85	0.41
5:C:232:ILE:HD12	5:C:330:HIS:O	2.19	0.41
6:D:67:ASP:HB3	6:D:68:TYR:HD2	1.85	0.41
6:D:616:PRO:HA	6:D:619:ILE:HG22	2.01	0.41
4:B:35:PHE:O	4:B:38:THR:HG22	2.20	0.41
5:C:4:SER:O	5:C:8:LYS:HG3	2.20	0.41
5:C:314:ASN:HD21	5:C:352:ARG:HG3	1.83	0.41
5:C:646:SER:HB3	5:C:649:GLN:HG3	2.02	0.41
5:C:742:TYR:C	5:C:744:GLY:N	2.78	0.41
5:C:756:TYR:CZ	5:C:766:ASN:ND2	2.88	0.41
6:D:644:MET:O	6:D:764:ARG:NH1	2.53	0.41
6:D:732:GLY:HA2	6:D:736:GLN:CD	2.45	0.41
6:D:1031:VAL:HG21	6:D:1088:VAL:HG11	2.02	0.41
6:D:1137:GLY:O	6:D:1140:ARG:HB3	2.20	0.41
6:D:1220:ILE:HD13	6:D:1220:ILE:HA	1.93	0.41
6:D:1237:VAL:HG11	6:D:1253:ILE:HG21	2.02	0.41
6:D:1242:ARG:C	6:D:1245:GLY:H	2.27	0.41
6:D:1272:SER:OG	6:D:1300:ALA:HB2	2.20	0.41
6:D:1321:SER:OG	6:D:1349:GLU:OE2	2.38	0.41
3:F:68:CYS:CA	3:F:72:LEU:HD13	2.50	0.41
4:A:23:HIS:HB3	4:A:206:GLU:OE1	2.20	0.41
5:C:101:ARG:HH21	5:C:118:LYS:HZ2	1.68	0.41
5:C:165:HIS:C	5:C:167:SER:N	2.78	0.41
5:C:188:PHE:CZ	5:C:194:LEU:HD13	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:224:PHE:CD1	5:C:347:ILE:HG13	2.54	0.41
5:C:1099:ASN:OD1	5:C:1101:LEU:N	2.42	0.41
6:D:452:LEU:HG	6:D:625:MET:HE3	2.00	0.41
6:D:699:ASP:O	6:D:703:THR:HG22	2.20	0.41
6:D:978:ARG:HG2	6:D:999:TYR:CD1	2.54	0.41
3:F:5:LEU:HD21	3:F:87:PHE:CD2	2.56	0.41
3:F:46:ALA:HB3	6:D:736:GLN:HG2	2.02	0.41
3:F:136:LEU:HG	3:F:149:TYR:HE1	1.83	0.41
4:B:44:ARG:HA	4:B:183:ILE:HD11	2.01	0.41
5:C:62:TYR:CE1	3:G:44:GLU:HA	2.56	0.41
5:C:268:ARG:CZ	5:C:270:THR:HG22	2.50	0.41
5:C:484:LEU:O	5:C:486:THR:N	2.53	0.41
5:C:705:GLU:O	5:C:706:ARG:C	2.62	0.41
5:C:958:LYS:O	5:C:962:GLU:HG2	2.20	0.41
6:D:1067:ARG:HD2	6:D:1072:LYS:HA	2.03	0.41
5:C:398:SER:OG	5:C:400:VAL:HB	2.20	0.41
5:C:546:GLU:O	5:C:549:ASP:N	2.53	0.41
5:C:809:GLY:C	5:C:811:ASN:N	2.79	0.41
5:C:813:GLU:HA	6:D:504:GLN:NE2	2.36	0.41
6:D:474:LEU:HD21	7:E:27:ALA:HB1	2.01	0.41
7:E:15:ASN:O	7:E:16:ARG:HB3	2.20	0.41
3:F:62:VAL:O	3:F:66:THR:OG1	2.28	0.41
5:C:27:LEU:HD13	5:C:663:VAL:HG11	2.03	0.41
5:C:149:LEU:HD21	5:C:451:ARG:HD3	2.03	0.41
5:C:667:LEU:HA	5:C:667:LEU:HD23	1.80	0.41
5:C:758:ARG:HG2	5:C:759:SER:O	2.20	0.41
5:C:927:THR:HG22	5:C:928:VAL:N	2.35	0.41
5:C:1079:ILE:HA	5:C:1079:ILE:HD12	1.75	0.41
5:C:1291:LEU:HD23	5:C:1291:LEU:HA	1.71	0.41
4:A:79:LEU:HD21	5:C:693:LEU:HD21	2.02	0.41
5:C:44:GLU:O	5:C:46:GLN:HG3	2.20	0.41
5:C:351:LEU:HA	5:C:354:ASP:OD2	2.21	0.41
5:C:741:MET:HG3	5:C:746:ALA:HB3	2.03	0.41
6:D:107:LEU:HA	6:D:276:ASN:ND2	2.35	0.41
6:D:432:LEU:HD23	6:D:432:LEU:HA	1.81	0.41
6:D:479:GLU:OE2	7:E:20:VAL:HG11	2.21	0.41
6:D:495:ASN:ND2	6:D:1247:LYS:HB2	2.33	0.41
6:D:580:TRP:C	6:D:582:ILE:H	2.29	0.41
6:D:1164:SER:O	6:D:1175:LEU:HD12	2.20	0.41
6:D:1321:SER:O	6:D:1324:SER:N	2.53	0.41
1:N:8:DA:C5	1:N:9:DC:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:197:ASP:N	4:B:197:ASP:OD1	2.54	0.41
5:C:53:PHE:HA	5:C:56:VAL:HG12	2.02	0.41
5:C:74:ARG:NH2	5:C:121:GLU:OE2	2.48	0.41
5:C:543:ALA:HB3	5:C:548:ARG:NH2	2.35	0.41
5:C:615:VAL:N	5:C:651:ASP:OD2	2.49	0.41
5:C:1149:TYR:HE1	5:C:1180:MET:HE3	1.84	0.41
5:C:1243:MET:SD	6:D:445:LYS:HB3	2.60	0.41
6:D:185:ILE:HD13	6:D:188:LEU:HD12	2.03	0.41
6:D:686:TRP:CD2	6:D:758:PRO:HG2	2.56	0.41
6:D:706:VAL:HG12	6:D:715:LYS:HA	2.01	0.41
6:D:1179:PRO:HB2	6:D:1182:GLY:N	2.36	0.41
2:T:27:DG:H1'	2:T:28:DG:O4'	2.21	0.41
3:F:137:ALA:O	3:F:147:SER:HA	2.21	0.41
4:A:74:VAL:HG21	4:A:131:CYS:HB2	2.03	0.41
4:A:222:THR:OG1	4:B:232:VAL:HG11	2.20	0.41
4:B:128:HIS:ND1	4:B:129:VAL:O	2.53	0.41
4:B:192:VAL:O	4:B:193:GLU:C	2.63	0.41
5:C:187:GLU:OE2	5:C:197:ARG:NH2	2.54	0.41
5:C:1192:GLU:CD	6:D:764:ARG:HE	2.22	0.41
6:D:809:VAL:HA	6:D:894:VAL:O	2.21	0.41
6:D:998:PRO:HG2	6:D:1020:TRP:CZ2	2.55	0.41
6:D:1071:GLY:HA3	6:D:1074:LEU:HD12	2.03	0.41
6:D:1177:ILE:O	6:D:1184:ASP:HB2	2.21	0.41
6:D:1287:ILE:HD12	6:D:1288:ALA:N	2.36	0.41
8:R:11:U:H2'	8:R:12:G:C8	2.56	0.41
4:A:52:PRO:HD3	4:A:219:ARG:HD2	2.03	0.41
4:A:228:LEU:HD21	4:B:224:LEU:HD12	2.04	0.41
5:C:4:SER:HB3	5:C:7:GLU:CD	2.45	0.41
5:C:765:ILE:HG13	5:C:787:PRO:HG3	2.03	0.41
5:C:1119:MET:SD	5:C:1228:GLY:HA2	2.61	0.41
6:D:139:LEU:HD23	6:D:139:LEU:HA	1.80	0.41
6:D:343:LEU:HD11	6:D:1348:LYS:HE2	2.03	0.41
6:D:884:SER:HB3	6:D:886:VAL:HG12	2.03	0.41
6:D:925:GLU:HB3	6:D:926:PRO:HD3	2.03	0.41
6:D:1037:PHE:CZ	6:D:1111:ASP:HB2	2.56	0.41
6:D:1292:LEU:HD23	6:D:1292:LEU:HA	1.89	0.41
6:D:1344:LEU:O	6:D:1345:ARG:C	2.63	0.41
2:T:15:DC:H6	2:T:15:DC:H2'	1.79	0.40
4:A:71:LYS:CE	4:A:140:ILE:HG22	2.51	0.40
5:C:478:ARG:HD2	5:C:492:MET:HG2	2.03	0.40
5:C:618:GLN:HA	5:C:654:ASP:OD2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:930:LEU:HA	6:D:930:LEU:HD23	1.90	0.40
4:B:51:MET:HE3	4:B:52:PRO:HD2	2.03	0.40
4:B:66:HIS:CD2	4:B:68:TYR:HB2	2.56	0.40
5:C:10:ARG:CZ	5:C:791:LEU:HD12	2.51	0.40
5:C:16:GLY:O	5:C:1155:VAL:HA	2.22	0.40
5:C:158:ASP:HB3	5:C:173:ASN:OD1	2.20	0.40
5:C:208:ILE:HG23	5:C:209:ILE:N	2.36	0.40
5:C:844:LYS:HE2	6:D:48:THR:HG22	2.03	0.40
6:D:349:TYR:CD1	6:D:472:LEU:HD21	2.56	0.40
6:D:364:HIS:CG	7:E:4:VAL:HG23	2.56	0.40
6:D:385:LEU:HA	6:D:385:LEU:HD23	1.91	0.40
6:D:528:THR:HG23	6:D:529:GLY:N	2.35	0.40
6:D:1249:ASN:HD21	6:D:1251:LYS:NZ	2.19	0.40
4:A:90:VAL:HG23	4:A:123:ILE:HD13	2.02	0.40
4:A:234:LEU:HD23	4:B:214:GLU:HG2	2.03	0.40
4:B:91:ARG:HH21	4:B:210:THR:HA	1.86	0.40
4:B:198:LEU:HD23	4:B:198:LEU:HA	1.82	0.40
5:C:663:VAL:HG23	5:C:664:GLY:N	2.37	0.40
5:C:685:MET:SD	5:C:1073:LYS:HE2	2.61	0.40
6:D:59:ALA:O	6:D:63:GLY:N	2.54	0.40
6:D:172:PHE:HB2	6:D:176:PHE:HB2	2.03	0.40
6:D:923:ILE:O	6:D:926:PRO:HD2	2.20	0.40
6:D:1021:ASP:OD2	6:D:1024:THR:OG1	2.30	0.40
6:D:1195:GLN:C	6:D:1196:LEU:HD12	2.46	0.40
2:T:7:DA:H2'	2:T:8:DT:C5	2.56	0.40
2:T:12:DT:H1'	2:T:13:DT:C5	2.56	0.40
5:C:268:ARG:NH2	5:C:270:THR:HA	2.37	0.40
5:C:820:GLU:HA	5:C:823:VAL:HG12	2.02	0.40
5:C:866:ASP:HA	5:C:872:TYR:CZ	2.56	0.40
5:C:1032:LYS:HD2	5:C:1035:LYS:HD2	2.03	0.40
3:F:111:ILE:O	3:F:111:ILE:HD12	2.21	0.40
4:A:70:THR:CG2	5:C:755:LYS:HE2	2.51	0.40
4:B:48:LEU:HD11	6:D:535:ARG:HG3	2.03	0.40
5:C:28:LEU:HD23	5:C:28:LEU:HA	1.92	0.40
5:C:555:TYR:CE2	5:C:637:ARG:CZ	3.04	0.40
5:C:678:ARG:NH2	5:C:1106:ARG:HE	2.19	0.40
5:C:724:VAL:HA	5:C:734:ILE:CD1	2.52	0.40
6:D:42:GLU:OE1	6:D:42:GLU:N	2.51	0.40
6:D:412:LEU:O	6:D:415:VAL:HG22	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	154/158 (98%)	136 (88%)	18 (12%)	0	100	100
3	G	154/158 (98%)	138 (90%)	16 (10%)	0	100	100
4	A	226/329 (69%)	201 (89%)	25 (11%)	0	100	100
4	B	227/329 (69%)	198 (87%)	29 (13%)	0	100	100
5	C	1315/1342 (98%)	1103 (84%)	212 (16%)	0	100	100
6	D	1356/1407 (96%)	1159 (86%)	197 (14%)	0	100	100
7	E	71/91 (78%)	64 (90%)	7 (10%)	0	100	100
All	All	3503/3814 (92%)	2999 (86%)	504 (14%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	137/139 (99%)	136 (99%)	1 (1%)	76	78
4	A	196/286 (68%)	196 (100%)	0	100	100
4	B	197/286 (69%)	197 (100%)	0	100	100
5	C	1138/1157 (98%)	1138 (100%)	0	100	100
6	D	1134/1168 (97%)	1132 (100%)	2 (0%)	87	87
7	E	63/75 (84%)	63 (100%)	0	100	100
All	All	2865/3111 (92%)	2862 (100%)	3 (0%)	87	89

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	111	ILE
6	D	1233	ILE
6	D	1261	LEU

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

Mol	Chain	Res	Type
4	A	41	ASN
4	A	75	GLN
4	B	66	HIS
4	B	84	ASN
4	B	132	HIS
5	C	69	GLN
5	C	150	HIS
5	C	165	HIS
5	C	314	ASN
5	C	327	GLN
5	C	387	ASN
5	C	437	ASN
5	C	573	ASN
5	C	580	GLN
5	C	618	GLN
5	C	673	HIS
5	C	688	GLN
5	C	799	ASN
5	C	808	ASN
5	C	1017	GLN
5	C	1116	HIS
5	C	1256	GLN
5	C	1257	GLN
5	C	1268	GLN
5	C	1313	HIS
6	D	45	ASN
6	D	232	ASN
6	D	341	ASN
6	D	365	GLN
6	D	488	ASN
6	D	817	HIS
6	D	861	ASN
6	D	865	HIS
6	D	936	HIS

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Mol	Chain	Res	Type
6	D	951	GLN
6	D	1049	GLN
6	D	1108	GLN
6	D	1195	GLN
6	D	1238	GLN
6	D	1259	GLN
6	D	1279	GLN
6	D	1350	ASN
6	D	1367	GLN
7	E	15	ASN
7	E	62	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	R	9/14 (64%)	3 (33%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	R	6	C
8	R	8	A
8	R	14	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

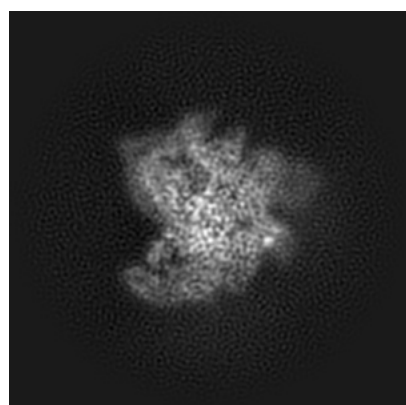
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4885. These allow visual inspection of the internal detail of the map and identification of artifacts.

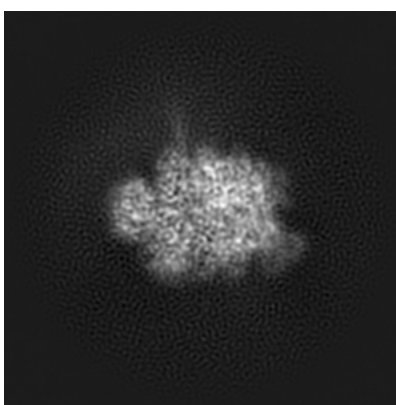
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

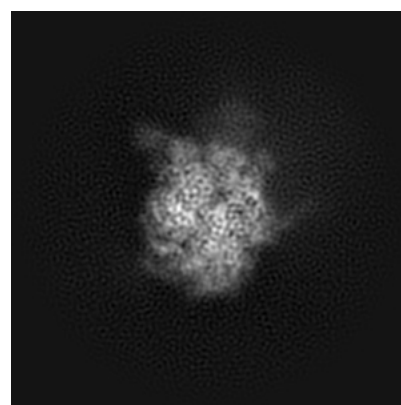
6.1.1 Primary map



X



Y

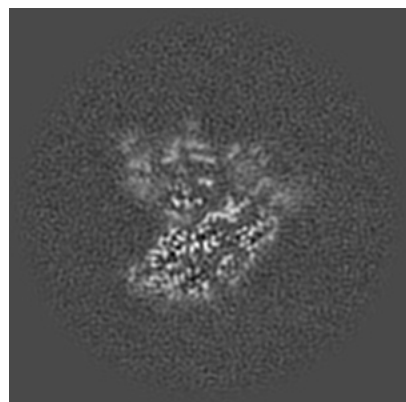


Z

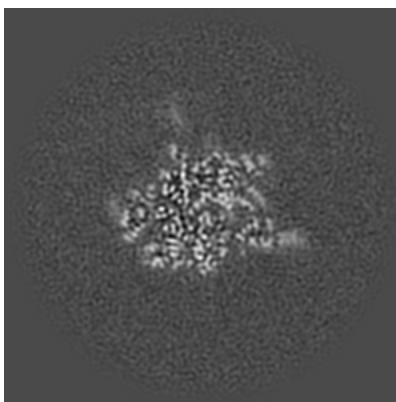
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

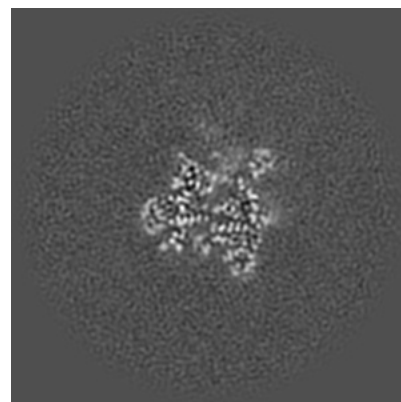
6.2.1 Primary map



X Index: 144



Y Index: 144

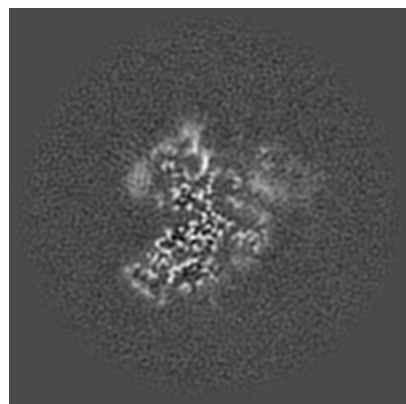


Z Index: 144

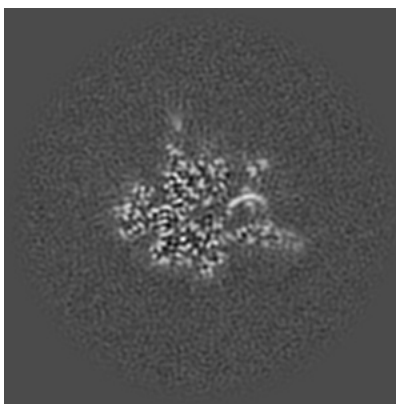
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

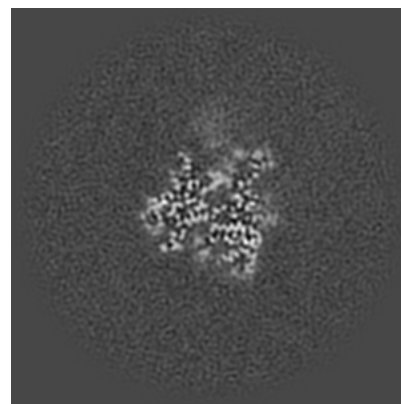
6.3.1 Primary map



X Index: 152



Y Index: 141

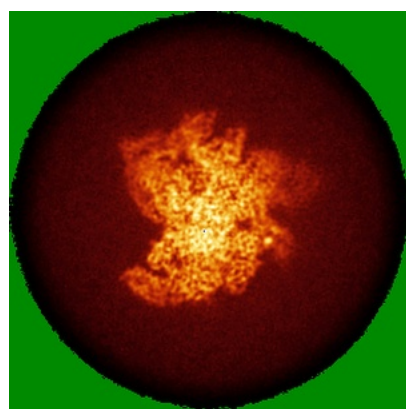


Z Index: 146

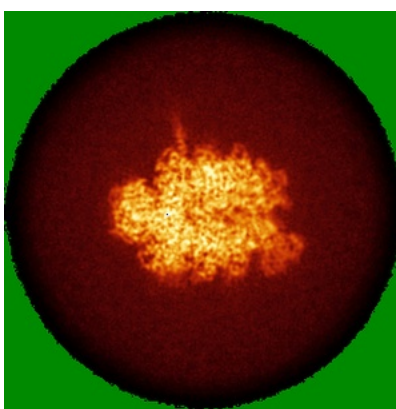
The images above show the largest variance slices of the map in three orthogonal directions.

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

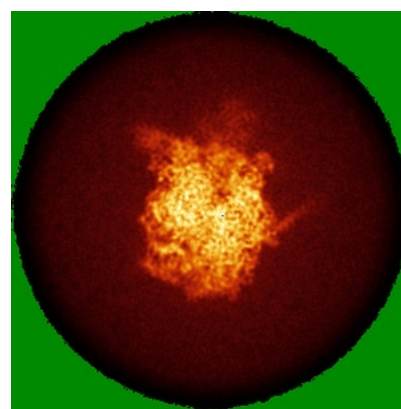
6.4.1 Primary map



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

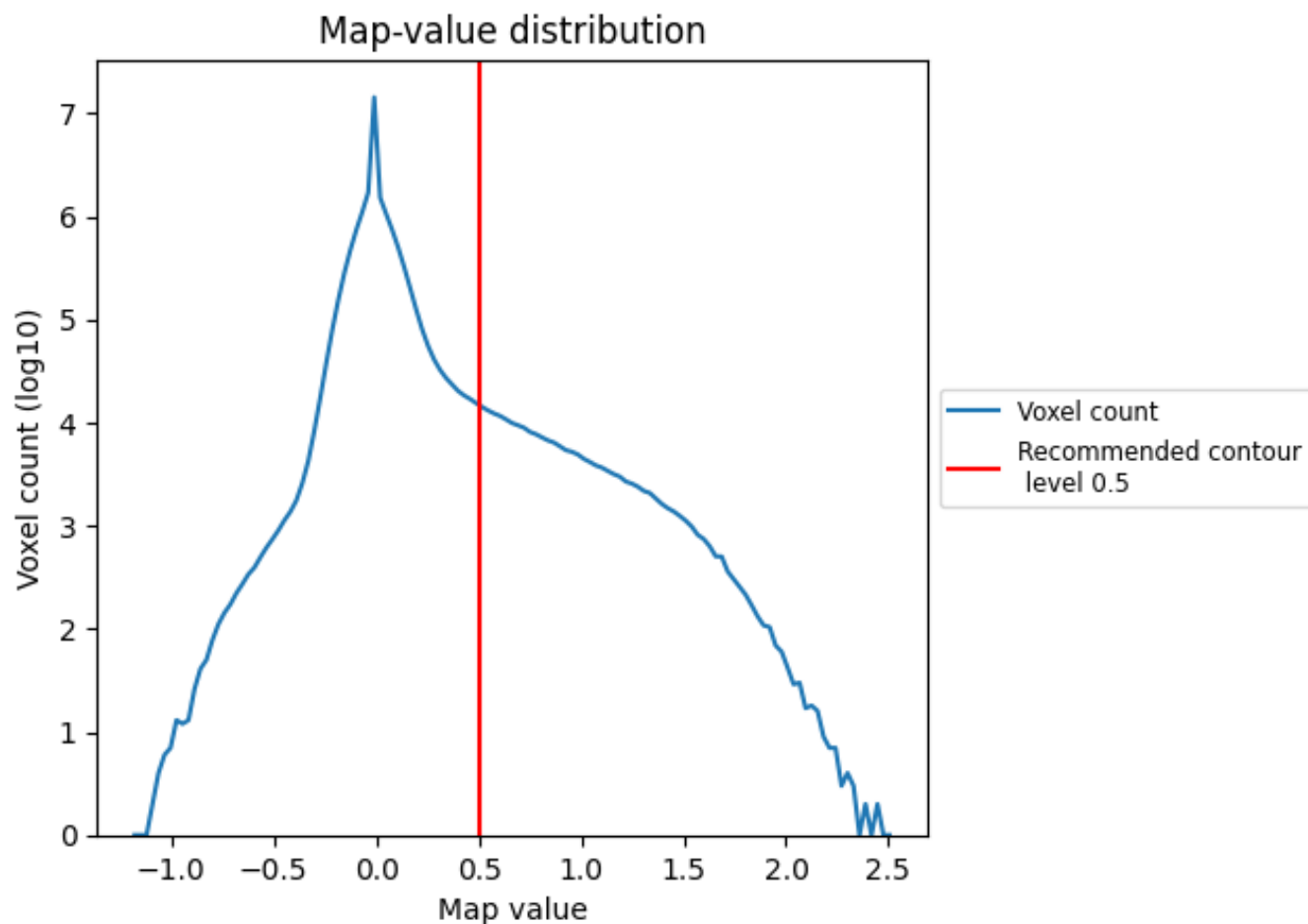
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

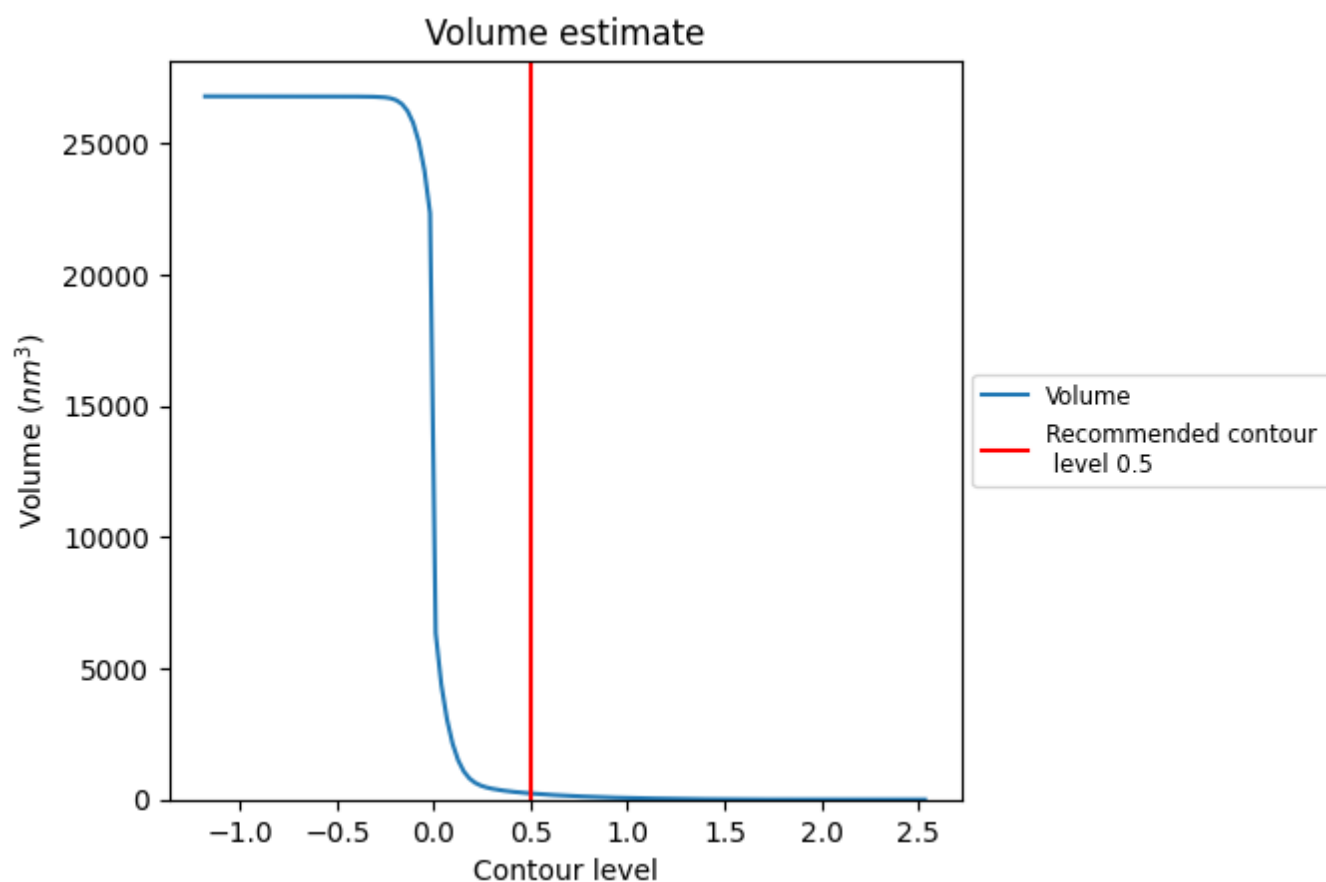
This section contains the results of statistical analysis of the map.

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.

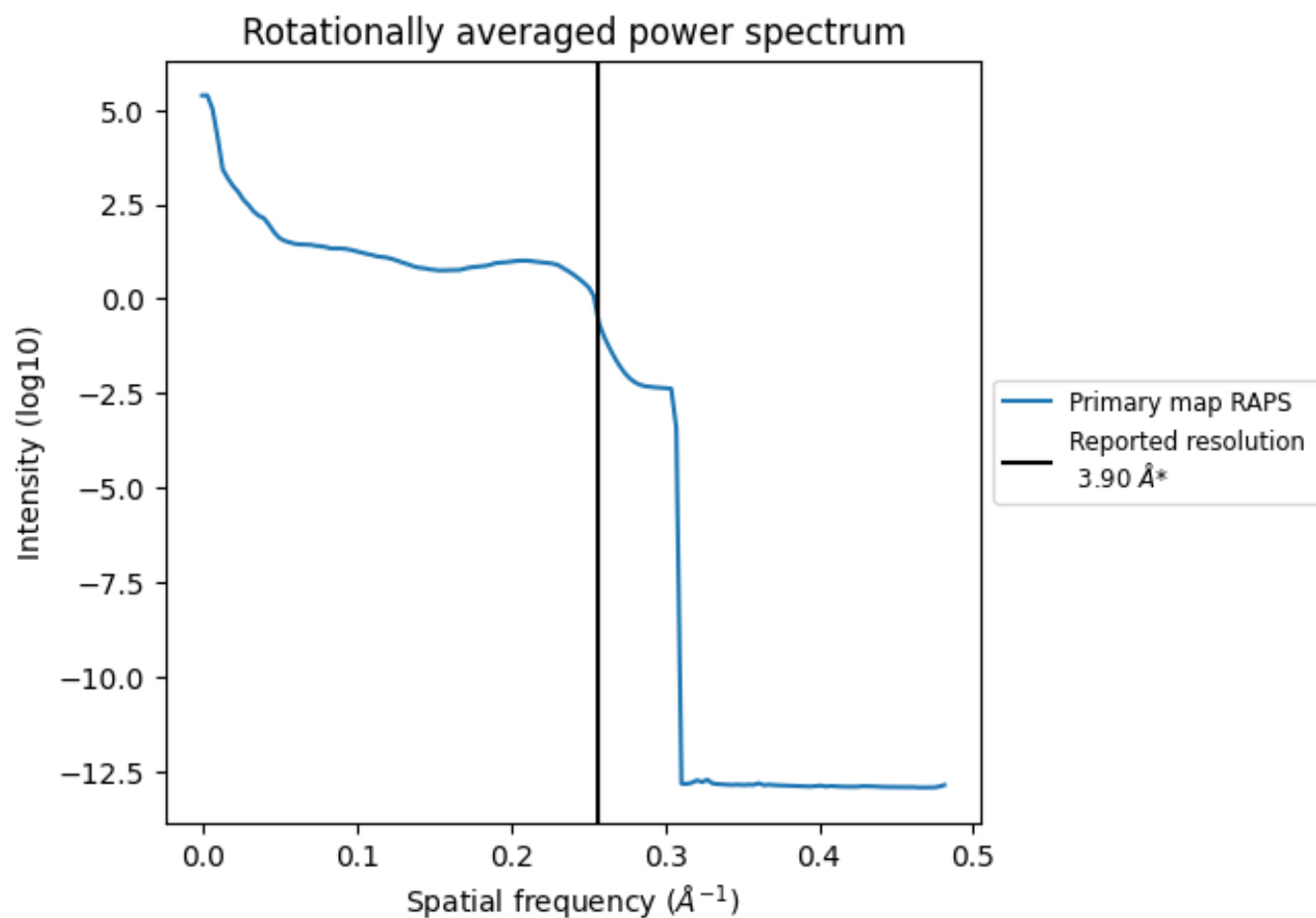
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 234 nm³; this corresponds to an approximate mass of 211 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 0.256 Å⁻¹

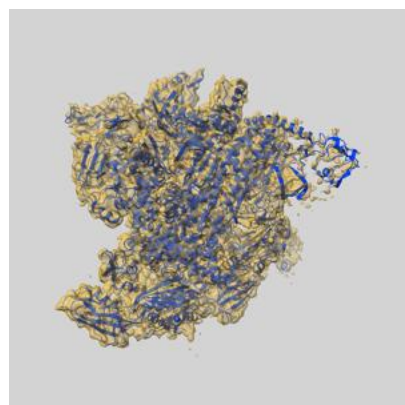
8 Fourier-Shell correlation

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

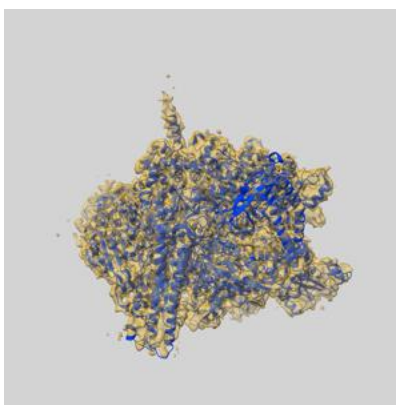
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4885 and PDB model 6RI7. Per-residue inclusion information can be found in section 3 on page 6.

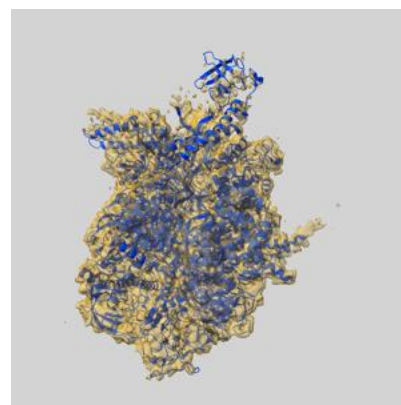
9.1 Map-model overlay [i](#)



X



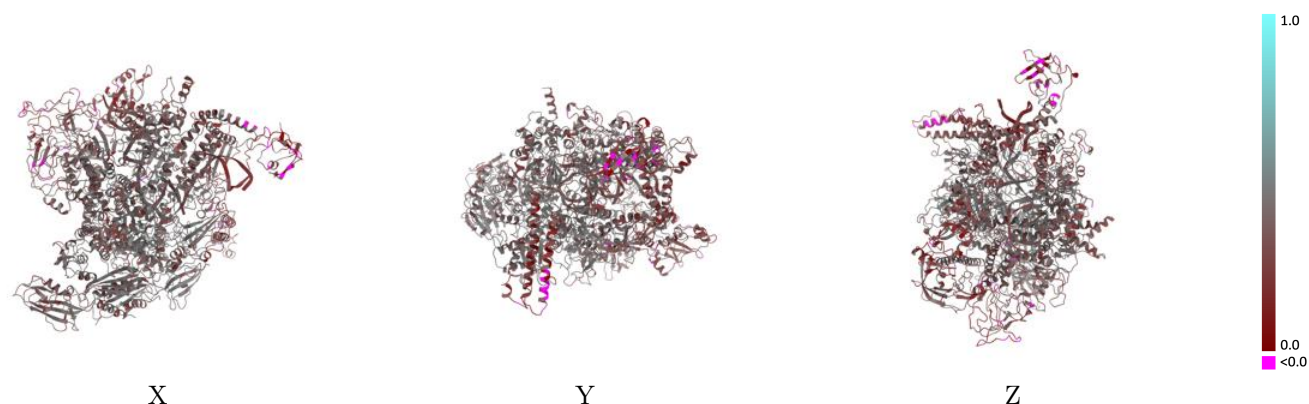
Y



Z

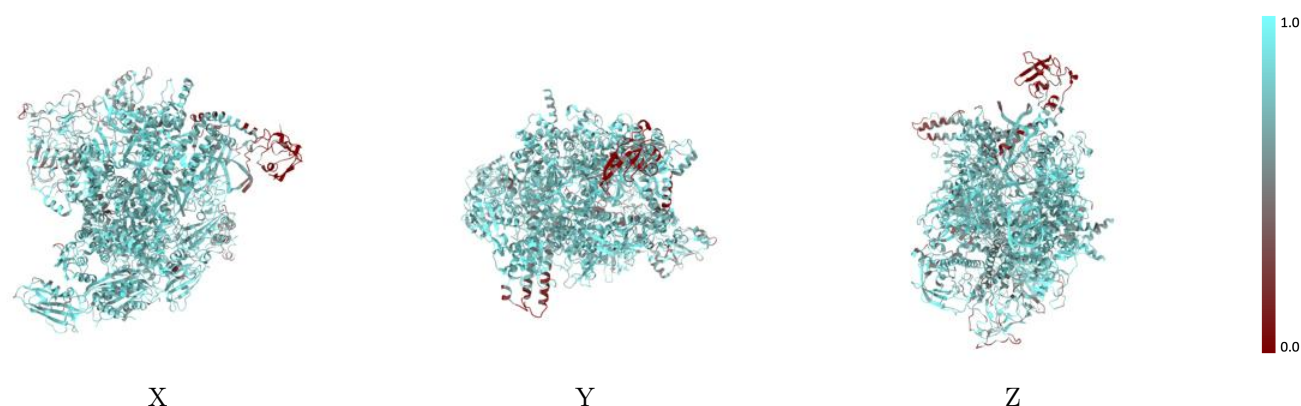
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



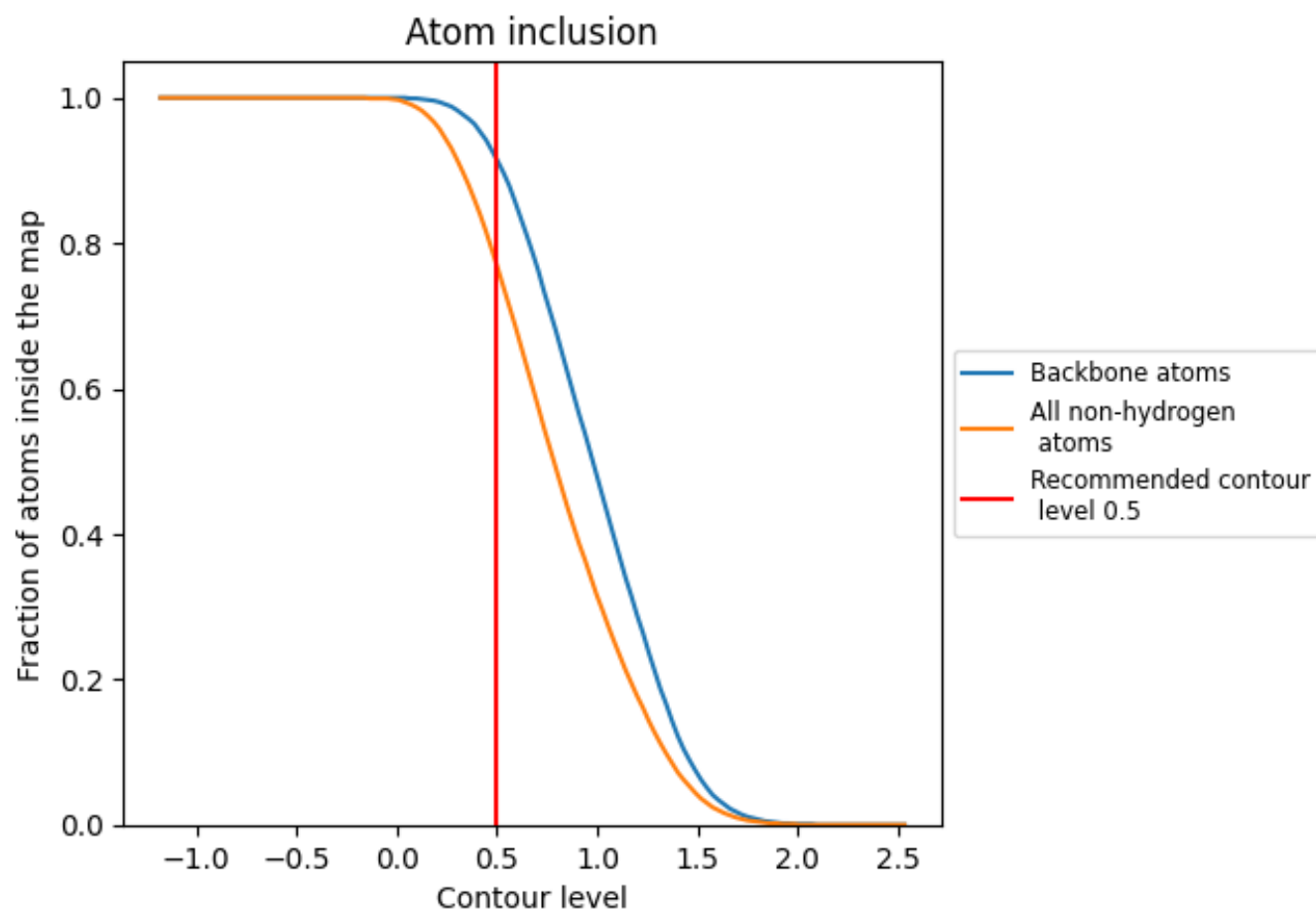
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7690	0.3690
A	0.8040	0.4150
B	0.7780	0.3800
C	0.7690	0.3720
D	0.7820	0.3730
E	0.7810	0.3650
F	0.7330	0.3410
G	0.3320	0.2530
N	0.8810	0.2870
R	0.9120	0.3970
T	0.8980	0.3540

1.0

0.0

<0.0