



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 05:52 AM UTC

PDB ID : 9OL6 / pdb_00009ol6
EMDB ID : EMD-70591
Title : Rabbit Ryanodine Receptor 1: DMSO Control Closed Conformation
Authors : Molinarolo, S.M.; Van Petegem, F.
Deposited on : 2025-05-12
Resolution : 3.11 Å(reported)
Based on initial model : 7TZC

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

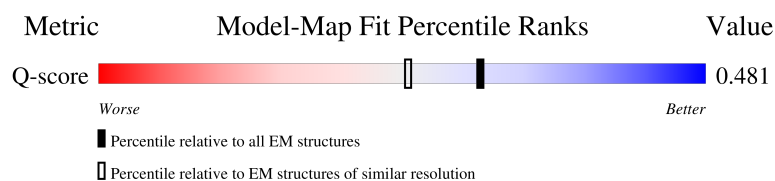
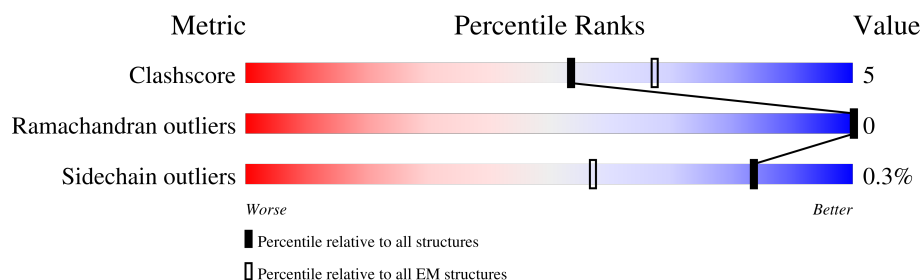
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

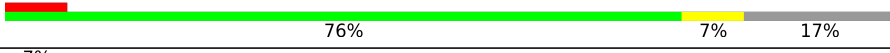
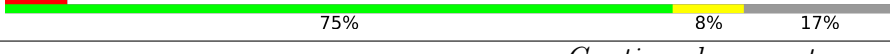
The reported resolution of this entry is 3.11 Å.

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	14465 (2.61 - 3.61)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	5037	
1	G	5037	
1	M	5037	
1	S	5037	

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Mol	Chain	Length	Quality of chain
2	B	111	90% 6%
2	H	111	90% 6%
2	N	111	90% 6%
2	T	111	90% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 133368 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	4185	Total	C	N	O	S	0	0
			32524	20790	5626	5890	218		
1	G	4185	Total	C	N	O	S	0	0
			32524	20790	5626	5890	218		
1	M	4185	Total	C	N	O	S	0	0
			32524	20790	5626	5890	218		
1	S	4185	Total	C	N	O	S	0	0
			32524	20790	5626	5890	218		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			816	514	144	154	4		
2	H	107	Total	C	N	O	S	0	0
			816	514	144	154	4		
2	N	107	Total	C	N	O	S	0	0
			816	514	144	154	4		
2	T	107	Total	C	N	O	S	0	0
			816	514	144	154	4		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	SER	-	expression tag	UNP P68106
B	-1	ASN	-	expression tag	UNP P68106
B	0	ALA	-	expression tag	UNP P68106
H	-2	SER	-	expression tag	UNP P68106
H	-1	ASN	-	expression tag	UNP P68106
H	0	ALA	-	expression tag	UNP P68106
N	-2	SER	-	expression tag	UNP P68106
N	-1	ASN	-	expression tag	UNP P68106
N	0	ALA	-	expression tag	UNP P68106

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Chain	Residue	Modelled	Actual	Comment	Reference
T	-2	SER	-	expression tag	UNP P68106
T	-1	ASN	-	expression tag	UNP P68106
T	0	ALA	-	expression tag	UNP P68106

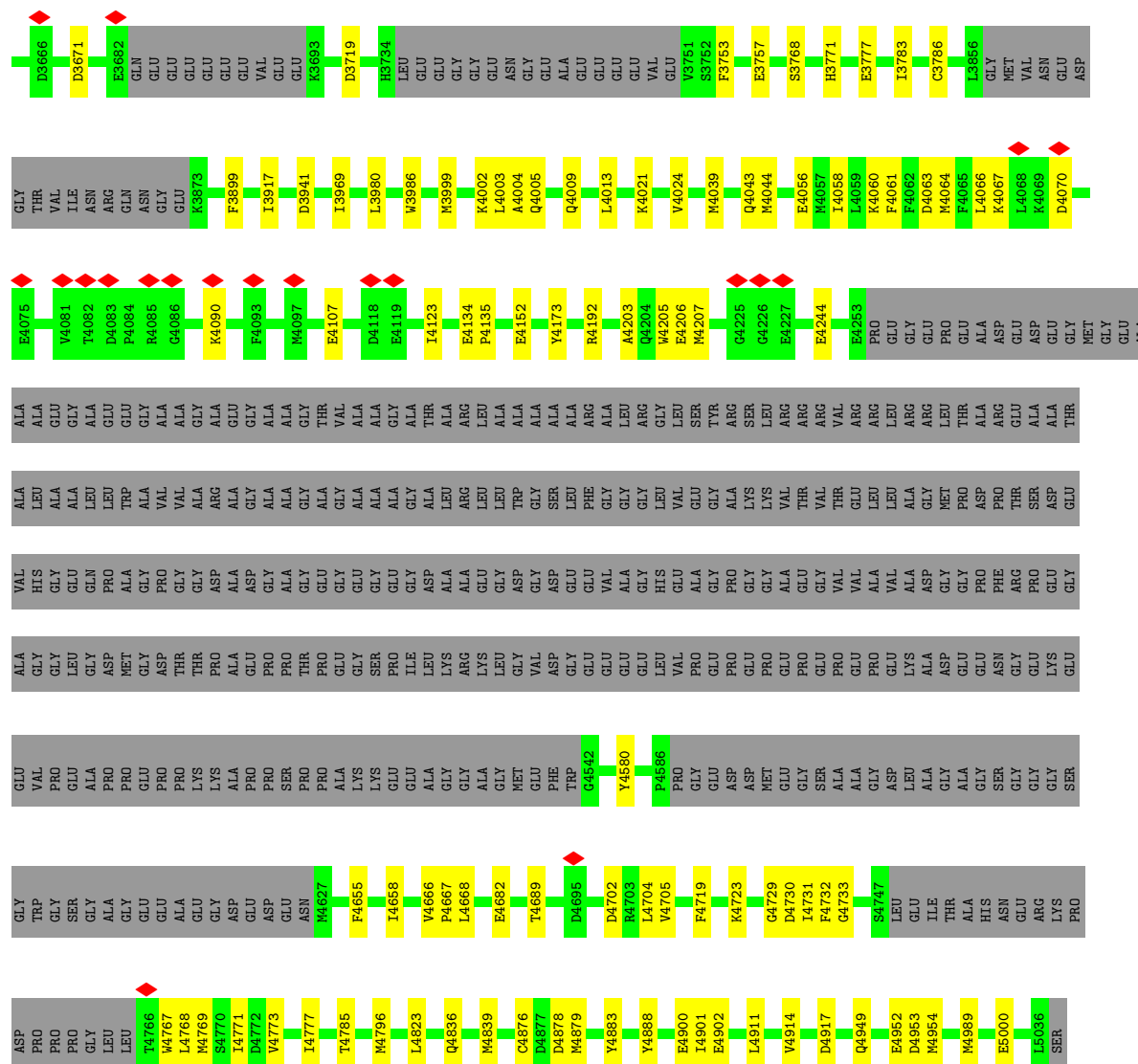
- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Ca 1	0
3	G	1	Total 1	Ca 1	0
3	M	1	Total 1	Ca 1	0
3	S	1	Total 1	Ca 1	0

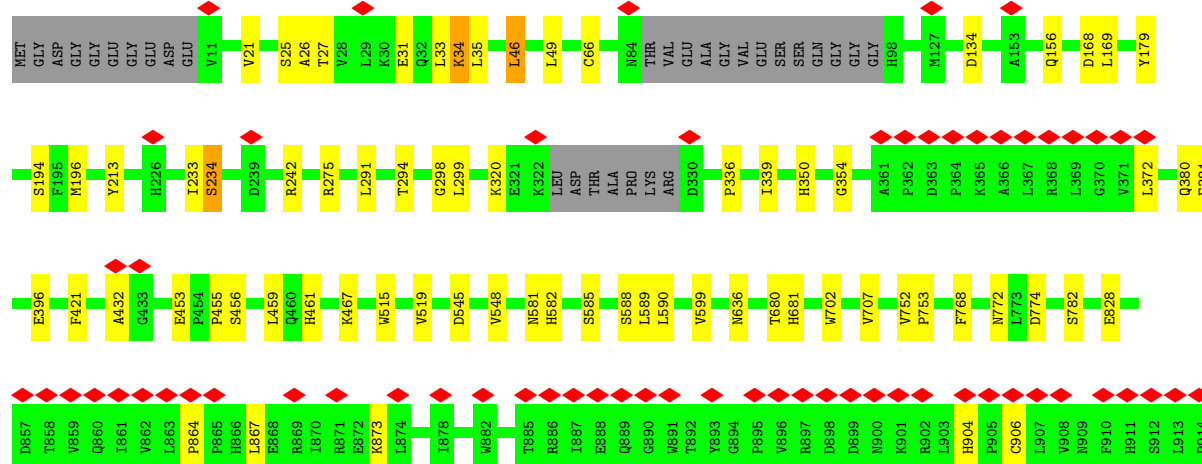
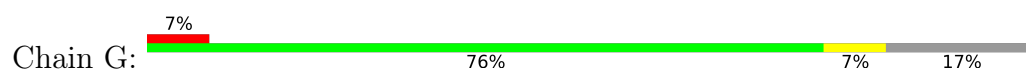
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total 1	Zn 1	0
4	G	1	Total 1	Zn 1	0
4	M	1	Total 1	Zn 1	0
4	S	1	Total 1	Zn 1	0





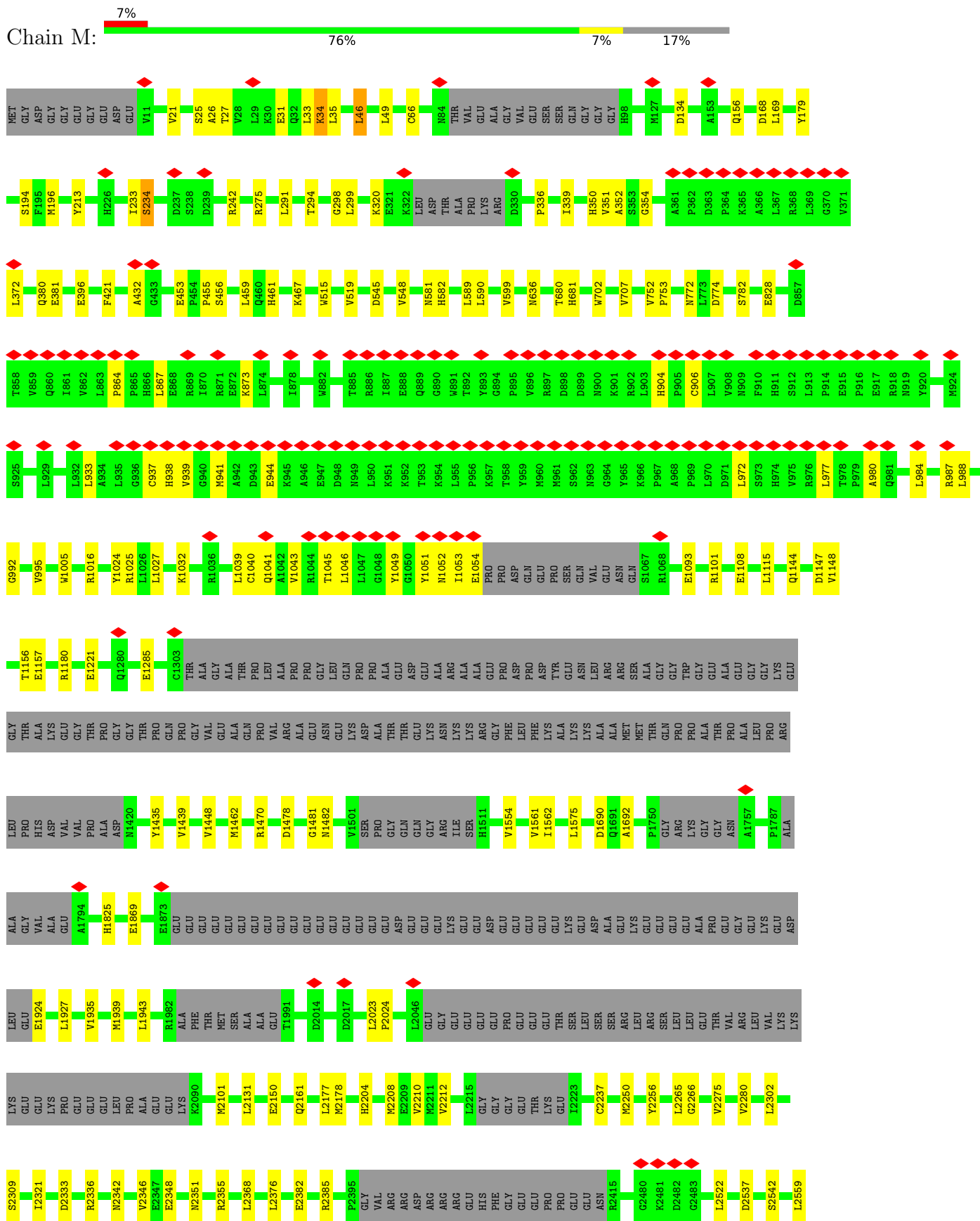
Molecule 1: Ryanodine receptor 1



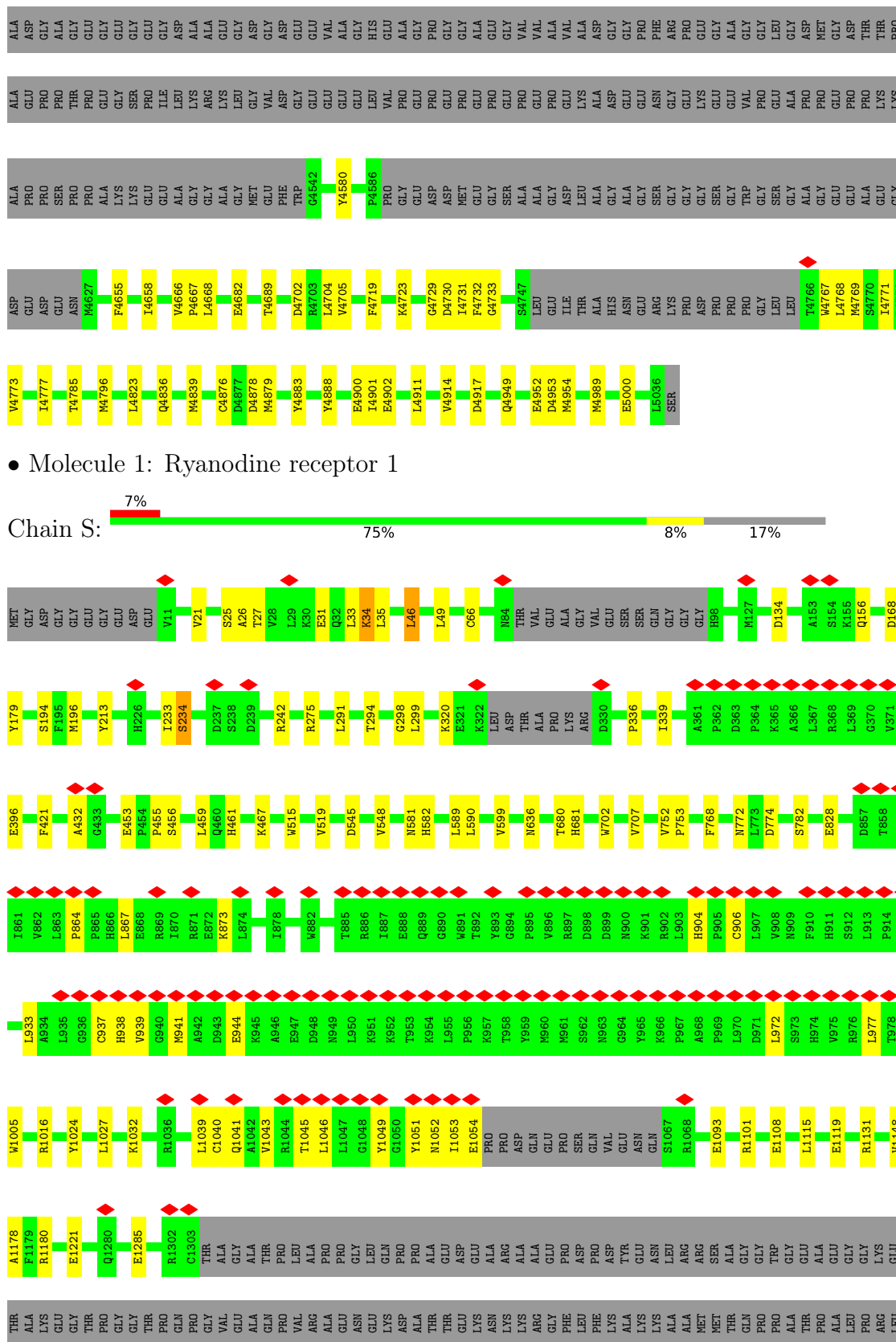




- Molecule 1: Ryanodine receptor 1











- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain N:  90% 6% .



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B

Chain T:  90% 6% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	126217	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.269	Depositor
Minimum map value	0.000	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.047	Depositor
Map size (Å)	491.52, 491.52, 491.52	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.96, 0.96, 0.96	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/33267	0.57	15/45152 (0.0%)
1	G	0.40	0/33267	0.57	16/45152 (0.0%)
1	M	0.40	0/33267	0.57	15/45152 (0.0%)
1	S	0.40	0/33267	0.57	16/45152 (0.0%)
2	B	0.77	0/832	0.70	0/1118
2	H	0.77	0/832	0.70	0/1118
2	N	0.78	0/832	0.70	0/1118
2	T	0.78	0/832	0.70	0/1118
All	All	0.41	0/136396	0.58	62/185080 (0.0%)

There are no bond length outliers.

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4005	GLN	N-CA-C	-7.38	103.87	113.17
1	G	4005	GLN	N-CA-C	-7.37	103.88	113.17
1	S	4005	GLN	N-CA-C	-7.36	103.90	113.17
1	M	4005	GLN	N-CA-C	-7.34	103.92	113.17
1	G	3157	ILE	CA-C-O	-6.40	117.06	122.63
1	A	3157	ILE	CA-C-O	-6.39	117.07	122.63
1	S	3157	ILE	CA-C-O	-6.37	117.09	122.63
1	M	3157	ILE	CA-C-O	-6.32	117.13	122.63
1	M	3564	GLU	N-CA-C	-6.21	101.22	110.23
1	S	3564	GLU	N-CA-C	-6.20	101.24	110.23
1	G	3564	GLU	N-CA-C	-6.19	101.26	110.23
1	A	3564	GLU	N-CA-C	-6.18	101.26	110.23
1	M	3463	GLU	N-CA-C	-5.93	105.96	112.72
1	G	3463	GLU	N-CA-C	-5.89	106.01	112.72
1	S	3463	GLU	N-CA-C	-5.88	106.02	112.72
1	A	3463	GLU	N-CA-C	-5.87	106.03	112.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	702	TRP	CA-C-O	-5.83	114.22	120.92
1	S	702	TRP	CA-C-O	-5.82	114.23	120.92
1	G	702	TRP	CA-C-O	-5.79	114.26	120.92
1	S	4768	LEU	N-CA-C	-5.79	104.60	111.03
1	M	4768	LEU	N-CA-C	-5.78	104.61	111.03
1	M	702	TRP	CA-C-O	-5.78	114.27	120.92
1	M	4769	MET	CA-C-O	-5.78	114.39	121.67
1	S	4769	MET	CA-C-O	-5.77	114.39	121.67
1	G	4769	MET	CA-C-O	-5.76	114.41	121.67
1	A	4769	MET	CA-C-O	-5.76	114.42	121.67
1	G	4768	LEU	N-CA-C	-5.76	104.64	111.03
1	A	4768	LEU	N-CA-C	-5.74	104.66	111.03
1	A	461	HIS	CA-C-O	-5.58	114.97	120.82
1	M	461	HIS	CA-C-O	-5.55	114.99	120.82
1	S	461	HIS	CA-C-O	-5.55	114.99	120.82
1	G	461	HIS	CA-C-O	-5.55	114.99	120.82
1	A	3579	LEU	N-CA-C	-5.45	102.36	110.20
1	G	3579	LEU	N-CA-C	-5.44	102.36	110.20
1	G	589	LEU	CA-C-O	-5.42	113.97	120.10
1	M	3579	LEU	N-CA-C	-5.41	102.41	110.20
1	M	589	LEU	CA-C-O	-5.40	114.00	120.10
1	S	3579	LEU	N-CA-C	-5.40	102.42	110.20
1	S	589	LEU	CA-C-O	-5.38	114.02	120.10
1	A	589	LEU	CA-C-O	-5.38	114.02	120.10
1	M	702	TRP	N-CA-C	-5.20	101.22	109.96
1	G	702	TRP	N-CA-C	-5.19	101.24	109.96
1	A	702	TRP	N-CA-C	-5.18	101.26	109.96
1	S	702	TRP	N-CA-C	-5.17	101.27	109.96
1	A	4883	TYR	CA-C-O	-5.17	115.37	120.70
1	G	4883	TYR	CA-C-O	-5.17	115.38	120.70
1	S	3385	ALA	N-CA-C	-5.16	105.65	111.28
1	G	234	SER	CA-C-O	-5.16	116.05	121.88
1	G	3567	PRO	N-CA-C	-5.15	106.37	113.53
1	S	234	SER	CA-C-O	-5.15	116.06	121.88
1	A	3385	ALA	N-CA-C	-5.14	105.68	111.28
1	A	3567	PRO	N-CA-C	-5.14	106.39	113.53
1	M	3567	PRO	N-CA-C	-5.14	106.39	113.53
1	G	3385	ALA	N-CA-C	-5.14	105.68	111.28
1	M	3385	ALA	N-CA-C	-5.14	105.68	111.28
1	S	3567	PRO	N-CA-C	-5.13	106.41	113.53
1	A	234	SER	CA-C-O	-5.12	116.09	121.88
1	M	4883	TYR	CA-C-O	-5.11	115.44	120.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	4883	TYR	CA-C-O	-5.11	115.44	120.70
1	M	234	SER	CA-C-O	-5.10	116.12	121.88
1	G	768	PHE	CA-C-O	-5.04	115.30	120.54
1	S	768	PHE	CA-C-O	-5.01	115.33	120.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32524	0	31610	354	0
1	G	32524	0	31610	351	0
1	M	32524	0	31610	353	0
1	S	32524	0	31610	358	0
2	B	816	0	815	3	0
2	H	816	0	815	3	0
2	N	816	0	815	3	0
2	T	816	0	815	3	0
3	A	1	0	0	0	0
3	G	1	0	0	0	0
3	M	1	0	0	0	0
3	S	1	0	0	0	0
4	A	1	0	0	0	0
4	G	1	0	0	0	0
4	M	1	0	0	0	0
4	S	1	0	0	0	0
All	All	133368	0	129700	1377	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 5.

All (1377) 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:A:939:VAL:HA	1:A:1053:ILE:HG22	1.36	1.08
1:G:939:VAL:HA	1:G:1053:ILE:HG22	1.36	1.07
1:S:939:VAL:HA	1:S:1053:ILE:HG22	1.35	1.03
1:M:939:VAL:HA	1:M:1053:ILE:HG22	1.36	1.01
1:G:3579:LEU:HD12	1:G:3580:PRO:HD3	1.46	0.97
1:M:3579:LEU:HD12	1:M:3580:PRO:HD3	1.46	0.97
1:A:3579:LEU:HD12	1:A:3580:PRO:HD3	1.46	0.97
1:S:3579:LEU:HD12	1:S:3580:PRO:HD3	1.46	0.97
1:G:1927:LEU:HD12	1:G:2101:MET:SD	2.06	0.96
1:A:1927:LEU:HD12	1:A:2101:MET:SD	2.06	0.95
1:M:1927:LEU:HD12	1:M:2101:MET:SD	2.06	0.95
1:S:1927:LEU:HD12	1:S:2101:MET:SD	2.06	0.94
1:S:1927:LEU:CD1	1:S:2101:MET:SD	2.60	0.90
1:M:1927:LEU:CD1	1:M:2101:MET:SD	2.60	0.89
1:A:1927:LEU:CD1	1:A:2101:MET:SD	2.60	0.89
1:G:1927:LEU:CD1	1:G:2101:MET:SD	2.60	0.89
1:M:1027:LEU:HD23	1:M:1032:LYS:CG	2.03	0.89
1:A:4767:TRP:CD1	1:A:4771:ILE:HD11	2.08	0.88
1:G:1027:LEU:HD23	1:G:1032:LYS:CG	2.04	0.88
1:S:4767:TRP:CD1	1:S:4771:ILE:HD11	2.08	0.88
1:G:4767:TRP:CD1	1:G:4771:ILE:HD11	2.08	0.88
1:S:1027:LEU:HD23	1:S:1032:LYS:CG	2.04	0.88
1:M:4767:TRP:CD1	1:M:4771:ILE:HD11	2.08	0.87
1:G:3579:LEU:HG	1:G:3580:PRO:HD2	1.56	0.87
1:A:3579:LEU:HG	1:A:3580:PRO:HD2	1.55	0.86
1:A:1027:LEU:HD23	1:A:1032:LYS:CG	2.04	0.86
1:M:3579:LEU:HG	1:M:3580:PRO:HD2	1.55	0.85
1:M:275:ARG:HD3	1:M:336:PRO:HG2	1.58	0.85
1:S:275:ARG:HD3	1:S:336:PRO:HG2	1.58	0.85
1:S:3579:LEU:HG	1:S:3580:PRO:HD2	1.56	0.85
1:A:396:GLU:OE2	1:A:396:GLU:N	2.09	0.85
1:M:4767:TRP:NE1	1:M:4771:ILE:HD11	1.92	0.85
1:S:396:GLU:N	1:S:396:GLU:OE2	2.09	0.85
1:G:275:ARG:HD3	1:G:336:PRO:HG2	1.58	0.85
1:G:4767:TRP:NE1	1:G:4771:ILE:HD11	1.92	0.85
1:A:275:ARG:HD3	1:A:336:PRO:HG2	1.58	0.84
1:G:939:VAL:CA	1:G:1053:ILE:HG22	2.07	0.84
1:A:939:VAL:CA	1:A:1053:ILE:HG22	2.07	0.84
1:G:4839:MET:HG2	1:M:4823:LEU:HD22	1.60	0.84
1:A:4823:LEU:HD22	1:S:4839:MET:HG2	1.60	0.84
1:M:396:GLU:OE2	1:M:396:GLU:N	2.09	0.84
1:A:4767:TRP:NE1	1:A:4771:ILE:HD11	1.92	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:4839:MET:HG3	1:S:4823:LEU:HD21	1.59	0.84
1:S:939:VAL:CA	1:S:1053:ILE:HG22	2.07	0.84
1:A:1027:LEU:HD23	1:A:1032:LYS:HG3	1.59	0.83
1:A:4839:MET:HG2	1:G:4823:LEU:HD22	1.60	0.83
1:G:1027:LEU:HD23	1:G:1032:LYS:HG3	1.59	0.83
1:A:4839:MET:HG3	1:G:4823:LEU:HD21	1.59	0.83
1:G:396:GLU:N	1:G:396:GLU:OE2	2.09	0.83
1:S:4767:TRP:NE1	1:S:4771:ILE:HD11	1.92	0.83
1:M:1027:LEU:HD23	1:M:1032:LYS:HG3	1.59	0.83
1:M:4839:MET:HG2	1:S:4823:LEU:HD22	1.60	0.83
1:A:4823:LEU:HD21	1:S:4839:MET:HG3	1.59	0.82
1:M:939:VAL:CA	1:M:1053:ILE:HG22	2.07	0.82
1:G:4839:MET:HG3	1:M:4823:LEU:HD21	1.59	0.82
1:G:1156:THR:OG1	1:G:1157:GLU:OE1	1.98	0.82
1:S:1027:LEU:HD23	1:S:1032:LYS:HG3	1.59	0.82
1:G:4917:ASP:OD2	1:M:4888:TYR:OH	1.99	0.81
1:M:2627:VAL:HG11	1:M:2910:THR:CG2	2.11	0.81
1:A:2627:VAL:HG11	1:A:2910:THR:CG2	2.11	0.81
1:S:2627:VAL:HG11	1:S:2910:THR:CG2	2.10	0.81
1:G:1561:VAL:HG12	1:G:1562:ILE:HG12	1.64	0.80
1:S:1156:THR:OG1	1:S:1157:GLU:OE1	1.98	0.80
1:A:1156:THR:OG1	1:A:1157:GLU:OE1	1.98	0.80
1:G:2627:VAL:HG11	1:G:2910:THR:CG2	2.11	0.80
1:S:275:ARG:HH11	1:S:336:PRO:HD2	1.47	0.80
1:M:1156:THR:OG1	1:M:1157:GLU:OE1	1.98	0.80
1:A:1561:VAL:HG12	1:A:1562:ILE:HG12	1.64	0.80
1:S:1561:VAL:HG12	1:S:1562:ILE:HG12	1.64	0.80
1:M:4917:ASP:OD2	1:S:4888:TYR:OH	1.99	0.80
1:M:1561:VAL:HG12	1:M:1562:ILE:HG12	1.64	0.79
1:M:4839:MET:CG	1:S:4823:LEU:CD2	2.61	0.79
1:S:4064:MET:HE3	1:S:4107:GLU:HB3	1.65	0.79
1:G:275:ARG:HH11	1:G:336:PRO:HD2	1.47	0.79
1:A:275:ARG:HH11	1:A:336:PRO:HD2	1.47	0.79
1:G:1108:GLU:N	1:G:1108:GLU:OE1	2.16	0.79
1:M:4064:MET:HE3	1:M:4107:GLU:HB3	1.65	0.79
1:A:4839:MET:CG	1:G:4823:LEU:CD2	2.61	0.79
1:A:4823:LEU:CD2	1:S:4839:MET:CG	2.61	0.79
1:M:1108:GLU:OE1	1:M:1108:GLU:N	2.16	0.78
1:M:2627:VAL:HG11	1:M:2910:THR:HG22	1.65	0.78
1:A:4888:TYR:OH	1:S:4917:ASP:OD2	1.99	0.78
1:M:275:ARG:HH11	1:M:336:PRO:HD2	1.47	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1108:GLU:OE1	1:A:1108:GLU:N	2.16	0.78
1:A:2627:VAL:HG11	1:A:2910:THR:HG22	1.64	0.78
1:A:4917:ASP:OD2	1:G:4888:TYR:OH	1.99	0.78
1:G:3286:GLU:OE2	1:G:3286:GLU:N	2.17	0.78
1:G:4839:MET:CG	1:M:4823:LEU:CD2	2.61	0.78
1:S:1108:GLU:N	1:S:1108:GLU:OE1	2.16	0.78
1:G:2627:VAL:HG11	1:G:2910:THR:HG22	1.64	0.78
1:M:3286:GLU:N	1:M:3286:GLU:OE2	2.17	0.78
1:A:3286:GLU:N	1:A:3286:GLU:OE2	2.17	0.77
1:S:2627:VAL:HG11	1:S:2910:THR:HG22	1.64	0.77
1:A:4064:MET:HE3	1:A:4107:GLU:HB3	1.65	0.77
1:A:4823:LEU:HD21	1:S:4839:MET:CG	2.14	0.77
1:A:4823:LEU:CD2	1:S:4839:MET:HG2	2.15	0.77
1:A:4839:MET:CG	1:G:4823:LEU:HD21	2.14	0.77
1:G:4064:MET:HE3	1:G:4107:GLU:HB3	1.65	0.77
1:M:4839:MET:HG2	1:S:4823:LEU:CD2	2.15	0.77
1:M:4839:MET:CG	1:S:4823:LEU:HD21	2.14	0.77
1:S:3286:GLU:OE2	1:S:3286:GLU:N	2.17	0.77
1:A:1024:TYR:CE1	1:A:1032:LYS:HG2	2.20	0.76
1:S:3783:ILE:O	1:S:3786:CYS:SG	2.43	0.76
1:M:3783:ILE:O	1:M:3786:CYS:SG	2.43	0.76
1:S:1024:TYR:CE1	1:S:1032:LYS:HG2	2.20	0.76
1:A:3783:ILE:O	1:A:3786:CYS:SG	2.43	0.76
1:G:3783:ILE:O	1:G:3786:CYS:SG	2.43	0.76
1:G:4839:MET:CG	1:M:4823:LEU:HD21	2.14	0.76
1:G:1024:TYR:CE1	1:G:1032:LYS:HG2	2.20	0.76
1:A:3169:LEU:CD1	1:A:3194:LEU:HD11	2.16	0.76
1:M:3169:LEU:CD1	1:M:3194:LEU:HD11	2.16	0.76
1:A:4004:ALA:HB2	1:A:4013:LEU:HD22	1.69	0.75
1:S:3169:LEU:CD1	1:S:3194:LEU:HD11	2.16	0.75
1:M:1024:TYR:CE1	1:M:1032:LYS:HG2	2.20	0.75
1:G:3169:LEU:CD1	1:G:3194:LEU:HD11	2.16	0.75
1:G:4839:MET:HG2	1:M:4823:LEU:CD2	2.16	0.75
1:A:275:ARG:HD3	1:A:336:PRO:CG	2.17	0.75
1:G:4004:ALA:HB2	1:G:4013:LEU:HD22	1.69	0.75
1:A:4839:MET:HG2	1:G:4823:LEU:CD2	2.15	0.74
1:S:456:SER:OG	1:S:459:LEU:HG	1.88	0.74
1:G:456:SER:OG	1:G:459:LEU:HG	1.88	0.74
1:A:456:SER:OG	1:A:459:LEU:HG	1.88	0.74
1:G:275:ARG:HD3	1:G:336:PRO:CG	2.17	0.74
1:M:1435:TYR:HB3	1:M:1575:LEU:HD23	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:1435:TYR:HB3	1:S:1575:LEU:HD23	1.70	0.74
1:G:3151:GLN:N	1:G:3151:GLN:OE1	2.21	0.74
1:M:456:SER:OG	1:M:459:LEU:HG	1.88	0.74
1:S:275:ARG:HD3	1:S:336:PRO:CG	2.17	0.74
1:A:3151:GLN:OE1	1:A:3151:GLN:N	2.21	0.74
1:M:275:ARG:HD3	1:M:336:PRO:CG	2.17	0.74
1:S:4004:ALA:HB2	1:S:4013:LEU:HD22	1.69	0.73
1:M:4004:ALA:HB2	1:M:4013:LEU:HD22	1.69	0.73
1:S:3151:GLN:N	1:S:3151:GLN:OE1	2.21	0.73
1:A:453:GLU:N	1:A:453:GLU:OE1	2.21	0.73
1:G:453:GLU:N	1:G:453:GLU:OE1	2.21	0.73
1:M:3151:GLN:N	1:M:3151:GLN:OE1	2.21	0.73
1:M:3753:PHE:HZ	1:M:4719:PHE:CZ	2.06	0.73
1:A:1435:TYR:HB3	1:A:1575:LEU:HD23	1.70	0.73
1:G:1943:LEU:HD11	1:G:2101:MET:HE1	1.71	0.73
1:M:1943:LEU:HD11	1:M:2101:MET:HE1	1.71	0.73
1:S:453:GLU:N	1:S:453:GLU:OE1	2.21	0.73
1:M:4207:MET:HE2	1:M:4207:MET:N	2.04	0.73
1:S:1943:LEU:HD11	1:S:2101:MET:HE1	1.71	0.73
1:M:453:GLU:N	1:M:453:GLU:OE1	2.21	0.73
1:S:3753:PHE:HZ	1:S:4719:PHE:CZ	2.07	0.73
1:G:1435:TYR:HB3	1:G:1575:LEU:HD23	1.70	0.73
1:G:4207:MET:N	1:G:4207:MET:HE2	2.04	0.73
1:G:3753:PHE:HZ	1:G:4719:PHE:CZ	2.06	0.72
1:S:3579:LEU:HD12	1:S:3580:PRO:CD	2.20	0.72
1:A:1825:HIS:CD2	1:G:3567:PRO:HG3	2.25	0.72
1:A:2670:GLU:O	1:A:2674:LEU:HD13	1.90	0.72
1:A:4207:MET:HE2	1:A:4207:MET:N	2.04	0.72
1:S:1027:LEU:HD23	1:S:1032:LYS:HG2	1.72	0.72
1:S:4207:MET:N	1:S:4207:MET:HE2	2.04	0.72
1:G:2628:PHE:CD1	1:G:2907:PRO:HG3	2.25	0.72
1:M:2628:PHE:CD1	1:M:2907:PRO:HG3	2.25	0.72
1:M:3579:LEU:HD12	1:M:3580:PRO:CD	2.20	0.72
1:G:2670:GLU:O	1:G:2674:LEU:HD13	1.90	0.72
1:M:2670:GLU:O	1:M:2674:LEU:HD13	1.90	0.72
1:A:3753:PHE:HZ	1:A:4719:PHE:CZ	2.07	0.72
1:A:1943:LEU:HD11	1:A:2101:MET:HE1	1.71	0.71
1:M:33:LEU:HD11	1:M:35:LEU:HD12	1.72	0.71
1:S:2628:PHE:CD1	1:S:2907:PRO:HG3	2.25	0.71
1:A:2628:PHE:CD1	1:A:2907:PRO:HG3	2.25	0.71
1:G:2628:PHE:HB2	1:G:2907:PRO:CD	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:33:LEU:HD11	1:G:35:LEU:HD12	1.72	0.71
1:A:3567:PRO:HG3	1:S:1825:HIS:CD2	2.25	0.71
1:M:2628:PHE:HB2	1:M:2907:PRO:CD	2.20	0.71
1:S:2628:PHE:HB2	1:S:2907:PRO:HD3	1.73	0.71
1:A:1027:LEU:HD23	1:A:1032:LYS:HG2	1.72	0.71
1:A:2628:PHE:HB2	1:A:2907:PRO:CD	2.20	0.71
1:G:941:MET:SD	1:G:944:GLU:HG2	2.31	0.71
1:G:1027:LEU:HD23	1:G:1032:LYS:HG2	1.72	0.71
1:A:941:MET:SD	1:A:944:GLU:HG2	2.31	0.71
1:M:1027:LEU:HD23	1:M:1032:LYS:HG2	1.72	0.71
1:S:2628:PHE:HB2	1:S:2907:PRO:CD	2.20	0.71
1:S:3427:PRO:HG2	1:S:3579:LEU:HD21	1.72	0.71
1:G:3579:LEU:HD12	1:G:3580:PRO:CD	2.20	0.71
1:M:1825:HIS:CD2	1:S:3567:PRO:HG3	2.25	0.71
1:A:3427:PRO:HG2	1:A:3579:LEU:HD21	1.72	0.70
1:G:2628:PHE:HB2	1:G:2907:PRO:HD3	1.73	0.70
1:A:980:ALA:O	1:A:984:LEU:HD13	1.92	0.70
1:S:2670:GLU:O	1:S:2674:LEU:HD13	1.90	0.70
1:S:4152:GLU:OE1	1:S:4192:ARG:NH1	2.24	0.70
1:A:33:LEU:HD11	1:A:35:LEU:HD12	1.72	0.70
1:G:1825:HIS:CD2	1:M:3567:PRO:HG3	2.25	0.70
1:G:4152:GLU:OE1	1:G:4192:ARG:NH1	2.24	0.70
1:S:980:ALA:O	1:S:984:LEU:HD13	1.92	0.70
1:M:4152:GLU:OE1	1:M:4192:ARG:NH1	2.24	0.70
1:S:941:MET:SD	1:S:944:GLU:HG2	2.31	0.70
1:A:4152:GLU:OE1	1:A:4192:ARG:NH1	2.24	0.70
1:G:980:ALA:O	1:G:984:LEU:HD13	1.92	0.70
1:M:941:MET:SD	1:M:944:GLU:HG2	2.31	0.70
1:M:3427:PRO:HG2	1:M:3579:LEU:HD21	1.72	0.70
1:A:2628:PHE:HB2	1:A:2907:PRO:HD3	1.73	0.70
1:G:3427:PRO:HG2	1:G:3579:LEU:HD21	1.72	0.70
1:S:33:LEU:HD11	1:S:35:LEU:HD12	1.72	0.70
1:M:2628:PHE:HB2	1:M:2907:PRO:HD3	1.73	0.70
1:M:3459:VAL:HG23	1:M:3464:ILE:HG23	1.73	0.70
1:G:2250:MET:HE2	1:G:2250:MET:HA	1.74	0.69
1:M:1943:LEU:CD1	1:M:2101:MET:HE1	2.22	0.69
1:S:1943:LEU:CD1	1:S:2101:MET:HE1	2.22	0.69
1:M:3579:LEU:HG	1:M:3580:PRO:CD	2.22	0.69
1:A:1943:LEU:CD1	1:A:2101:MET:HE1	2.22	0.69
1:A:3579:LEU:HD12	1:A:3580:PRO:CD	2.20	0.69
1:G:3999:MET:O	1:G:4003:LEU:HG	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:939:VAL:HA	1:S:1053:ILE:CG2	2.20	0.69
1:A:3579:LEU:HG	1:A:3580:PRO:CD	2.22	0.69
1:G:3579:LEU:HG	1:G:3580:PRO:CD	2.22	0.69
1:G:1943:LEU:CD1	1:G:2101:MET:HE1	2.22	0.69
1:M:3999:MET:O	1:M:4003:LEU:HG	1.93	0.69
1:S:3427:PRO:CG	1:S:3579:LEU:HD21	2.23	0.69
1:A:3459:VAL:HG23	1:A:3464:ILE:HG23	1.73	0.69
1:M:980:ALA:O	1:M:984:LEU:HD13	1.92	0.68
1:S:3579:LEU:HG	1:S:3580:PRO:CD	2.22	0.68
1:A:2250:MET:HE2	1:A:2250:MET:HA	1.75	0.68
1:A:3427:PRO:CG	1:A:3579:LEU:HD21	2.23	0.68
1:S:2250:MET:HE2	1:S:2250:MET:HA	1.75	0.68
1:A:4244:GLU:OE1	1:A:4668:LEU:HD13	1.93	0.68
1:G:4244:GLU:OE1	1:G:4668:LEU:HD13	1.93	0.68
1:S:4244:GLU:OE1	1:S:4668:LEU:HD13	1.93	0.68
1:G:3459:VAL:HG23	1:G:3464:ILE:HG23	1.73	0.68
1:M:2250:MET:HA	1:M:2250:MET:HE2	1.74	0.68
1:M:4767:TRP:CD2	1:M:4767:TRP:O	2.47	0.68
1:S:3459:VAL:HG23	1:S:3464:ILE:HG23	1.73	0.68
1:S:4767:TRP:O	1:S:4767:TRP:CD2	2.47	0.68
1:A:4767:TRP:CD2	1:A:4767:TRP:O	2.47	0.68
1:M:4244:GLU:OE1	1:M:4668:LEU:HD13	1.93	0.68
1:A:3999:MET:O	1:A:4003:LEU:HG	1.93	0.67
1:G:4767:TRP:O	1:G:4767:TRP:CD2	2.47	0.67
1:G:3427:PRO:CG	1:G:3579:LEU:HD21	2.23	0.67
1:M:3427:PRO:CG	1:M:3579:LEU:HD21	2.23	0.67
1:M:2333:ASP:OD1	1:M:2336:ARG:NH2	2.28	0.67
1:S:3999:MET:O	1:S:4003:LEU:HG	1.93	0.67
1:M:2537:ASP:O	1:M:2593:ARG:NH1	2.28	0.67
1:A:2537:ASP:O	1:A:2593:ARG:NH1	2.28	0.67
1:S:2333:ASP:OD1	1:S:2336:ARG:NH2	2.28	0.67
1:G:2333:ASP:OD1	1:G:2336:ARG:NH2	2.28	0.66
1:S:2537:ASP:O	1:S:2593:ARG:NH1	2.28	0.66
1:A:2333:ASP:OD1	1:A:2336:ARG:NH2	2.28	0.66
1:G:2537:ASP:O	1:G:2593:ARG:NH1	2.28	0.66
1:G:1927:LEU:HD11	1:G:2101:MET:SD	2.36	0.66
1:A:1927:LEU:HD11	1:A:2101:MET:SD	2.36	0.66
1:M:35:LEU:HD22	1:M:49:LEU:HB3	1.78	0.66
1:A:3579:LEU:CD1	1:A:3580:PRO:HD3	2.25	0.66
1:S:1927:LEU:HD11	1:S:2101:MET:SD	2.36	0.66
1:S:3283:ARG:HH22	1:S:3287:ARG:HH22	1.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:3579:LEU:CD1	1:M:3580:PRO:CD	2.74	0.65
1:S:3579:LEU:CD1	1:S:3580:PRO:CD	2.74	0.65
1:S:275:ARG:NH1	1:S:336:PRO:HD2	2.11	0.65
1:G:35:LEU:HD22	1:G:49:LEU:HB3	1.78	0.65
1:M:3969:ILE:HD11	1:M:3980:LEU:CD1	2.27	0.65
1:A:4767:TRP:O	1:A:4767:TRP:CE3	2.50	0.65
1:G:938:HIS:O	1:G:1053:ILE:HA	1.97	0.65
1:G:3579:LEU:CG	1:G:3580:PRO:HD2	2.27	0.65
1:A:275:ARG:NH1	1:A:336:PRO:HD2	2.11	0.65
1:A:3579:LEU:CD1	1:A:3580:PRO:CD	2.74	0.65
1:G:275:ARG:NH1	1:G:336:PRO:HD2	2.11	0.65
1:G:3579:LEU:CD1	1:G:3580:PRO:CD	2.74	0.65
1:M:4767:TRP:O	1:M:4767:TRP:CE3	2.50	0.65
1:S:3579:LEU:CG	1:S:3580:PRO:HD2	2.27	0.65
1:S:4767:TRP:O	1:S:4767:TRP:CE3	2.50	0.65
1:G:939:VAL:HA	1:G:1053:ILE:CG2	2.20	0.65
1:M:937:CYS:SG	1:M:984:LEU:HG	2.37	0.65
1:A:938:HIS:O	1:A:1053:ILE:HA	1.97	0.64
1:M:938:HIS:O	1:M:1053:ILE:HA	1.97	0.64
1:G:3579:LEU:CD1	1:G:3580:PRO:HD3	2.25	0.64
1:S:984:LEU:HD12	1:S:987:ARG:HH11	1.62	0.64
1:A:3283:ARG:HH22	1:A:3287:ARG:HH22	1.44	0.64
1:M:3579:LEU:CG	1:M:3580:PRO:HD2	2.27	0.64
1:A:35:LEU:HD22	1:A:49:LEU:HB3	1.78	0.64
1:A:3579:LEU:CG	1:A:3580:PRO:HD2	2.27	0.64
1:A:3969:ILE:HD11	1:A:3980:LEU:CD1	2.27	0.64
1:M:3283:ARG:HH22	1:M:3287:ARG:HH22	1.44	0.64
1:S:3969:ILE:HD11	1:S:3980:LEU:CD1	2.27	0.64
1:G:3969:ILE:HD11	1:G:3980:LEU:CD1	2.27	0.64
1:A:984:LEU:HD12	1:A:987:ARG:HH11	1.62	0.64
1:M:1927:LEU:HD11	1:M:2101:MET:SD	2.36	0.64
1:M:275:ARG:NH1	1:M:336:PRO:HD2	2.11	0.64
1:M:3106:MET:HE3	1:M:3132:THR:HB	1.80	0.64
1:S:938:HIS:O	1:S:1053:ILE:HA	1.97	0.64
1:A:937:CYS:SG	1:A:984:LEU:HG	2.37	0.64
1:G:937:CYS:SG	1:G:984:LEU:HG	2.37	0.64
1:S:2627:VAL:CG1	1:S:2910:THR:CG2	2.76	0.64
1:S:4064:MET:CE	1:S:4107:GLU:HB3	2.28	0.64
1:G:3283:ARG:HH22	1:G:3287:ARG:HH22	1.44	0.63
1:G:3310:ASP:OD1	1:G:3350:ARG:NH2	2.32	0.63
1:S:35:LEU:HD22	1:S:49:LEU:HB3	1.78	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:937:CYS:SG	1:S:984:LEU:HG	2.37	0.63
1:G:3106:MET:HE3	1:G:3132:THR:HB	1.80	0.63
1:G:2627:VAL:CG1	1:G:2910:THR:CG2	2.76	0.63
1:G:4064:MET:HA	1:G:4067:LYS:HD3	1.81	0.63
1:M:581:ASN:OD1	1:M:582:HIS:CD2	2.52	0.63
1:M:4064:MET:HA	1:M:4067:LYS:HD3	1.81	0.63
1:A:2627:VAL:CG1	1:A:2910:THR:CG2	2.76	0.63
1:S:3310:ASP:OD1	1:S:3350:ARG:NH2	2.32	0.63
1:A:581:ASN:OD1	1:A:582:HIS:CD2	2.52	0.63
1:M:984:LEU:HD12	1:M:987:ARG:HH11	1.62	0.63
1:M:2627:VAL:CG1	1:M:2910:THR:CG2	2.76	0.63
1:M:4064:MET:CE	1:M:4107:GLU:HB3	2.28	0.63
1:S:581:ASN:OD1	1:S:582:HIS:CD2	2.52	0.63
1:A:3310:ASP:OD1	1:A:3350:ARG:NH2	2.31	0.63
1:S:3106:MET:HE3	1:S:3132:THR:HB	1.80	0.63
1:G:213:TYR:CD1	1:G:339:ILE:O	2.52	0.62
1:A:3106:MET:HE3	1:A:3132:THR:HB	1.80	0.62
1:G:984:LEU:HD12	1:G:987:ARG:HH11	1.63	0.62
1:G:4767:TRP:O	1:G:4767:TRP:CE3	2.50	0.62
1:S:213:TYR:CD1	1:S:339:ILE:O	2.52	0.62
1:A:2693:GLN:OE1	1:A:2693:GLN:N	2.32	0.62
1:G:581:ASN:OD1	1:G:582:HIS:CD2	2.52	0.62
1:M:3310:ASP:OD1	1:M:3350:ARG:NH2	2.32	0.62
1:A:1825:HIS:CD2	1:G:3567:PRO:HB3	2.35	0.62
1:M:1825:HIS:CD2	1:S:3567:PRO:HB3	2.35	0.62
1:M:2693:GLN:OE1	1:M:2693:GLN:N	2.32	0.62
1:A:4064:MET:CE	1:A:4107:GLU:HB3	2.28	0.62
1:G:1825:HIS:NE2	1:M:3567:PRO:HB3	2.15	0.62
1:M:213:TYR:CD1	1:M:339:ILE:O	2.52	0.62
1:A:3169:LEU:CD1	1:A:3194:LEU:CD1	2.78	0.62
1:G:2693:GLN:N	1:G:2693:GLN:OE1	2.32	0.62
1:A:1825:HIS:CD2	1:G:3567:PRO:CG	2.83	0.62
1:G:3592:ILE:O	1:G:3596:VAL:HG23	2.00	0.62
1:M:1825:HIS:CD2	1:S:3567:PRO:CG	2.83	0.62
1:A:1005:TRP:CE3	1:A:1016:ARG:C	2.78	0.62
1:G:1005:TRP:CE3	1:G:1016:ARG:C	2.78	0.62
1:S:1005:TRP:CE3	1:S:1016:ARG:C	2.78	0.62
1:A:3567:PRO:HB3	1:S:1825:HIS:CD2	2.35	0.61
1:M:1825:HIS:NE2	1:S:3567:PRO:HB3	2.14	0.61
1:A:3567:PRO:CG	1:S:1825:HIS:CD2	2.83	0.61
1:M:3169:LEU:CD1	1:M:3194:LEU:CD1	2.78	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1825:HIS:CD2	1:M:3567:PRO:CG	2.83	0.61
1:G:4064:MET:CE	1:G:4107:GLU:HB3	2.28	0.61
1:M:1005:TRP:CE3	1:M:1016:ARG:C	2.78	0.61
1:M:2862:LEU:CD1	1:M:2932:MET:HE1	2.30	0.61
1:S:4064:MET:HA	1:S:4067:LYS:HD3	1.80	0.61
1:A:1825:HIS:NE2	1:G:3567:PRO:HB3	2.14	0.61
1:A:2862:LEU:CD1	1:A:2932:MET:HE1	2.30	0.61
1:A:3567:PRO:HB3	1:S:1825:HIS:NE2	2.15	0.61
1:G:4767:TRP:CE2	1:G:4771:ILE:HD11	2.36	0.61
1:S:2693:GLN:N	1:S:2693:GLN:OE1	2.32	0.61
1:A:3433:GLU:OE1	1:A:3436:ARG:NH1	2.34	0.61
1:A:4064:MET:HA	1:A:4067:LYS:HD3	1.81	0.61
1:G:1157:GLU:OE1	1:G:1157:GLU:N	2.34	0.61
1:G:1825:HIS:CD2	1:M:3567:PRO:HB3	2.35	0.61
1:M:2580:ASP:OD1	1:M:2581:SER:N	2.33	0.61
1:S:3169:LEU:CD1	1:S:3194:LEU:CD1	2.78	0.61
1:A:213:TYR:CD1	1:A:339:ILE:O	2.52	0.61
1:A:3592:ILE:O	1:A:3596:VAL:HG23	2.00	0.61
1:M:939:VAL:HA	1:M:1053:ILE:CG2	2.20	0.61
1:M:1157:GLU:OE1	1:M:1157:GLU:N	2.34	0.61
1:S:1157:GLU:OE1	1:S:1157:GLU:N	2.34	0.61
1:S:2862:LEU:CD1	1:S:2932:MET:HE1	2.30	0.61
1:S:2580:ASP:OD1	1:S:2581:SER:N	2.33	0.61
1:G:2580:ASP:OD1	1:G:2581:SER:N	2.33	0.61
1:G:2862:LEU:CD1	1:G:2932:MET:HE1	2.30	0.61
1:A:4767:TRP:CE2	1:A:4771:ILE:HD11	2.36	0.61
1:G:3169:LEU:CD1	1:G:3194:LEU:CD1	2.78	0.61
1:S:3433:GLU:OE1	1:S:3436:ARG:NH1	2.34	0.61
1:A:581:ASN:OD1	1:A:582:HIS:N	2.34	0.60
1:A:2580:ASP:OD1	1:A:2581:SER:N	2.33	0.60
1:G:4954:MET:HA	1:G:4954:MET:HE2	1.83	0.60
1:M:581:ASN:OD1	1:M:582:HIS:N	2.34	0.60
1:M:4954:MET:HE2	1:M:4954:MET:HA	1.83	0.60
1:A:3283:ARG:HH22	1:A:3287:ARG:NH2	1.99	0.60
1:A:3573:MET:O	1:A:3574:ALA:C	2.44	0.60
1:S:3283:ARG:HH22	1:S:3287:ARG:NH2	1.99	0.60
1:S:2342:ASN:ND2	1:S:2342:ASN:O	2.35	0.60
1:A:4954:MET:HE2	1:A:4954:MET:HA	1.83	0.60
1:G:3433:GLU:OE1	1:G:3436:ARG:NH1	2.34	0.60
1:M:3433:GLU:OE1	1:M:3436:ARG:NH1	2.34	0.60
1:M:3592:ILE:O	1:M:3596:VAL:HG23	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:4767:TRP:CE2	1:M:4771:ILE:HD11	2.36	0.60
1:S:4954:MET:HA	1:S:4954:MET:HE2	1.83	0.60
1:A:1157:GLU:OE1	1:A:1157:GLU:N	2.34	0.60
1:M:2342:ASN:O	1:M:2342:ASN:ND2	2.35	0.60
1:S:2280:VAL:HG22	1:S:2280:VAL:O	2.02	0.60
1:S:3592:ILE:O	1:S:3596:VAL:HG23	2.00	0.60
1:M:2628:PHE:HD1	1:M:2907:PRO:HG3	1.67	0.60
1:M:3283:ARG:HH22	1:M:3287:ARG:NH2	1.99	0.60
1:A:939:VAL:HA	1:A:1053:ILE:CG2	2.20	0.60
1:G:581:ASN:OD1	1:G:582:HIS:N	2.34	0.60
1:G:873:LYS:HB3	1:G:1049:TYR:CZ	2.37	0.60
1:G:3573:MET:O	1:G:3574:ALA:C	2.44	0.60
1:M:972:LEU:HD11	1:M:1045:THR:OG1	2.02	0.60
1:S:581:ASN:OD1	1:S:582:HIS:N	2.34	0.60
1:G:320:LYS:NZ	1:G:381:GLU:O	2.35	0.60
1:A:873:LYS:HB3	1:A:1049:TYR:CZ	2.37	0.59
1:S:972:LEU:HD11	1:S:1045:THR:OG1	2.02	0.59
1:S:3573:MET:O	1:S:3574:ALA:C	2.44	0.59
1:S:4767:TRP:CE2	1:S:4771:ILE:HD11	2.36	0.59
1:G:545:ASP:HA	1:G:548:VAL:HG22	1.85	0.59
1:G:3283:ARG:HH22	1:G:3287:ARG:NH2	1.99	0.59
1:G:972:LEU:HD11	1:G:1045:THR:OG1	2.02	0.59
1:A:2280:VAL:O	1:A:2280:VAL:HG22	2.02	0.59
1:G:2280:VAL:HG22	1:G:2280:VAL:O	2.02	0.59
1:A:545:ASP:HA	1:A:548:VAL:HG22	1.85	0.59
1:S:3671:ASP:OD2	1:S:3671:ASP:N	2.35	0.59
1:A:320:LYS:NZ	1:A:381:GLU:O	2.35	0.59
1:A:1027:LEU:CD2	1:A:1032:LYS:HG3	2.33	0.59
1:M:545:ASP:HA	1:M:548:VAL:HG22	1.84	0.59
1:M:3671:ASP:OD2	1:M:3671:ASP:N	2.35	0.59
1:S:873:LYS:HB3	1:S:1049:TYR:CZ	2.37	0.59
1:A:972:LEU:HD11	1:A:1045:THR:OG1	2.02	0.59
1:M:320:LYS:NZ	1:M:381:GLU:O	2.35	0.59
1:M:873:LYS:HB3	1:M:1049:TYR:CZ	2.37	0.59
1:M:3573:MET:O	1:M:3574:ALA:C	2.44	0.59
1:S:2628:PHE:HD1	1:S:2907:PRO:HG3	1.67	0.59
1:G:3192:GLU:OE2	1:G:3196:ARG:NE	2.36	0.59
1:M:2280:VAL:O	1:M:2280:VAL:HG22	2.02	0.59
1:A:2342:ASN:O	1:A:2342:ASN:ND2	2.35	0.58
1:G:2342:ASN:ND2	1:G:2342:ASN:O	2.35	0.58
1:G:3671:ASP:N	1:G:3671:ASP:OD2	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:933:LEU:HD21	1:M:939:VAL:HG12	1.85	0.58
1:S:933:LEU:HD21	1:S:939:VAL:HG12	1.85	0.58
1:S:1052:ASN:ND2	1:S:1054:GLU:OE2	2.36	0.58
1:M:2542:SER:HG	1:M:2594:SER:HG	1.48	0.58
1:G:3154:ASP:O	1:G:3158:LEU:HD21	2.03	0.58
1:S:3154:ASP:O	1:S:3158:LEU:HD21	2.03	0.58
1:S:3192:GLU:OE2	1:S:3196:ARG:NE	2.36	0.58
1:A:1052:ASN:ND2	1:A:1054:GLU:OE2	2.36	0.58
1:S:320:LYS:NZ	1:S:381:GLU:O	2.35	0.58
1:A:3154:ASP:O	1:A:3158:LEU:HD21	2.03	0.58
1:S:2628:PHE:HB2	1:S:2907:PRO:CG	2.34	0.58
1:A:33:LEU:HD12	1:A:33:LEU:C	2.29	0.58
1:A:3579:LEU:CG	1:A:3580:PRO:CD	2.82	0.58
1:A:3986:TRP:CE3	1:A:3986:TRP:HA	2.39	0.58
1:M:3154:ASP:O	1:M:3158:LEU:HD21	2.03	0.58
1:S:27:THR:HA	1:S:31:GLU:O	2.04	0.58
1:S:33:LEU:C	1:S:33:LEU:HD12	2.29	0.58
1:S:213:TYR:HD1	1:S:339:ILE:O	1.87	0.58
1:S:545:ASP:HA	1:S:548:VAL:HG22	1.84	0.58
1:S:3579:LEU:CD1	1:S:3580:PRO:HD3	2.25	0.57
1:S:3579:LEU:CG	1:S:3580:PRO:CD	2.82	0.57
1:G:213:TYR:HD1	1:G:339:ILE:O	1.87	0.57
1:M:33:LEU:HD12	1:M:33:LEU:C	2.29	0.57
1:M:939:VAL:HG23	1:M:1053:ILE:CG2	2.34	0.57
1:M:27:THR:HA	1:M:31:GLU:O	2.04	0.57
1:M:2628:PHE:HB2	1:M:2907:PRO:CG	2.34	0.57
1:G:939:VAL:HG23	1:G:1053:ILE:CG2	2.34	0.57
1:S:864:PRO:HG2	1:S:867:LEU:HB2	1.86	0.57
1:A:2628:PHE:HD1	1:A:2907:PRO:HG3	1.67	0.57
1:G:933:LEU:HD21	1:G:939:VAL:HG12	1.85	0.57
1:G:4878:ASP:OD1	1:G:4879:MET:N	2.37	0.57
1:A:4682:GLU:OE2	1:A:4723:LYS:HE2	2.05	0.57
1:G:3579:LEU:CG	1:G:3580:PRO:CD	2.82	0.57
1:M:213:TYR:HD1	1:M:339:ILE:O	1.87	0.57
1:M:3579:LEU:CG	1:M:3580:PRO:CD	2.82	0.57
1:A:828:GLU:OE1	1:A:828:GLU:N	2.36	0.57
1:G:33:LEU:C	1:G:33:LEU:HD12	2.29	0.57
1:M:1052:ASN:ND2	1:M:1054:GLU:OE2	2.36	0.57
1:A:864:PRO:HG2	1:A:867:LEU:HB2	1.87	0.57
1:A:933:LEU:HD21	1:A:939:VAL:HG12	1.85	0.57
1:M:33:LEU:CD1	1:M:35:LEU:HD12	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:828:GLU:OE1	1:M:828:GLU:N	2.36	0.57
1:M:3986:TRP:HA	1:M:3986:TRP:CE3	2.39	0.57
1:M:4878:ASP:OD1	1:M:4879:MET:N	2.37	0.57
1:S:3986:TRP:HA	1:S:3986:TRP:CE3	2.39	0.57
1:G:864:PRO:HG2	1:G:867:LEU:HB2	1.87	0.56
1:G:2628:PHE:HD1	1:G:2907:PRO:HG3	1.67	0.56
1:A:27:THR:HA	1:A:31:GLU:O	2.04	0.56
1:A:213:TYR:HD1	1:A:339:ILE:O	1.87	0.56
1:A:939:VAL:HG23	1:A:1053:ILE:CG2	2.34	0.56
1:A:4658:ILE:HD11	1:A:4796:MET:HB2	1.88	0.56
1:A:4878:ASP:OD1	1:A:4879:MET:N	2.37	0.56
1:A:4949:GLN:C	1:A:4949:GLN:OE1	2.49	0.56
1:G:707:VAL:HG23	1:G:782:SER:HB3	1.87	0.56
1:S:939:VAL:HG23	1:S:1053:ILE:CG2	2.34	0.56
1:S:3753:PHE:CZ	1:S:4719:PHE:CZ	2.92	0.56
1:A:2628:PHE:HB2	1:A:2907:PRO:CG	2.34	0.56
1:A:3671:ASP:OD2	1:A:3671:ASP:N	2.35	0.56
1:G:27:THR:HA	1:G:31:GLU:O	2.04	0.56
1:G:33:LEU:CD1	1:G:35:LEU:HD12	2.35	0.56
1:G:2628:PHE:HB2	1:G:2907:PRO:CG	2.34	0.56
1:M:1027:LEU:CD2	1:M:1032:LYS:HG3	2.33	0.56
1:M:3753:PHE:CZ	1:M:4719:PHE:CZ	2.91	0.56
1:M:4682:GLU:OE2	1:M:4723:LYS:HE2	2.05	0.56
1:M:4949:GLN:C	1:M:4949:GLN:OE1	2.48	0.56
1:S:2807:TRP:HB3	1:S:2808:PRO:HD3	1.88	0.56
1:A:3753:PHE:CZ	1:A:4719:PHE:CZ	2.92	0.56
1:G:1052:ASN:ND2	1:G:1054:GLU:OE2	2.36	0.56
1:G:3128:ASN:OD1	1:G:3129:LEU:N	2.39	0.56
1:G:3986:TRP:HA	1:G:3986:TRP:CE3	2.39	0.56
1:S:3157:ILE:O	1:S:3158:LEU:HD13	2.06	0.56
1:S:4878:ASP:OD1	1:S:4879:MET:N	2.37	0.56
1:A:33:LEU:CD1	1:A:35:LEU:HD12	2.35	0.56
1:S:4949:GLN:C	1:S:4949:GLN:OE1	2.49	0.56
1:A:1093:GLU:HB2	1:A:1148:VAL:HG22	1.88	0.56
1:M:3192:GLU:OE2	1:M:3196:ARG:NE	2.36	0.56
1:A:3128:ASN:OD1	1:A:3129:LEU:N	2.39	0.56
1:S:33:LEU:CD1	1:S:35:LEU:HD12	2.35	0.56
1:S:4682:GLU:OE2	1:S:4723:LYS:HE2	2.05	0.56
1:G:3157:ILE:O	1:G:3158:LEU:HD13	2.06	0.56
1:G:4949:GLN:C	1:G:4949:GLN:OE1	2.49	0.56
1:M:707:VAL:HG23	1:M:782:SER:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:3128:ASN:OD1	1:S:3129:LEU:N	2.39	0.56
1:A:707:VAL:HG23	1:A:782:SER:HB3	1.87	0.56
1:M:3157:ILE:O	1:M:3158:LEU:HD13	2.06	0.56
1:A:2212:VAL:HG11	1:A:2256:TYR:OH	2.06	0.55
1:G:3283:ARG:HH12	1:G:3287:ARG:CZ	2.19	0.55
1:M:2212:VAL:HG11	1:M:2256:TYR:OH	2.06	0.55
1:M:3128:ASN:OD1	1:M:3129:LEU:N	2.39	0.55
1:S:1093:GLU:HB2	1:S:1148:VAL:HG22	1.88	0.55
1:A:3283:ARG:HH12	1:A:3287:ARG:CZ	2.19	0.55
1:M:864:PRO:HG2	1:M:867:LEU:HB2	1.86	0.55
1:A:2807:TRP:HB3	1:A:2808:PRO:HD3	1.88	0.55
1:G:864:PRO:HG3	1:G:867:LEU:HD12	1.89	0.55
1:S:707:VAL:HG23	1:S:782:SER:HB3	1.87	0.55
1:S:2212:VAL:HG11	1:S:2256:TYR:OH	2.06	0.55
1:S:2542:SER:OG	1:S:2594:SER:OG	2.25	0.55
1:G:2212:VAL:HG11	1:G:2256:TYR:OH	2.06	0.55
1:G:2348:GLU:OE1	1:G:2348:GLU:N	2.38	0.55
1:G:2807:TRP:HB3	1:G:2808:PRO:HD3	1.88	0.55
1:S:2778:GLY:HA3	1:S:2787:THR:HB	1.89	0.55
1:S:3777:GLU:OE1	1:S:3777:GLU:N	2.39	0.55
1:A:3157:ILE:O	1:A:3158:LEU:HD13	2.06	0.55
1:G:1027:LEU:CD2	1:G:1032:LYS:HG3	2.33	0.55
1:G:3753:PHE:CZ	1:G:4719:PHE:CZ	2.91	0.55
1:M:977:LEU:HD11	1:M:1040:CYS:SG	2.47	0.55
1:M:1093:GLU:HB2	1:M:1148:VAL:HG22	1.88	0.55
1:M:4658:ILE:HD11	1:M:4796:MET:HB2	1.87	0.55
1:G:4658:ILE:HD11	1:G:4796:MET:HB2	1.87	0.55
1:G:4682:GLU:OE2	1:G:4723:LYS:HE2	2.05	0.55
1:S:828:GLU:OE1	1:S:828:GLU:N	2.36	0.55
1:S:4658:ILE:HD11	1:S:4796:MET:HB2	1.87	0.55
1:A:977:LEU:HD11	1:A:1040:CYS:SG	2.47	0.55
1:A:2627:VAL:CG1	1:A:2910:THR:HG21	2.37	0.55
1:G:977:LEU:HD11	1:G:1040:CYS:SG	2.47	0.55
1:G:1093:GLU:HB2	1:G:1148:VAL:HG22	1.88	0.55
1:M:2807:TRP:HB3	1:M:2808:PRO:HD3	1.88	0.55
1:M:3579:LEU:CD1	1:M:3580:PRO:HD3	2.25	0.54
1:A:3192:GLU:OE2	1:A:3196:ARG:NE	2.36	0.54
1:G:828:GLU:OE1	1:G:828:GLU:N	2.36	0.54
1:M:2627:VAL:CG1	1:M:2910:THR:HG21	2.37	0.54
1:M:3283:ARG:HH12	1:M:3287:ARG:CZ	2.19	0.54
1:S:864:PRO:HG3	1:S:867:LEU:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:3283:ARG:HH12	1:S:3287:ARG:CZ	2.19	0.54
1:A:864:PRO:HG3	1:A:867:LEU:HD12	1.89	0.54
1:G:988:LEU:HB3	1:G:1039:LEU:HD13	1.90	0.54
1:M:26:ALA:O	1:M:33:LEU:HG	2.08	0.54
1:M:988:LEU:HB3	1:M:1039:LEU:HD13	1.90	0.54
1:M:4729:GLY:O	1:M:4733:GLY:N	2.41	0.54
1:S:977:LEU:HD11	1:S:1040:CYS:SG	2.47	0.54
1:G:2309:SER:HB3	1:G:2321:ILE:O	2.08	0.54
1:S:2627:VAL:CG1	1:S:2910:THR:HG21	2.37	0.54
1:A:4729:GLY:O	1:A:4733:GLY:N	2.41	0.54
1:G:2627:VAL:CG1	1:G:2910:THR:HG21	2.37	0.54
1:M:34:LYS:HA	1:M:34:LYS:HE2	1.90	0.54
1:M:2778:GLY:HA3	1:M:2787:THR:HB	1.89	0.54
1:S:4729:GLY:O	1:S:4733:GLY:N	2.41	0.54
1:A:2778:GLY:HA3	1:A:2787:THR:HB	1.89	0.54
1:A:3777:GLU:N	1:A:3777:GLU:OE1	2.39	0.54
1:G:4729:GLY:O	1:G:4733:GLY:N	2.41	0.54
1:M:2309:SER:HB3	1:M:2321:ILE:O	2.08	0.54
1:S:26:ALA:O	1:S:33:LEU:HG	2.08	0.54
1:S:3527:PRO:HD2	1:S:3573:MET:HE1	1.90	0.54
1:A:275:ARG:CD	1:A:336:PRO:HG2	2.36	0.53
1:A:3527:PRO:HD2	1:A:3573:MET:HE1	1.90	0.53
1:M:2348:GLU:OE1	1:M:2348:GLU:N	2.38	0.53
1:S:988:LEU:HB3	1:S:1039:LEU:HD13	1.90	0.53
1:G:3777:GLU:OE1	1:G:3777:GLU:N	2.39	0.53
1:G:4952:GLU:C	1:G:4952:GLU:OE1	2.52	0.53
1:M:4952:GLU:OE1	1:M:4952:GLU:C	2.52	0.53
1:S:196:MET:HE3	1:S:196:MET:HA	1.91	0.53
1:A:2309:SER:HB3	1:A:2321:ILE:O	2.08	0.53
1:A:4952:GLU:OE1	1:A:4952:GLU:C	2.52	0.53
1:G:2778:GLY:HA3	1:G:2787:THR:HB	1.89	0.53
1:G:3169:LEU:HD13	1:G:3194:LEU:CD1	2.38	0.53
1:M:864:PRO:HG3	1:M:867:LEU:HD12	1.88	0.53
1:M:3527:PRO:HD2	1:M:3573:MET:HE1	1.90	0.53
1:A:3169:LEU:HD13	1:A:3194:LEU:CD1	2.38	0.53
1:M:196:MET:HE3	1:M:196:MET:HA	1.91	0.53
1:S:3169:LEU:HD13	1:S:3194:LEU:CD1	2.38	0.53
1:S:4244:GLU:OE2	1:S:4244:GLU:HA	2.09	0.53
1:A:26:ALA:O	1:A:33:LEU:HG	2.08	0.53
1:G:3579:LEU:CD1	1:G:3580:PRO:HD2	2.38	0.53
1:M:3169:LEU:HD13	1:M:3194:LEU:CD1	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:1027:LEU:CD2	1:S:1032:LYS:HG3	2.33	0.53
1:S:2309:SER:HB3	1:S:2321:ILE:O	2.08	0.53
1:S:4952:GLU:C	1:S:4952:GLU:OE1	2.52	0.53
2:B:17:PRO:HA	2:B:107:LEU:HD21	1.91	0.53
1:M:3579:LEU:CD1	1:M:3580:PRO:HD2	2.38	0.53
1:S:3579:LEU:CD1	1:S:3580:PRO:HD2	2.38	0.53
1:A:3579:LEU:CD1	1:A:3580:PRO:HD2	2.38	0.53
1:G:196:MET:HE3	1:G:196:MET:HA	1.91	0.53
1:G:3527:PRO:HD2	1:G:3573:MET:HE1	1.90	0.53
1:S:372:LEU:C	1:S:372:LEU:HD13	2.34	0.53
1:A:34:LYS:HA	1:A:34:LYS:HE2	1.90	0.52
1:A:988:LEU:HB3	1:A:1039:LEU:HD13	1.90	0.52
1:M:2542:SER:OG	1:M:2594:SER:OG	2.25	0.52
1:A:372:LEU:C	1:A:372:LEU:HD13	2.34	0.52
1:G:1041:GLN:HA	1:G:1041:GLN:OE1	2.10	0.52
1:M:4244:GLU:OE2	1:M:4244:GLU:HA	2.09	0.52
1:S:34:LYS:HE2	1:S:34:LYS:HA	1.90	0.52
1:A:988:LEU:HD23	1:A:1039:LEU:HD22	1.92	0.52
1:A:2542:SER:HG	1:A:2594:SER:HG	1.57	0.52
1:G:26:ALA:O	1:G:33:LEU:HG	2.08	0.52
1:A:977:LEU:HD21	1:A:1043:VAL:HG12	1.92	0.52
1:A:1041:GLN:OE1	1:A:1041:GLN:HA	2.10	0.52
1:A:4244:GLU:OE2	1:A:4244:GLU:HA	2.09	0.52
1:S:3753:PHE:HZ	1:S:4719:PHE:CE2	2.28	0.52
1:A:2542:SER:OG	1:A:2594:SER:OG	2.25	0.52
1:A:4689:THR:HG22	1:A:4732:PHE:CZ	2.45	0.52
1:M:3777:GLU:N	1:M:3777:GLU:OE1	2.39	0.52
2:T:17:PRO:HA	2:T:107:LEU:HD21	1.91	0.52
1:G:977:LEU:HD21	1:G:1043:VAL:HG12	1.92	0.52
1:M:772:ASN:ND2	1:M:1470:ARG:HA	2.25	0.52
1:M:3753:PHE:HZ	1:M:4719:PHE:CE2	2.28	0.52
1:S:988:LEU:HD23	1:S:1039:LEU:HD22	1.92	0.52
1:A:421:PHE:HB3	1:A:432:ALA:HB3	1.92	0.52
1:M:977:LEU:HD21	1:M:1043:VAL:HG12	1.92	0.52
1:M:4205:TRP:CE3	1:M:4989:MET:HE1	2.45	0.52
1:M:4689:THR:HG22	1:M:4732:PHE:CZ	2.45	0.52
1:S:1024:TYR:HE1	1:S:1032:LYS:HG2	1.74	0.52
1:A:196:MET:HE3	1:A:196:MET:HA	1.91	0.52
1:G:34:LYS:HE2	1:G:34:LYS:HA	1.90	0.52
1:G:372:LEU:C	1:G:372:LEU:HD13	2.34	0.52
1:G:3753:PHE:HZ	1:G:4719:PHE:CE2	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:772:ASN:ND2	1:S:1470:ARG:HA	2.25	0.52
1:G:275:ARG:CD	1:G:336:PRO:HG2	2.36	0.51
1:G:4205:TRP:CE3	1:G:4989:MET:HE1	2.45	0.51
1:S:2542:SER:HG	1:S:2594:SER:HG	1.57	0.51
1:M:372:LEU:HD13	1:M:372:LEU:C	2.35	0.51
2:N:17:PRO:HA	2:N:107:LEU:HD21	1.91	0.51
2:H:17:PRO:HA	2:H:107:LEU:HD21	1.91	0.51
1:M:1041:GLN:OE1	1:M:1041:GLN:HA	2.10	0.51
1:S:977:LEU:HD21	1:S:1043:VAL:HG12	1.92	0.51
2:B:12:ASP:OD2	2:B:13:GLY:N	2.44	0.51
1:G:4244:GLU:OE2	1:G:4244:GLU:HA	2.09	0.51
1:G:4689:THR:HG22	1:G:4732:PHE:CZ	2.45	0.51
1:M:1046:LEU:C	1:M:1046:LEU:HD13	2.36	0.51
1:M:2150:GLU:OE1	1:M:2150:GLU:N	2.44	0.51
1:M:3528:THR:HG23	1:M:3573:MET:HE3	1.93	0.51
1:S:1046:LEU:HD13	1:S:1046:LEU:C	2.36	0.51
1:A:772:ASN:ND2	1:A:1470:ARG:HA	2.25	0.51
1:A:4206:GLU:C	1:A:4207:MET:HE2	2.36	0.51
1:G:233:ILE:HD12	1:G:242:ARG:HB3	1.93	0.51
1:G:4063:ASP:O	1:G:4067:LYS:HG3	2.11	0.51
1:S:4205:TRP:CE3	1:S:4989:MET:HE1	2.45	0.51
1:S:4689:THR:HG22	1:S:4732:PHE:CZ	2.45	0.51
1:A:3753:PHE:HZ	1:A:4719:PHE:CE2	2.28	0.51
1:S:3528:THR:HG23	1:S:3573:MET:HE3	1.93	0.51
1:S:4004:ALA:CB	1:S:4013:LEU:HD22	2.40	0.51
1:S:4730:ASP:OD1	1:S:4731:ILE:N	2.44	0.51
1:A:3105:LYS:HD3	1:A:3105:LYS:O	2.11	0.51
1:G:988:LEU:HD23	1:G:1039:LEU:HD22	1.92	0.51
1:M:3105:LYS:HD3	1:M:3105:LYS:O	2.11	0.51
1:S:421:PHE:HB3	1:S:432:ALA:HB3	1.92	0.51
1:S:4206:GLU:C	1:S:4207:MET:HE2	2.36	0.51
2:T:12:ASP:OD2	2:T:13:GLY:N	2.44	0.51
1:A:1046:LEU:C	1:A:1046:LEU:HD13	2.36	0.51
1:M:988:LEU:HD23	1:M:1039:LEU:HD22	1.92	0.51
1:M:421:PHE:HB3	1:M:432:ALA:HB3	1.92	0.51
1:M:4063:ASP:O	1:M:4067:LYS:HG3	2.11	0.51
1:M:4836:GLN:N	1:M:4836:GLN:OE1	2.44	0.51
1:A:2634:ASN:OD1	1:A:2637:ALA:N	2.44	0.51
1:G:4836:GLN:OE1	1:G:4836:GLN:N	2.44	0.51
2:N:12:ASP:OD2	2:N:13:GLY:N	2.44	0.51
1:S:1041:GLN:HA	1:S:1041:GLN:OE1	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:12:ASP:OD2	2:H:13:GLY:N	2.44	0.50
1:M:3156:VAL:HG13	1:M:3157:ILE:N	2.27	0.50
1:S:3105:LYS:O	1:S:3105:LYS:HD3	2.11	0.50
1:S:4063:ASP:O	1:S:4067:LYS:HG3	2.11	0.50
1:A:4063:ASP:O	1:A:4067:LYS:HG3	2.11	0.50
1:G:421:PHE:HB3	1:G:432:ALA:HB3	1.92	0.50
1:G:2634:ASN:OD1	1:G:2637:ALA:N	2.44	0.50
1:G:4206:GLU:C	1:G:4207:MET:HE2	2.36	0.50
1:M:1869:GLU:OE1	1:M:1869:GLU:N	2.40	0.50
1:A:4205:TRP:CE3	1:A:4989:MET:HE1	2.45	0.50
1:S:2634:ASN:OD1	1:S:2637:ALA:N	2.44	0.50
1:G:772:ASN:ND2	1:G:1470:ARG:HA	2.25	0.50
1:S:233:ILE:HD12	1:S:242:ARG:HB3	1.93	0.50
1:S:2150:GLU:N	1:S:2150:GLU:OE1	2.44	0.50
1:A:4767:TRP:O	1:A:4767:TRP:CG	2.65	0.50
1:G:3528:THR:HG23	1:G:3573:MET:HE3	1.93	0.50
1:M:941:MET:HA	1:M:1051:TYR:HA	1.94	0.50
1:S:3156:VAL:HG13	1:S:3157:ILE:N	2.27	0.50
1:A:939:VAL:O	1:A:939:VAL:HG13	2.11	0.50
1:G:4730:ASP:OD1	1:G:4731:ILE:N	2.44	0.50
1:S:941:MET:HA	1:S:1051:TYR:HA	1.94	0.50
1:G:939:VAL:HG13	1:G:939:VAL:O	2.11	0.50
1:S:1869:GLU:OE1	1:S:1869:GLU:N	2.40	0.50
1:G:1046:LEU:HD13	1:G:1046:LEU:C	2.36	0.50
1:G:3283:ARG:NH1	1:G:3287:ARG:CZ	2.75	0.50
1:M:2634:ASN:OD1	1:M:2637:ALA:N	2.44	0.50
1:M:3110:LEU:C	1:M:3110:LEU:HD13	2.37	0.50
1:S:939:VAL:HG13	1:S:939:VAL:O	2.12	0.50
1:G:275:ARG:HD3	1:G:336:PRO:CD	2.42	0.50
1:S:3283:ARG:NH1	1:S:3287:ARG:CZ	2.75	0.50
1:A:233:ILE:HD12	1:A:242:ARG:HB3	1.93	0.49
1:G:4767:TRP:O	1:G:4767:TRP:CG	2.65	0.49
1:G:291:LEU:HD11	1:G:299:LEU:HD11	1.93	0.49
1:G:1024:TYR:HE1	1:G:1032:LYS:HG2	1.74	0.49
1:G:3110:LEU:HD13	1:G:3110:LEU:C	2.37	0.49
1:M:233:ILE:HD12	1:M:242:ARG:HB3	1.93	0.49
1:M:275:ARG:HD3	1:M:336:PRO:CD	2.42	0.49
1:M:4767:TRP:O	1:M:4767:TRP:CG	2.65	0.49
1:S:275:ARG:HD3	1:S:336:PRO:CD	2.42	0.49
1:A:275:ARG:HD3	1:A:336:PRO:CD	2.42	0.49
1:A:977:LEU:CD2	1:A:1043:VAL:CG1	2.91	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:2542:SER:OG	1:G:2594:SER:OG	2.25	0.49
1:G:3105:LYS:O	1:G:3105:LYS:HD3	2.11	0.49
1:M:4066:LEU:HD11	1:M:4173:TYR:CD1	2.47	0.49
1:S:291:LEU:HD11	1:S:299:LEU:HD11	1.93	0.49
1:S:939:VAL:CB	1:S:1053:ILE:HG22	2.43	0.49
1:A:2150:GLU:OE1	1:A:2150:GLU:N	2.44	0.49
1:A:3283:ARG:NH1	1:A:3287:ARG:CZ	2.75	0.49
1:G:2542:SER:HG	1:G:2594:SER:HG	1.57	0.49
1:G:4066:LEU:HD11	1:G:4173:TYR:CE1	2.48	0.49
1:M:2628:PHE:C	1:M:2628:PHE:CD2	2.90	0.49
1:M:4730:ASP:OD1	1:M:4731:ILE:N	2.44	0.49
1:S:4066:LEU:HD11	1:S:4173:TYR:CE1	2.48	0.49
1:A:3110:LEU:HD11	1:A:3183:VAL:CG1	2.43	0.49
1:A:3528:THR:HG23	1:A:3573:MET:HE3	1.93	0.49
1:G:1478:ASP:OD1	1:G:1482:ASN:N	2.45	0.49
1:M:2382:GLU:OE1	1:M:2385:ARG:NH1	2.45	0.49
1:M:3283:ARG:NH1	1:M:3287:ARG:CZ	2.75	0.49
1:M:4066:LEU:HD11	1:M:4173:TYR:CE1	2.48	0.49
1:M:4206:GLU:C	1:M:4207:MET:HE2	2.36	0.49
1:G:941:MET:HA	1:G:1051:TYR:HA	1.94	0.49
1:G:2150:GLU:N	1:G:2150:GLU:OE1	2.44	0.49
1:G:4066:LEU:HD11	1:G:4173:TYR:CD1	2.47	0.49
1:M:939:VAL:HG13	1:M:939:VAL:O	2.11	0.49
1:S:4767:TRP:O	1:S:4767:TRP:CG	2.65	0.49
1:A:941:MET:HA	1:A:1051:TYR:HA	1.94	0.49
1:A:1024:TYR:HE1	1:A:1032:LYS:HG2	1.74	0.49
1:A:2348:GLU:OE1	1:A:2348:GLU:N	2.38	0.49
1:A:2966:TRP:HA	1:A:2969:ILE:HD12	1.95	0.49
1:A:4004:ALA:CB	1:A:4013:LEU:HD22	2.40	0.49
1:G:3110:LEU:HD11	1:G:3183:VAL:CG1	2.43	0.49
1:M:4003:LEU:HD23	1:M:4009:GLN:NE2	2.28	0.49
1:S:2966:TRP:HA	1:S:2969:ILE:HD12	1.95	0.49
1:G:1285:GLU:HB2	1:G:1462:MET:HE1	1.95	0.49
1:M:291:LEU:HD11	1:M:299:LEU:HD11	1.93	0.49
1:M:939:VAL:CB	1:M:1053:ILE:HG22	2.43	0.49
1:S:3110:LEU:HD13	1:S:3110:LEU:C	2.37	0.49
1:S:3110:LEU:HD11	1:S:3183:VAL:CG1	2.43	0.49
1:S:4836:GLN:N	1:S:4836:GLN:OE1	2.44	0.49
1:A:4066:LEU:HD11	1:A:4173:TYR:CD1	2.47	0.49
1:G:1435:TYR:CB	1:G:1575:LEU:HD23	2.41	0.49
1:G:4056:GLU:C	1:G:4060:LYS:HE2	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:937:CYS:SG	1:M:984:LEU:CG	3.01	0.49
1:A:939:VAL:CB	1:A:1053:ILE:HG22	2.43	0.49
1:A:1435:TYR:CB	1:A:1575:LEU:HD23	2.41	0.49
1:A:3110:LEU:C	1:A:3110:LEU:HD13	2.37	0.49
1:A:4003:LEU:HD23	1:A:4009:GLN:NE2	2.28	0.49
1:A:4836:GLN:N	1:A:4836:GLN:OE1	2.44	0.49
1:M:1285:GLU:HB2	1:M:1462:MET:HE1	1.95	0.49
1:A:291:LEU:HD11	1:A:299:LEU:HD11	1.93	0.48
1:A:4730:ASP:OD1	1:A:4731:ILE:N	2.44	0.48
1:M:2967:MET:HE3	1:M:2967:MET:HA	1.95	0.48
1:S:977:LEU:CD2	1:S:1043:VAL:CG1	2.91	0.48
1:S:2522:LEU:O	1:S:2522:LEU:HD23	2.13	0.48
1:S:4056:GLU:C	1:S:4060:LYS:HE2	2.38	0.48
1:A:937:CYS:SG	1:A:984:LEU:CG	3.01	0.48
1:A:2628:PHE:C	1:A:2628:PHE:CD2	2.90	0.48
1:G:275:ARG:HD3	1:G:336:PRO:HD2	1.95	0.48
1:G:937:CYS:SG	1:G:984:LEU:CG	3.01	0.48
1:S:4066:LEU:HD11	1:S:4173:TYR:CD1	2.48	0.48
1:A:3156:VAL:HG13	1:A:3157:ILE:N	2.27	0.48
1:A:4066:LEU:HD11	1:A:4173:TYR:CE1	2.48	0.48
1:G:3156:VAL:HG13	1:G:3157:ILE:N	2.27	0.48
1:M:977:LEU:CD2	1:M:1043:VAL:CG1	2.91	0.48
1:S:2628:PHE:C	1:S:2628:PHE:CD2	2.90	0.48
1:A:275:ARG:HD3	1:A:336:PRO:HD2	1.95	0.48
1:G:977:LEU:CD2	1:G:1043:VAL:CG1	2.91	0.48
1:G:4003:LEU:HD23	1:G:4009:GLN:NE2	2.28	0.48
1:M:3428:ASN:OD1	1:M:3429:ALA:N	2.46	0.48
1:S:3514:LEU:HD13	1:S:3514:LEU:O	2.14	0.48
1:A:4911:LEU:HA	1:A:4914:VAL:HG22	1.95	0.48
1:G:939:VAL:CB	1:G:1053:ILE:HG22	2.43	0.48
1:G:2522:LEU:O	1:G:2522:LEU:HD23	2.13	0.48
1:G:3169:LEU:HD13	1:G:3194:LEU:HD11	1.95	0.48
1:M:46:LEU:HD11	1:M:134:ASP:HB3	1.96	0.48
1:A:1285:GLU:HB2	1:A:1462:MET:HE1	1.95	0.48
1:A:3428:ASN:OD1	1:A:3429:ALA:N	2.46	0.48
1:A:4056:GLU:C	1:A:4060:LYS:HE2	2.38	0.48
1:G:3514:LEU:HD13	1:G:3514:LEU:O	2.14	0.48
1:M:2966:TRP:HA	1:M:2969:ILE:HD12	1.95	0.48
1:M:3110:LEU:HD11	1:M:3183:VAL:CG1	2.42	0.48
1:A:3514:LEU:HD13	1:A:3514:LEU:O	2.14	0.48
1:G:2628:PHE:CD2	1:G:2628:PHE:C	2.91	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3428:ASN:OD1	1:G:3429:ALA:N	2.46	0.48
1:S:937:CYS:SG	1:S:984:LEU:CG	3.01	0.48
1:A:2967:MET:HE3	1:A:2967:MET:HA	1.95	0.48
1:M:977:LEU:HD21	1:M:1043:VAL:CG1	2.44	0.48
1:M:2522:LEU:HD23	1:M:2522:LEU:O	2.13	0.48
1:S:3428:ASN:OD1	1:S:3429:ALA:N	2.46	0.48
1:A:1478:ASP:OD1	1:A:1482:ASN:N	2.45	0.48
1:G:2966:TRP:HA	1:G:2969:ILE:HD12	1.95	0.48
1:A:2522:LEU:HD23	1:A:2522:LEU:O	2.13	0.48
1:S:1285:GLU:HB2	1:S:1462:MET:HE1	1.95	0.48
1:A:977:LEU:HD21	1:A:1043:VAL:CG1	2.44	0.47
1:A:2368:LEU:HD11	1:A:2376:LEU:HD11	1.96	0.47
1:A:3157:ILE:C	1:A:3158:LEU:HD22	2.39	0.47
1:A:3169:LEU:HD13	1:A:3194:LEU:HD11	1.95	0.47
1:A:3528:THR:HG23	1:A:3573:MET:CE	2.44	0.47
1:G:2368:LEU:HD11	1:G:2376:LEU:HD11	1.96	0.47
1:G:4901:ILE:HG22	1:G:4902:GLU:N	2.29	0.47
1:S:46:LEU:HD11	1:S:134:ASP:HB3	1.96	0.47
1:S:275:ARG:HD3	1:S:336:PRO:HD2	1.95	0.47
1:A:46:LEU:HD11	1:A:134:ASP:HB3	1.96	0.47
1:A:4901:ILE:HG22	1:A:4902:GLU:N	2.29	0.47
1:G:4911:LEU:HA	1:G:4914:VAL:HG22	1.95	0.47
1:M:4056:GLU:C	1:M:4060:LYS:HE2	2.38	0.47
1:M:4911:LEU:HA	1:M:4914:VAL:HG22	1.95	0.47
1:S:937:CYS:SG	1:S:984:LEU:CD2	3.02	0.47
1:S:2382:GLU:OE1	1:S:2385:ARG:NH1	2.45	0.47
1:S:4003:LEU:HD23	1:S:4009:GLN:NE2	2.28	0.47
1:G:977:LEU:HD21	1:G:1043:VAL:CG1	2.44	0.47
1:M:3528:THR:HG23	1:M:3573:MET:CE	2.44	0.47
1:S:1180:ARG:HB2	1:S:1180:ARG:NH1	2.29	0.47
1:S:1561:VAL:O	1:S:1562:ILE:HD13	2.14	0.47
1:A:2131:LEU:C	1:A:2131:LEU:HD12	2.40	0.47
1:A:2382:GLU:OE1	1:A:2385:ARG:NH1	2.45	0.47
1:M:275:ARG:HD3	1:M:336:PRO:HD2	1.95	0.47
1:M:2131:LEU:C	1:M:2131:LEU:HD12	2.40	0.47
1:M:4702:ASP:O	1:M:4705:VAL:HG12	2.15	0.47
1:A:3459:VAL:HG23	1:A:3464:ILE:CG2	2.44	0.47
1:G:1180:ARG:HB2	1:G:1180:ARG:NH1	2.29	0.47
1:G:3157:ILE:C	1:G:3158:LEU:HD22	2.39	0.47
1:G:3409:TYR:CE1	1:G:3513:THR:HG21	2.50	0.47
1:M:1825:HIS:CD2	1:S:3567:PRO:CB	2.98	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:977:LEU:HD21	1:S:1043:VAL:CG1	2.44	0.47
1:S:3157:ILE:C	1:S:3158:LEU:HD22	2.39	0.47
1:A:1825:HIS:CD2	1:G:3567:PRO:CB	2.98	0.47
1:M:3283:ARG:HH12	1:M:3287:ARG:NH2	2.12	0.47
1:A:941:MET:HE3	1:A:944:GLU:OE2	2.14	0.47
1:A:1180:ARG:NH1	1:A:1180:ARG:HB2	2.29	0.47
1:A:3539:ARG:NH1	1:A:3552:PHE:CE2	2.83	0.47
1:A:3567:PRO:CB	1:S:1825:HIS:CD2	2.98	0.47
1:A:4666:VAL:N	1:A:4667:PRO:HD2	2.30	0.47
1:G:46:LEU:HD11	1:G:134:ASP:HB3	1.96	0.47
1:G:380:GLN:OE1	1:G:380:GLN:N	2.47	0.47
1:G:941:MET:HE3	1:G:944:GLU:OE2	2.14	0.47
1:G:2382:GLU:OE1	1:G:2385:ARG:NH1	2.45	0.47
1:G:2967:MET:HE3	1:G:2967:MET:HA	1.95	0.47
1:G:3283:ARG:HH12	1:G:3287:ARG:NH2	2.12	0.47
1:G:3539:ARG:NH1	1:G:3552:PHE:CE2	2.83	0.47
1:G:3753:PHE:HZ	1:G:4719:PHE:HZ	1.61	0.47
1:G:4702:ASP:O	1:G:4705:VAL:HG12	2.15	0.47
1:M:941:MET:HE3	1:M:944:GLU:OE2	2.15	0.47
1:M:3157:ILE:C	1:M:3158:LEU:HD22	2.39	0.47
1:M:3409:TYR:CE1	1:M:3513:THR:HG21	2.50	0.47
1:S:941:MET:HE3	1:S:944:GLU:OE2	2.15	0.47
1:S:1478:ASP:OD1	1:S:1482:ASN:N	2.45	0.47
1:S:3283:ARG:HH12	1:S:3287:ARG:NH2	2.12	0.47
1:S:4666:VAL:N	1:S:4667:PRO:HD2	2.30	0.47
1:S:4911:LEU:HA	1:S:4914:VAL:HG22	1.95	0.47
1:G:937:CYS:SG	1:G:984:LEU:CD2	3.03	0.47
1:G:1561:VAL:O	1:G:1562:ILE:HD13	2.14	0.47
1:G:4004:ALA:CB	1:G:4013:LEU:HD22	2.40	0.47
1:G:4666:VAL:N	1:G:4667:PRO:HD2	2.30	0.47
1:M:3514:LEU:HD13	1:M:3514:LEU:O	2.14	0.47
1:S:2368:LEU:HD11	1:S:2376:LEU:HD11	1.96	0.47
1:S:2967:MET:HE3	1:S:2967:MET:HA	1.95	0.47
1:A:977:LEU:CD2	1:A:1043:VAL:HG12	2.45	0.47
1:A:2522:LEU:HD23	1:A:2522:LEU:C	2.40	0.47
1:G:3528:THR:HG23	1:G:3573:MET:CE	2.44	0.47
1:M:2368:LEU:HD11	1:M:2376:LEU:HD11	1.96	0.47
1:M:3753:PHE:HZ	1:M:4719:PHE:HZ	1.61	0.47
1:A:4058:ILE:O	1:A:4061:PHE:HB3	2.15	0.47
1:M:1561:VAL:O	1:M:1562:ILE:HD13	2.14	0.47
1:S:4901:ILE:HG22	1:S:4902:GLU:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:GLN:OE1	1:A:380:GLN:N	2.47	0.46
1:A:1561:VAL:O	1:A:1562:ILE:HD13	2.14	0.46
1:A:3283:ARG:HH12	1:A:3287:ARG:NH2	2.12	0.46
1:A:3941:ASP:O	1:A:4002:LYS:NZ	2.48	0.46
1:G:2131:LEU:HD12	1:G:2131:LEU:C	2.40	0.46
1:M:275:ARG:CD	1:M:336:PRO:HG2	2.36	0.46
1:M:937:CYS:SG	1:M:984:LEU:CD2	3.03	0.46
1:M:1180:ARG:NH1	1:M:1180:ARG:HB2	2.29	0.46
1:S:275:ARG:CD	1:S:336:PRO:HG2	2.36	0.46
1:A:937:CYS:SG	1:A:984:LEU:CD2	3.03	0.46
1:A:3409:TYR:CE1	1:A:3513:THR:HG21	2.50	0.46
1:G:4658:ILE:HD12	1:G:4796:MET:HE3	1.97	0.46
1:M:977:LEU:CD2	1:M:1043:VAL:HG12	2.45	0.46
1:M:2862:LEU:HD11	1:M:2932:MET:HE1	1.97	0.46
1:M:3941:ASP:O	1:M:4002:LYS:NZ	2.48	0.46
1:A:1869:GLU:OE1	1:A:1869:GLU:N	2.40	0.46
1:A:2302:LEU:HD23	1:A:2302:LEU:O	2.16	0.46
1:G:977:LEU:CD2	1:G:1043:VAL:HG12	2.45	0.46
1:M:1435:TYR:CB	1:M:1575:LEU:HD23	2.41	0.46
1:M:3539:ARG:NH1	1:M:3552:PHE:CE2	2.83	0.46
1:S:977:LEU:CD2	1:S:1043:VAL:HG12	2.45	0.46
1:S:3528:THR:HG23	1:S:3573:MET:CE	2.44	0.46
1:S:3539:ARG:NH1	1:S:3552:PHE:CE2	2.83	0.46
1:S:4702:ASP:O	1:S:4705:VAL:HG12	2.15	0.46
1:A:3999:MET:HG3	1:A:4003:LEU:HD11	1.98	0.46
1:S:2131:LEU:HD12	1:S:2131:LEU:C	2.40	0.46
1:S:3156:VAL:HG13	1:S:3157:ILE:HG13	1.98	0.46
1:A:4658:ILE:HD12	1:A:4796:MET:HE3	1.97	0.46
1:G:2302:LEU:O	1:G:2302:LEU:HD23	2.16	0.46
1:G:4705:VAL:HG22	1:G:4705:VAL:O	2.15	0.46
1:M:1024:TYR:HE1	1:M:1032:LYS:HG2	1.74	0.46
1:M:3156:VAL:HG13	1:M:3157:ILE:HG13	1.98	0.46
1:S:2348:GLU:OE1	1:S:2348:GLU:N	2.38	0.46
1:S:2522:LEU:HD23	1:S:2522:LEU:C	2.40	0.46
1:A:992:GLY:O	1:A:995:VAL:HG12	2.16	0.46
1:A:2825:LYS:HE3	1:A:2827:ARG:O	2.16	0.46
1:A:4580:TYR:O	1:S:4878:ASP:OD1	2.34	0.46
1:A:4702:ASP:O	1:A:4705:VAL:HG12	2.15	0.46
1:G:156:GLN:OE1	1:G:156:GLN:N	2.48	0.46
1:G:992:GLY:O	1:G:995:VAL:HG12	2.16	0.46
1:G:2522:LEU:HD23	1:G:2522:LEU:C	2.40	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:4878:ASP:OD1	1:M:4580:TYR:O	2.34	0.46
1:A:2862:LEU:HD11	1:A:2932:MET:HE1	1.97	0.46
1:G:2897:LYS:O	1:G:2897:LYS:HG2	2.16	0.46
1:G:4058:ILE:O	1:G:4061:PHE:HB3	2.15	0.46
1:M:992:GLY:O	1:M:995:VAL:HG12	2.16	0.46
1:S:2825:LYS:HE3	1:S:2827:ARG:O	2.16	0.46
1:S:4658:ILE:HD12	1:S:4796:MET:HE3	1.97	0.46
1:M:1478:ASP:OD1	1:M:1482:ASN:N	2.45	0.46
1:M:2825:LYS:HE3	1:M:2827:ARG:O	2.16	0.46
1:S:3409:TYR:CE1	1:S:3513:THR:HG21	2.50	0.46
1:S:4058:ILE:O	1:S:4061:PHE:HB3	2.15	0.46
1:G:3999:MET:HG3	1:G:4003:LEU:HD11	1.98	0.46
1:M:2522:LEU:HD23	1:M:2522:LEU:C	2.40	0.46
1:M:4705:VAL:O	1:M:4705:VAL:HG22	2.15	0.46
1:M:4785:THR:O	1:M:4785:THR:HG22	2.16	0.46
1:S:4039:MET:HE3	1:S:4043:GLN:OE1	2.15	0.46
1:S:4785:THR:HG22	1:S:4785:THR:O	2.16	0.46
1:A:1690:ASP:OD1	1:A:1692:ALA:N	2.49	0.46
1:A:4705:VAL:O	1:A:4705:VAL:HG22	2.15	0.46
1:S:992:GLY:O	1:S:995:VAL:HG12	2.16	0.46
1:S:2161:GLN:NE2	1:S:2177:LEU:HD12	2.31	0.46
1:G:1825:HIS:CD2	1:M:3567:PRO:CB	2.98	0.45
1:G:2161:GLN:NE2	1:G:2177:LEU:HD12	2.31	0.45
1:G:2825:LYS:HE3	1:G:2827:ARG:O	2.16	0.45
1:G:4039:MET:HE3	1:G:4043:GLN:OE1	2.15	0.45
1:M:2897:LYS:HG2	1:M:2897:LYS:O	2.16	0.45
1:S:1435:TYR:CB	1:S:1575:LEU:HD23	2.41	0.45
1:S:2897:LYS:O	1:S:2897:LYS:HG2	2.16	0.45
1:A:2897:LYS:O	1:A:2897:LYS:HG2	2.16	0.45
1:A:4878:ASP:OD1	1:G:4580:TYR:O	2.33	0.45
1:G:3222:LYS:O	1:G:3227:ARG:NH1	2.49	0.45
1:M:1575:LEU:HD12	1:M:1575:LEU:C	2.42	0.45
1:M:2302:LEU:HD23	1:M:2302:LEU:O	2.16	0.45
1:M:4666:VAL:N	1:M:4667:PRO:HD2	2.30	0.45
1:M:4878:ASP:OD1	1:S:4580:TYR:O	2.33	0.45
1:M:4901:ILE:HG22	1:M:4902:GLU:N	2.30	0.45
1:S:1575:LEU:C	1:S:1575:LEU:HD12	2.42	0.45
1:S:3169:LEU:HD11	1:S:3194:LEU:HD11	1.96	0.45
1:M:4039:MET:HE3	1:M:4043:GLN:OE1	2.15	0.45
1:M:4058:ILE:O	1:M:4061:PHE:HB3	2.15	0.45
1:A:1575:LEU:HD12	1:A:1575:LEU:C	2.42	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2822:THR:OG1	1:A:2938:THR:OG1	2.34	0.45
1:A:3222:LYS:O	1:A:3227:ARG:NH1	2.49	0.45
1:S:3222:LYS:O	1:S:3227:ARG:NH1	2.49	0.45
1:S:4705:VAL:HG22	1:S:4705:VAL:O	2.15	0.45
1:A:2237:CYS:SG	1:A:2275:VAL:HG12	2.57	0.45
1:G:2212:VAL:HG11	1:G:2256:TYR:CZ	2.52	0.45
1:G:2237:CYS:SG	1:G:2275:VAL:HG12	2.57	0.45
1:G:2862:LEU:HD11	1:G:2932:MET:HE1	1.97	0.45
1:G:3941:ASP:O	1:G:4002:LYS:NZ	2.48	0.45
1:M:156:GLN:OE1	1:M:156:GLN:N	2.48	0.45
1:M:3222:LYS:O	1:M:3227:ARG:NH1	2.49	0.45
1:M:3663:LEU:HD12	1:M:3663:LEU:C	2.42	0.45
1:M:4203:ALA:O	1:M:4207:MET:HE3	2.16	0.45
1:M:4658:ILE:HD12	1:M:4796:MET:HE3	1.97	0.45
1:S:294:THR:O	1:S:298:GLY:N	2.46	0.45
1:S:2023:LEU:HB3	1:S:2024:PRO:HD2	1.99	0.45
1:G:772:ASN:HD21	1:G:1470:ARG:HA	1.82	0.45
1:G:4203:ALA:O	1:G:4207:MET:HE3	2.16	0.45
1:M:2822:THR:OG1	1:M:2938:THR:OG1	2.35	0.45
1:M:4004:ALA:CB	1:M:4013:LEU:HD22	2.40	0.45
1:S:2862:LEU:HD11	1:S:2932:MET:HE1	1.97	0.45
1:S:3999:MET:HG3	1:S:4003:LEU:HD11	1.98	0.45
1:A:772:ASN:HD21	1:A:1470:ARG:HA	1.82	0.45
1:A:2023:LEU:HB3	1:A:2024:PRO:HD2	1.99	0.45
1:A:4203:ALA:O	1:A:4207:MET:HE3	2.16	0.45
1:A:4785:THR:O	1:A:4785:THR:HG22	2.16	0.45
1:G:3081:MET:HE1	1:G:3092:LEU:HD23	1.99	0.45
1:S:4203:ALA:O	1:S:4207:MET:HE3	2.16	0.45
1:G:1869:GLU:OE1	1:G:1869:GLU:N	2.40	0.45
1:M:3999:MET:HG3	1:M:4003:LEU:HD11	1.98	0.45
1:S:2302:LEU:O	1:S:2302:LEU:HD23	2.16	0.45
1:A:3663:LEU:C	1:A:3663:LEU:HD12	2.42	0.45
1:G:1478:ASP:OD1	1:G:1481:GLY:N	2.50	0.45
1:G:1575:LEU:C	1:G:1575:LEU:HD12	2.42	0.45
1:M:3459:VAL:HG23	1:M:3464:ILE:CG2	2.44	0.45
1:S:774:ASP:OD1	1:S:774:ASP:N	2.50	0.45
1:A:1439:VAL:HG13	1:A:1439:VAL:O	2.17	0.45
1:A:2212:VAL:HG11	1:A:2256:TYR:CZ	2.52	0.45
1:A:3105:LYS:HD3	1:A:3105:LYS:C	2.42	0.45
1:A:4773:VAL:HG22	1:A:4777:ILE:HD11	1.99	0.45
1:G:3156:VAL:HG13	1:G:3157:ILE:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3366:ARG:HA	1:G:3441:ILE:HD11	1.99	0.45
1:A:2161:GLN:NE2	1:A:2177:LEU:HD12	2.31	0.44
1:G:294:THR:O	1:G:298:GLY:N	2.46	0.44
1:G:372:LEU:HD13	1:G:372:LEU:O	2.18	0.44
1:G:2768:PHE:O	1:G:2772:GLN:HG2	2.17	0.44
1:G:4900:GLU:O	1:G:4901:ILE:HD13	2.17	0.44
1:M:2161:GLN:NE2	1:M:2177:LEU:HD12	2.31	0.44
1:M:2212:VAL:HG11	1:M:2256:TYR:CZ	2.52	0.44
1:M:3050:VAL:O	1:M:3050:VAL:HG12	2.17	0.44
1:M:3366:ARG:HA	1:M:3441:ILE:HD11	1.99	0.44
1:S:2212:VAL:HG11	1:S:2256:TYR:CZ	2.52	0.44
1:S:2237:CYS:SG	1:S:2275:VAL:HG12	2.57	0.44
1:A:1478:ASP:OD1	1:A:1481:GLY:N	2.50	0.44
1:A:3156:VAL:HG13	1:A:3157:ILE:HG13	1.98	0.44
1:A:4039:MET:HE3	1:A:4043:GLN:OE1	2.15	0.44
1:G:1690:ASP:OD1	1:G:1692:ALA:N	2.49	0.44
1:G:4773:VAL:HG22	1:G:4777:ILE:HD11	1.99	0.44
1:M:1439:VAL:O	1:M:1439:VAL:HG13	2.17	0.44
1:M:1690:ASP:OD1	1:M:1692:ALA:N	2.49	0.44
1:S:1690:ASP:OD1	1:S:1692:ALA:N	2.49	0.44
1:S:4773:VAL:HG22	1:S:4777:ILE:HD11	1.99	0.44
1:A:3062:PRO:HA	1:A:3065:VAL:HG22	1.99	0.44
1:G:2822:THR:OG1	1:G:2938:THR:OG1	2.35	0.44
1:G:3158:LEU:HD22	1:G:3158:LEU:N	2.33	0.44
1:G:3319:ILE:HD11	1:G:3338:LEU:HD21	2.00	0.44
1:M:2763:HIS:HE1	1:M:2790:MET:O	2.01	0.44
1:S:179:TYR:N	1:S:194:SER:O	2.50	0.44
1:S:3663:LEU:C	1:S:3663:LEU:HD12	2.42	0.44
1:A:2351:ASN:O	1:A:2355:ARG:HG3	2.18	0.44
1:A:3081:MET:HE1	1:A:3092:LEU:HD23	1.99	0.44
1:A:3655:GLU:O	1:A:3655:GLU:OE1	2.35	0.44
1:G:179:TYR:N	1:G:194:SER:O	2.51	0.44
1:M:3655:GLU:O	1:M:3655:GLU:OE1	2.35	0.44
1:M:2237:CYS:SG	1:M:2275:VAL:HG12	2.57	0.44
1:M:3081:MET:HE1	1:M:3092:LEU:HD23	1.99	0.44
1:M:4900:GLU:O	1:M:4901:ILE:HD13	2.17	0.44
1:S:3050:VAL:O	1:S:3050:VAL:HG12	2.17	0.44
1:A:2768:PHE:O	1:A:2772:GLN:HG2	2.17	0.44
1:A:3319:ILE:HD11	1:A:3338:LEU:HD21	2.00	0.44
1:A:4900:GLU:O	1:A:4901:ILE:HD13	2.17	0.44
1:G:3062:PRO:HA	1:G:3065:VAL:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3655:GLU:OE1	1:G:3655:GLU:O	2.35	0.44
1:G:4785:THR:HG22	1:G:4785:THR:O	2.16	0.44
1:M:380:GLN:OE1	1:M:380:GLN:N	2.47	0.44
1:S:156:GLN:OE1	1:S:156:GLN:N	2.48	0.44
1:S:2768:PHE:O	1:S:2772:GLN:HG2	2.17	0.44
1:S:3105:LYS:HD3	1:S:3105:LYS:C	2.42	0.44
1:S:3158:LEU:HD22	1:S:3158:LEU:N	2.33	0.44
1:S:3655:GLU:OE1	1:S:3655:GLU:O	2.35	0.44
1:A:1144:GLN:N	1:A:1147:ASP:OD2	2.47	0.44
1:A:2763:HIS:HE1	1:A:2790:MET:O	2.01	0.44
1:A:3232:LEU:HD22	1:A:3232:LEU:N	2.33	0.44
1:A:3366:ARG:HA	1:A:3441:ILE:HD11	1.99	0.44
1:G:515:TRP:O	1:G:519:VAL:HG23	2.18	0.44
1:M:372:LEU:HD13	1:M:372:LEU:O	2.18	0.44
1:M:3169:LEU:HD13	1:M:3194:LEU:HD11	1.95	0.44
1:S:3105:LYS:HE2	1:S:3105:LYS:HA	2.00	0.44
1:A:3050:VAL:HG12	1:A:3050:VAL:O	2.17	0.44
1:G:1439:VAL:HG13	1:G:1439:VAL:O	2.17	0.44
1:G:3105:LYS:HD3	1:G:3105:LYS:C	2.42	0.44
1:G:3232:LEU:N	1:G:3232:LEU:HD22	2.33	0.44
1:S:772:ASN:HD21	1:S:1470:ARG:HA	1.82	0.44
1:S:1478:ASP:OD1	1:S:1481:GLY:N	2.50	0.44
1:S:2351:ASN:O	1:S:2355:ARG:HG3	2.18	0.44
1:A:372:LEU:HD13	1:A:372:LEU:O	2.18	0.44
1:A:774:ASP:N	1:A:774:ASP:OD1	2.50	0.44
1:M:1478:ASP:OD1	1:M:1481:GLY:N	2.50	0.44
1:M:2768:PHE:O	1:M:2772:GLN:HG2	2.18	0.44
1:S:372:LEU:HD13	1:S:372:LEU:O	2.18	0.44
1:S:2874:MET:HE1	1:S:2937:VAL:HG12	2.00	0.44
1:S:3003:LEU:HB2	1:S:3004:PRO:HD3	2.00	0.44
1:S:3366:ARG:HA	1:S:3441:ILE:HD11	1.99	0.44
1:S:3539:ARG:NH1	1:S:3552:PHE:CD2	2.86	0.44
1:S:3941:ASP:O	1:S:4002:LYS:NZ	2.48	0.44
1:A:179:TYR:N	1:A:194:SER:O	2.51	0.43
1:A:3158:LEU:HD22	1:A:3158:LEU:N	2.33	0.43
1:G:590:LEU:HD13	1:G:599:VAL:HB	2.00	0.43
1:G:2023:LEU:HB3	1:G:2024:PRO:HD2	1.99	0.43
1:G:3663:LEU:C	1:G:3663:LEU:HD12	2.42	0.43
1:M:772:ASN:HD21	1:M:1470:ARG:HA	1.82	0.43
1:S:380:GLN:OE1	1:S:380:GLN:N	2.47	0.43
1:A:515:TRP:O	1:A:519:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:939:VAL:CB	1:A:1053:ILE:CG2	2.97	0.43
1:A:3169:LEU:HD11	1:A:3194:LEU:HD11	1.96	0.43
1:M:3169:LEU:HD11	1:M:3194:LEU:HD11	1.96	0.43
1:S:3152:PHE:O	1:S:3156:VAL:HG12	2.18	0.43
1:G:2204:HIS:O	1:G:2208:MET:HG3	2.18	0.43
1:M:939:VAL:CB	1:M:1053:ILE:CG2	2.96	0.43
1:M:2023:LEU:HB3	1:M:2024:PRO:HD2	1.99	0.43
1:M:3105:LYS:HD3	1:M:3105:LYS:C	2.42	0.43
1:M:3539:ARG:NH1	1:M:3552:PHE:CD2	2.86	0.43
1:S:3062:PRO:HA	1:S:3065:VAL:HG22	1.99	0.43
1:S:4900:GLU:O	1:S:4901:ILE:HD13	2.17	0.43
1:G:3003:LEU:HB2	1:G:3004:PRO:HD3	2.00	0.43
1:G:3050:VAL:O	1:G:3050:VAL:HG12	2.17	0.43
1:M:590:LEU:HD13	1:M:599:VAL:HB	2.00	0.43
1:M:4244:GLU:OE1	1:M:4668:LEU:HD22	2.18	0.43
1:S:234:SER:HB2	1:S:242:ARG:HG2	2.00	0.43
1:S:1448:VAL:HG22	1:S:1554:VAL:HG23	2.01	0.43
1:S:1935:VAL:O	1:S:1939:MET:HG2	2.18	0.43
1:A:2204:HIS:O	1:A:2208:MET:HG3	2.18	0.43
1:A:3105:LYS:HE2	1:A:3105:LYS:HA	2.00	0.43
1:A:3152:PHE:O	1:A:3156:VAL:HG12	2.18	0.43
1:A:4244:GLU:OE1	1:A:4668:LEU:HD22	2.18	0.43
1:G:1935:VAL:O	1:G:1939:MET:HG2	2.18	0.43
1:G:4244:GLU:OE1	1:G:4668:LEU:HD22	2.19	0.43
1:M:3003:LEU:HB2	1:M:3004:PRO:HD3	2.00	0.43
1:M:3062:PRO:HA	1:M:3065:VAL:HG22	1.99	0.43
1:M:3158:LEU:HD22	1:M:3158:LEU:N	2.33	0.43
1:M:4773:VAL:HG22	1:M:4777:ILE:HD11	1.99	0.43
1:S:1439:VAL:O	1:S:1439:VAL:HG13	2.17	0.43
1:M:515:TRP:O	1:M:519:VAL:HG23	2.18	0.43
1:M:4134:GLU:HB3	1:M:4135:PRO:HD3	2.01	0.43
1:S:1221:GLU:N	1:S:1221:GLU:OE1	2.52	0.43
1:S:2204:HIS:O	1:S:2208:MET:HG3	2.18	0.43
1:S:2763:HIS:HE1	1:S:2790:MET:O	2.01	0.43
1:S:3081:MET:HE1	1:S:3092:LEU:HD23	1.99	0.43
1:G:2351:ASN:O	1:G:2355:ARG:HG3	2.18	0.43
1:M:179:TYR:N	1:M:194:SER:O	2.51	0.43
1:M:234:SER:HB2	1:M:242:ARG:HG2	2.00	0.43
1:M:2204:HIS:O	1:M:2208:MET:HG3	2.18	0.43
1:S:4134:GLU:HB3	1:S:4135:PRO:HD3	2.01	0.43
1:A:234:SER:HB2	1:A:242:ARG:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1924:GLU:N	1:A:1924:GLU:OE1	2.52	0.43
1:A:4655:PHE:N	1:A:4796:MET:HE1	2.34	0.43
1:G:3719:ASP:OD1	1:G:3719:ASP:O	2.37	0.43
1:M:1935:VAL:O	1:M:1939:MET:HG2	2.18	0.43
1:M:3152:PHE:O	1:M:3156:VAL:HG12	2.18	0.43
1:M:4655:PHE:N	1:M:4796:MET:HE1	2.34	0.43
1:A:1448:VAL:HG22	1:A:1554:VAL:HG23	2.01	0.43
1:G:234:SER:HB2	1:G:242:ARG:HG2	2.00	0.43
1:G:2763:HIS:HE1	1:G:2790:MET:O	2.01	0.43
1:G:3539:ARG:NH1	1:G:3552:PHE:CD2	2.86	0.43
1:G:4655:PHE:N	1:G:4796:MET:HE1	2.34	0.43
1:M:1448:VAL:HG22	1:M:1554:VAL:HG23	2.01	0.43
1:M:3232:LEU:N	1:M:3232:LEU:HD22	2.33	0.43
1:S:3169:LEU:HD13	1:S:3194:LEU:HD11	1.95	0.43
1:S:3719:ASP:O	1:S:3719:ASP:OD1	2.37	0.43
1:A:707:VAL:HG23	1:A:782:SER:CB	2.48	0.43
1:A:1935:VAL:O	1:A:1939:MET:HG2	2.18	0.43
1:G:707:VAL:HG23	1:G:782:SER:CB	2.48	0.43
1:G:774:ASP:OD1	1:G:774:ASP:N	2.50	0.43
1:G:1101:ARG:NH1	1:G:1115:LEU:O	2.52	0.43
1:G:1924:GLU:N	1:G:1924:GLU:OE1	2.52	0.43
1:G:4134:GLU:HB3	1:G:4135:PRO:HD3	2.01	0.43
1:M:707:VAL:HG23	1:M:782:SER:CB	2.48	0.43
1:S:4244:GLU:OE1	1:S:4668:LEU:HD22	2.19	0.43
1:A:34:LYS:HA	1:A:34:LYS:CE	2.49	0.42
1:A:156:GLN:OE1	1:A:156:GLN:N	2.48	0.42
1:A:2346:VAL:HG13	1:A:2346:VAL:O	2.19	0.42
1:A:3539:ARG:NH1	1:A:3552:PHE:CD2	2.86	0.42
1:A:4063:ASP:OD1	1:A:4064:MET:N	2.52	0.42
1:A:4134:GLU:HB3	1:A:4135:PRO:HD3	2.01	0.42
1:G:3105:LYS:HE2	1:G:3105:LYS:HA	2.00	0.42
1:G:3152:PHE:O	1:G:3156:VAL:HG12	2.18	0.42
1:M:864:PRO:CG	1:M:867:LEU:HD12	2.49	0.42
1:M:3719:ASP:OD1	1:M:3719:ASP:O	2.37	0.42
1:S:590:LEU:HD13	1:S:599:VAL:HB	2.00	0.42
1:S:937:CYS:SG	1:S:984:LEU:HD21	2.59	0.42
1:S:939:VAL:CB	1:S:1053:ILE:CG2	2.97	0.42
1:S:3232:LEU:N	1:S:3232:LEU:HD22	2.33	0.42
1:S:3319:ILE:HD11	1:S:3338:LEU:HD21	2.00	0.42
1:S:3365:LEU:HD21	1:S:3405:LEU:HD23	2.01	0.42
1:A:3003:LEU:HB2	1:A:3004:PRO:HD3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3610:GLU:OE1	1:A:3610:GLU:N	2.52	0.42
1:G:864:PRO:CG	1:G:867:LEU:HD12	2.50	0.42
1:G:939:VAL:CB	1:G:1053:ILE:CG2	2.97	0.42
1:G:1448:VAL:HG22	1:G:1554:VAL:HG23	2.01	0.42
1:G:3365:LEU:HD21	1:G:3405:LEU:HD23	2.01	0.42
1:S:33:LEU:HD11	1:S:35:LEU:CD1	2.47	0.42
1:S:515:TRP:O	1:S:519:VAL:HG23	2.18	0.42
1:G:2265:LEU:O	1:G:2266:GLY:C	2.63	0.42
1:M:21:VAL:HG12	1:M:66:CYS:HA	2.01	0.42
1:M:680:THR:HG22	1:M:681:HIS:N	2.34	0.42
1:M:774:ASP:OD1	1:M:774:ASP:N	2.50	0.42
1:S:4655:PHE:N	1:S:4796:MET:HE1	2.34	0.42
1:S:4880:MET:HE2	1:S:4880:MET:HB2	1.97	0.42
1:A:2874:MET:HE1	1:A:2937:VAL:HG12	2.00	0.42
1:A:3365:LEU:HD21	1:A:3405:LEU:HD23	2.01	0.42
1:A:3719:ASP:OD1	1:A:3719:ASP:O	2.37	0.42
1:G:2874:MET:HE1	1:G:2937:VAL:HG12	2.00	0.42
1:M:937:CYS:SG	1:M:984:LEU:HD21	2.59	0.42
1:M:1221:GLU:OE1	1:M:1221:GLU:N	2.52	0.42
1:M:4063:ASP:OD1	1:M:4064:MET:N	2.52	0.42
1:M:5000:GLU:OE1	1:M:5000:GLU:N	2.50	0.42
1:S:3917:ILE:HD13	1:S:3917:ILE:N	2.34	0.42
1:G:1221:GLU:N	1:G:1221:GLU:OE1	2.52	0.42
1:G:3110:LEU:HD12	1:G:3175:LEU:HD21	2.02	0.42
1:G:3459:VAL:HG23	1:G:3464:ILE:CG2	2.44	0.42
1:G:4063:ASP:OD1	1:G:4064:MET:N	2.52	0.42
1:M:2351:ASN:O	1:M:2355:ARG:HG3	2.18	0.42
1:S:2822:THR:OG1	1:S:2938:THR:OG1	2.35	0.42
1:A:590:LEU:HD13	1:A:599:VAL:HB	2.00	0.42
1:A:937:CYS:SG	1:A:984:LEU:HD21	2.59	0.42
1:A:1101:ARG:NH1	1:A:1115:LEU:O	2.52	0.42
1:A:2750:LYS:HG2	1:A:2750:LYS:O	2.19	0.42
1:G:3917:ILE:N	1:G:3917:ILE:HD13	2.34	0.42
1:M:1924:GLU:N	1:M:1924:GLU:OE1	2.52	0.42
1:M:2874:MET:HE1	1:M:2937:VAL:HG12	2.00	0.42
1:S:34:LYS:HA	1:S:34:LYS:CE	2.49	0.42
1:S:1101:ARG:NH1	1:S:1115:LEU:O	2.52	0.42
1:S:4063:ASP:OD1	1:S:4064:MET:N	2.52	0.42
1:A:3917:ILE:HD13	1:A:3917:ILE:N	2.34	0.42
1:G:33:LEU:HD11	1:G:35:LEU:CD1	2.47	0.42
1:G:2178:MET:SD	1:G:2210:VAL:HG11	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:2967:MET:HE3	1:G:2967:MET:CA	2.49	0.42
1:M:3319:ILE:HD11	1:M:3338:LEU:HD21	2.00	0.42
1:S:4887:MET:HE3	1:S:4887:MET:HB3	1.97	0.42
1:A:1221:GLU:OE1	1:A:1221:GLU:N	2.52	0.42
1:A:2178:MET:SD	1:A:2210:VAL:HG11	2.60	0.42
1:A:2630:VAL:N	1:A:2631:PRO:HD2	2.35	0.42
1:G:21:VAL:HG12	1:G:66:CYS:HA	2.01	0.42
1:G:680:THR:HG22	1:G:681:HIS:N	2.34	0.42
1:G:2750:LYS:O	1:G:2750:LYS:HG2	2.20	0.42
1:M:2265:LEU:O	1:M:2266:GLY:C	2.62	0.42
1:M:2346:VAL:O	1:M:2346:VAL:HG13	2.19	0.42
1:A:455:PRO:HG3	1:A:467:LYS:HB3	2.02	0.42
1:A:680:THR:HG22	1:A:681:HIS:N	2.34	0.42
1:A:2967:MET:HE3	1:A:2967:MET:CA	2.49	0.42
1:A:3753:PHE:O	1:A:3757:GLU:HG2	2.20	0.42
1:G:2346:VAL:HG13	1:G:2346:VAL:O	2.19	0.42
1:G:2628:PHE:HD1	1:G:2907:PRO:CG	2.33	0.42
1:M:3110:LEU:HD12	1:M:3175:LEU:HD21	2.02	0.42
1:M:3917:ILE:HD13	1:M:3917:ILE:N	2.34	0.42
1:S:680:THR:HG22	1:S:681:HIS:N	2.34	0.42
1:S:2178:MET:SD	1:S:2210:VAL:HG11	2.60	0.42
1:S:2288:LEU:O	1:S:3849:ARG:NH1	2.51	0.42
1:S:3320:LEU:HA	1:S:3323:ILE:HG22	2.02	0.42
1:A:294:THR:O	1:A:298:GLY:N	2.46	0.42
1:G:34:LYS:HA	1:G:34:LYS:CE	2.49	0.42
1:G:2630:VAL:N	1:G:2631:PRO:HD2	2.35	0.42
1:M:1101:ARG:NH1	1:M:1115:LEU:O	2.52	0.42
1:M:2630:VAL:N	1:M:2631:PRO:HD2	2.35	0.42
1:M:2967:MET:HE3	1:M:2967:MET:CA	2.49	0.42
1:M:3105:LYS:HA	1:M:3105:LYS:HE2	2.00	0.42
1:A:977:LEU:CD2	1:A:1043:VAL:HG11	2.50	0.41
1:M:455:PRO:HG3	1:M:467:LYS:HB3	2.02	0.41
1:M:1144:GLN:N	1:M:1147:ASP:OD2	2.47	0.41
1:S:2630:VAL:N	1:S:2631:PRO:HD2	2.35	0.41
1:S:2967:MET:HE3	1:S:2967:MET:CA	2.49	0.41
1:S:3459:VAL:HG23	1:S:3464:ILE:CG2	2.44	0.41
1:A:904:HIS:HE1	1:A:906:CYS:SG	2.43	0.41
1:G:1131:ARG:NH1	1:G:1178:ALA:O	2.54	0.41
1:M:2178:MET:SD	1:M:2210:VAL:HG11	2.60	0.41
1:M:4093:PHE:O	1:M:4097:MET:HG2	2.20	0.41
1:S:3110:LEU:HD12	1:S:3175:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:LEU:HD11	1:A:35:LEU:CD1	2.47	0.41
1:A:1024:TYR:O	1:A:1025:ARG:C	2.63	0.41
1:A:3305:THR:HG22	1:A:3307:VAL:H	1.85	0.41
1:G:937:CYS:SG	1:G:984:LEU:HD21	2.60	0.41
1:G:977:LEU:CD2	1:G:1043:VAL:HG11	2.50	0.41
1:M:3320:LEU:HA	1:M:3323:ILE:HG22	2.02	0.41
1:M:3610:GLU:OE1	1:M:3610:GLU:N	2.52	0.41
1:S:2750:LYS:O	1:S:2750:LYS:HG2	2.19	0.41
1:S:3999:MET:HE2	1:S:3999:MET:HA	2.02	0.41
1:A:984:LEU:HD12	1:A:987:ARG:NH1	2.34	0.41
1:G:456:SER:HG	1:G:459:LEU:HG	1.79	0.41
1:G:3610:GLU:OE1	1:G:3610:GLU:N	2.52	0.41
2:H:38:ASP:OD1	2:H:39:SER:N	2.54	0.41
1:S:1039:LEU:HD23	1:S:1039:LEU:HA	1.95	0.41
1:S:2265:LEU:O	1:S:2266:GLY:C	2.62	0.41
1:S:2346:VAL:O	1:S:2346:VAL:HG13	2.19	0.41
1:A:864:PRO:CG	1:A:867:LEU:HD12	2.50	0.41
1:A:3110:LEU:HD12	1:A:3175:LEU:HD21	2.02	0.41
1:G:350:HIS:O	1:G:354:GLY:N	2.48	0.41
1:G:904:HIS:HE1	1:G:906:CYS:SG	2.43	0.41
1:G:2580:ASP:OD1	1:G:2580:ASP:C	2.64	0.41
1:G:3169:LEU:HD11	1:G:3194:LEU:HD11	1.96	0.41
1:G:3753:PHE:O	1:G:3757:GLU:HG2	2.20	0.41
1:M:1024:TYR:O	1:M:1025:ARG:C	2.63	0.41
1:M:2750:LYS:HG2	1:M:2750:LYS:O	2.19	0.41
1:M:3365:LEU:HD21	1:M:3405:LEU:HD23	2.01	0.41
1:M:3999:MET:HE2	1:M:3999:MET:HA	2.02	0.41
1:S:3610:GLU:OE1	1:S:3610:GLU:N	2.52	0.41
1:S:3753:PHE:HZ	1:S:4719:PHE:HZ	1.62	0.41
1:A:1131:ARG:NH1	1:A:1178:ALA:O	2.54	0.41
1:A:3320:LEU:HA	1:A:3323:ILE:HG22	2.02	0.41
1:G:1024:TYR:O	1:G:1025:ARG:C	2.63	0.41
1:G:2522:LEU:HD22	1:G:2578:MET:HE3	2.03	0.41
1:M:25:SER:HB3	1:M:34:LYS:HE3	2.02	0.41
1:M:3753:PHE:O	1:M:3757:GLU:HG2	2.20	0.41
1:S:21:VAL:HG12	1:S:66:CYS:HA	2.01	0.41
1:S:864:PRO:CG	1:S:867:LEU:HD12	2.50	0.41
1:S:1924:GLU:N	1:S:1924:GLU:OE1	2.52	0.41
1:A:4911:LEU:O	1:A:4914:VAL:HG22	2.21	0.41
2:B:38:ASP:OD1	2:B:39:SER:N	2.54	0.41
1:M:33:LEU:HD11	1:M:35:LEU:CD1	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:752:VAL:O	1:M:752:VAL:HG13	2.21	0.41
1:M:3986:TRP:HA	1:M:3986:TRP:HE3	1.86	0.41
1:S:3753:PHE:O	1:S:3757:GLU:HG2	2.20	0.41
1:S:4767:TRP:CZ2	1:S:4771:ILE:HG12	2.56	0.41
1:A:21:VAL:HG12	1:A:66:CYS:HA	2.01	0.41
1:A:25:SER:HB3	1:A:34:LYS:HE3	2.03	0.41
1:A:752:VAL:HG13	1:A:752:VAL:O	2.21	0.41
1:A:4839:MET:HG3	1:G:4823:LEU:CD2	2.32	0.41
1:A:5000:GLU:OE1	1:A:5000:GLU:N	2.49	0.41
1:G:4767:TRP:CZ2	1:G:4771:ILE:HG12	2.56	0.41
1:M:2628:PHE:HD1	1:M:2907:PRO:CG	2.33	0.41
1:M:4091:LYS:HB2	1:M:4091:LYS:HE2	1.89	0.41
1:M:4767:TRP:CE2	1:M:4771:ILE:CD1	3.04	0.41
1:S:33:LEU:CD1	1:S:35:LEU:CD1	2.99	0.41
1:A:1067:SER:OG	1:A:1070:ASP:OD2	2.34	0.41
1:A:1461:ASP:OD1	1:A:1462:MET:N	2.54	0.41
1:A:2628:PHE:HD1	1:A:2907:PRO:CG	2.32	0.41
1:A:4767:TRP:CZ2	1:A:4771:ILE:HG12	2.56	0.41
1:G:455:PRO:HG3	1:G:467:LYS:HB3	2.02	0.41
1:G:4911:LEU:O	1:G:4914:VAL:HG22	2.21	0.41
1:M:34:LYS:HA	1:M:34:LYS:CE	2.49	0.41
1:M:977:LEU:CD2	1:M:1043:VAL:HG11	2.50	0.41
1:M:2580:ASP:OD1	1:M:2580:ASP:C	2.64	0.41
1:M:2994:GLU:OE1	1:M:2994:GLU:N	2.52	0.41
1:M:3256:LEU:HD21	1:M:3266:MET:SD	2.61	0.41
1:M:3768:SER:HA	1:M:3771:HIS:CD2	2.56	0.41
1:S:168:ASP:C	1:S:169:LEU:HD12	2.46	0.41
1:S:453:GLU:OE1	1:S:453:GLU:CA	2.68	0.41
1:S:455:PRO:HG3	1:S:467:LYS:HB3	2.02	0.41
1:S:977:LEU:CD2	1:S:1043:VAL:HG11	2.50	0.41
1:S:1119:GLU:OE1	1:S:1119:GLU:N	2.48	0.41
1:S:4021:LYS:O	1:S:4024:VAL:HG12	2.21	0.41
1:A:2522:LEU:HD22	1:A:2578:MET:HE3	2.03	0.41
1:A:3256:LEU:HD21	1:A:3266:MET:SD	2.61	0.41
1:A:3999:MET:HE2	1:A:3999:MET:HA	2.02	0.41
1:A:4067:LYS:HA	1:A:4070:ASP:OD2	2.21	0.41
1:G:168:ASP:C	1:G:169:LEU:HD12	2.46	0.41
1:G:752:VAL:HG13	1:G:752:VAL:O	2.21	0.41
1:G:4093:PHE:O	1:G:4097:MET:HG2	2.20	0.41
1:G:4704:LEU:O	1:G:4704:LEU:HD23	2.21	0.41
1:M:3305:THR:HG22	1:M:3307:VAL:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:752:VAL:O	1:S:753:PRO:C	2.63	0.41
1:S:1461:ASP:OD1	1:S:1462:MET:N	2.54	0.41
1:S:2138:LEU:N	1:S:2139:PRO:CD	2.84	0.41
1:S:3362:ILE:HB	1:S:3437:MET:HE2	2.03	0.41
1:G:3362:ILE:HB	1:G:3437:MET:HE2	2.03	0.40
1:G:3768:SER:HA	1:G:3771:HIS:CD2	2.56	0.40
1:M:168:ASP:C	1:M:169:LEU:HD12	2.46	0.40
1:M:904:HIS:HE1	1:M:906:CYS:SG	2.43	0.40
1:M:3753:PHE:CE2	1:M:3757:GLU:HG3	2.56	0.40
1:S:904:HIS:HE1	1:S:906:CYS:SG	2.43	0.40
1:S:4093:PHE:O	1:S:4097:MET:HG2	2.20	0.40
1:A:33:LEU:CD1	1:A:35:LEU:CD1	2.99	0.40
1:A:2138:LEU:N	1:A:2139:PRO:CD	2.84	0.40
1:A:3324:VAL:O	1:A:3327:LEU:HD23	2.21	0.40
1:A:3768:SER:HA	1:A:3771:HIS:CD2	2.56	0.40
1:A:4090:LYS:HG2	1:A:4123:ILE:HD11	2.03	0.40
1:G:752:VAL:O	1:G:753:PRO:C	2.63	0.40
1:G:2865:VAL:HG21	1:G:2932:MET:HE2	2.04	0.40
1:M:752:VAL:O	1:M:753:PRO:C	2.63	0.40
1:S:25:SER:HB3	1:S:34:LYS:HE3	2.03	0.40
1:S:752:VAL:O	1:S:752:VAL:HG13	2.21	0.40
1:S:3156:VAL:CG1	1:S:3157:ILE:N	2.84	0.40
1:S:3256:LEU:HD21	1:S:3266:MET:SD	2.61	0.40
1:S:3305:THR:HG22	1:S:3307:VAL:H	1.85	0.40
1:S:4911:LEU:O	1:S:4914:VAL:HG22	2.21	0.40
1:A:939:VAL:HG23	1:A:1053:ILE:HG23	2.03	0.40
1:A:2265:LEU:O	1:A:2266:GLY:C	2.62	0.40
1:A:3567:PRO:CB	1:S:1825:HIS:NE2	2.83	0.40
1:G:25:SER:HB3	1:G:34:LYS:HE3	2.03	0.40
1:G:1461:ASP:OD1	1:G:1462:MET:N	2.54	0.40
1:G:4767:TRP:CE2	1:G:4771:ILE:CD1	3.04	0.40
1:M:294:THR:O	1:M:298:GLY:N	2.46	0.40
1:M:351:VAL:HG23	1:M:352:ALA:N	2.37	0.40
1:M:2522:LEU:HD22	1:M:2578:MET:HE3	2.03	0.40
1:M:3156:VAL:CG1	1:M:3157:ILE:N	2.85	0.40
1:M:4704:LEU:O	1:M:4704:LEU:HD23	2.22	0.40
1:M:4767:TRP:CZ2	1:M:4771:ILE:HG12	2.56	0.40
2:N:38:ASP:OD1	2:N:39:SER:N	2.54	0.40
1:S:2580:ASP:OD1	1:S:2580:ASP:C	2.63	0.40
1:S:3324:VAL:O	1:S:3327:LEU:HD23	2.21	0.40
1:S:3753:PHE:CE2	1:S:3757:GLU:HG3	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:4767:TRP:CE2	1:S:4771:ILE:CD1	3.04	0.40
2:T:38:ASP:OD1	2:T:39:SER:N	2.54	0.40
1:A:789:VAL:HG12	1:A:790:ARG:N	2.37	0.40
1:A:4704:LEU:HD23	1:A:4704:LEU:O	2.21	0.40
1:G:585:SER:O	1:G:588:SER:HB2	2.22	0.40
1:G:2994:GLU:OE1	1:G:2994:GLU:N	2.52	0.40
1:M:350:HIS:O	1:M:354:GLY:N	2.48	0.40
1:M:1825:HIS:NE2	1:S:3567:PRO:CB	2.83	0.40
1:M:4021:LYS:O	1:M:4024:VAL:HG12	2.21	0.40
1:S:1131:ARG:NH1	1:S:1178:ALA:O	2.54	0.40
1:S:2995:ILE:N	1:S:2995:ILE:HD12	2.37	0.40
1:S:3934:TYR:CD1	1:S:3999:MET:HE1	2.57	0.40
1:A:2995:ILE:N	1:A:2995:ILE:HD12	2.37	0.40
1:A:4021:LYS:O	1:A:4024:VAL:HG12	2.21	0.40
1:A:4044:MET:HE3	1:A:4044:MET:HB2	2.01	0.40
1:G:3087:ILE:HG23	1:G:3088:VAL:N	2.37	0.40
1:G:3156:VAL:CG1	1:G:3157:ILE:N	2.85	0.40
1:G:3305:THR:HG22	1:G:3307:VAL:H	1.85	0.40
1:G:4067:LYS:HA	1:G:4070:ASP:OD2	2.21	0.40
1:M:4911:LEU:O	1:M:4914:VAL:HG22	2.21	0.40
1:S:707:VAL:HG23	1:S:782:SER:CB	2.48	0.40
1:S:3768:SER:HA	1:S:3771:HIS:CD2	2.56	0.40
1:S:3959:LYS:HE3	1:S:4022:ASP:OD2	2.22	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	A	4129/5037 (82%)	4034 (98%)	95 (2%)	0	100	100
1	G	4129/5037 (82%)	4034 (98%)	95 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	4129/5037 (82%)	4034 (98%)	95 (2%)	0	100	100
1	S	4129/5037 (82%)	4035 (98%)	94 (2%)	0	100	100
2	B	105/111 (95%)	102 (97%)	3 (3%)	0	100	100
2	H	105/111 (95%)	102 (97%)	3 (3%)	0	100	100
2	N	105/111 (95%)	102 (97%)	3 (3%)	0	100	100
2	T	105/111 (95%)	102 (97%)	3 (3%)	0	100	100
All	All	16936/20592 (82%)	16545 (98%)	391 (2%)	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	
1	A	3402/4276 (80%)	3393 (100%)	9 (0%)	86	86
1	G	3402/4276 (80%)	3394 (100%)	8 (0%)	87	87
1	M	3402/4276 (80%)	3393 (100%)	9 (0%)	86	86
1	S	3402/4276 (80%)	3394 (100%)	8 (0%)	87	87
2	B	87/91 (96%)	86 (99%)	1 (1%)	65	76
2	H	87/91 (96%)	86 (99%)	1 (1%)	65	76
2	N	87/91 (96%)	86 (99%)	1 (1%)	65	76
2	T	87/91 (96%)	86 (99%)	1 (1%)	65	76
All	All	13956/17468 (80%)	13918 (100%)	38 (0%)	84	86

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LYS
1	A	46	LEU
1	A	636	ASN
1	A	2559	LEU

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Mol	Chain	Res	Type
1	A	3025	LEU
1	A	3569	LEU
1	A	3899	PHE
1	A	4876	CYS
1	A	4953	ASP
2	B	26	HIS
1	G	34	LYS
1	G	46	LEU
1	G	636	ASN
1	G	3025	LEU
1	G	3569	LEU
1	G	3899	PHE
1	G	4876	CYS
1	G	4953	ASP
2	H	26	HIS
1	M	34	LYS
1	M	46	LEU
1	M	636	ASN
1	M	2559	LEU
1	M	3025	LEU
1	M	3569	LEU
1	M	3899	PHE
1	M	4876	CYS
1	M	4953	ASP
2	N	26	HIS
1	S	34	LYS
1	S	46	LEU
1	S	636	ASN
1	S	3025	LEU
1	S	3569	LEU
1	S	3899	PHE
1	S	4876	CYS
1	S	4953	ASP
2	T	26	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (162) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN
1	A	54	ASN
1	A	57	ASN
1	A	151	HIS

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Mol	Chain	Res	Type
1	A	460	GLN
1	A	461	HIS
1	A	582	HIS
1	A	736	HIS
1	A	772	ASN
1	A	866	HIS
1	A	909	ASN
1	A	911	HIS
1	A	1158	ASN
1	A	1281	ASN
1	A	1560	ASN
1	A	1571	ASN
1	A	1640	HIS
1	A	1775	HIS
1	A	1953	HIS
1	A	2125	HIS
1	A	2194	HIS
1	A	2441	HIS
1	A	2520	HIS
1	A	2773	ASN
1	A	2780	ASN
1	A	2877	GLN
1	A	2931	GLN
1	A	2991	HIS
1	A	3150	HIS
1	A	3326	ASN
1	A	3449	HIS
1	A	3450	ASN
1	A	3927	GLN
1	A	3994	HIS
1	A	3998	HIS
1	A	4009	GLN
1	A	4034	ASN
1	A	4109	GLN
1	A	4223	ASN
1	A	4997	ASN
2	B	95	ASN
1	G	23	GLN
1	G	54	ASN
1	G	57	ASN
1	G	151	HIS
1	G	460	GLN

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Mol	Chain	Res	Type
1	G	461	HIS
1	G	582	HIS
1	G	736	HIS
1	G	772	ASN
1	G	866	HIS
1	G	909	ASN
1	G	911	HIS
1	G	1158	ASN
1	G	1560	ASN
1	G	1571	ASN
1	G	1611	HIS
1	G	1640	HIS
1	G	1775	HIS
1	G	1953	HIS
1	G	2125	HIS
1	G	2194	HIS
1	G	2284	ASN
1	G	2520	HIS
1	G	2773	ASN
1	G	2780	ASN
1	G	2877	GLN
1	G	2931	GLN
1	G	2991	HIS
1	G	3150	HIS
1	G	3326	ASN
1	G	3450	ASN
1	G	3994	HIS
1	G	3998	HIS
1	G	4009	GLN
1	G	4034	ASN
1	G	4109	GLN
1	G	4691	GLN
1	G	4997	ASN
2	H	66	GLN
2	H	95	ASN
1	M	23	GLN
1	M	54	ASN
1	M	57	ASN
1	M	151	HIS
1	M	460	GLN
1	M	461	HIS
1	M	582	HIS

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Mol	Chain	Res	Type
1	M	736	HIS
1	M	772	ASN
1	M	866	HIS
1	M	909	ASN
1	M	911	HIS
1	M	1158	ASN
1	M	1560	ASN
1	M	1571	ASN
1	M	1611	HIS
1	M	1640	HIS
1	M	1660	GLN
1	M	1775	HIS
1	M	1953	HIS
1	M	2125	HIS
1	M	2194	HIS
1	M	2441	HIS
1	M	2520	HIS
1	M	2773	ASN
1	M	2780	ASN
1	M	2877	GLN
1	M	2931	GLN
1	M	2991	HIS
1	M	3150	HIS
1	M	3268	HIS
1	M	3326	ASN
1	M	3449	HIS
1	M	3450	ASN
1	M	3994	HIS
1	M	3998	HIS
1	M	4009	GLN
1	M	4034	ASN
1	M	4109	GLN
1	M	4223	ASN
1	M	4997	ASN
2	N	95	ASN
1	S	23	GLN
1	S	54	ASN
1	S	57	ASN
1	S	151	HIS
1	S	460	GLN
1	S	461	HIS
1	S	582	HIS

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Mol	Chain	Res	Type
1	S	736	HIS
1	S	772	ASN
1	S	866	HIS
1	S	909	ASN
1	S	911	HIS
1	S	1158	ASN
1	S	1560	ASN
1	S	1571	ASN
1	S	1611	HIS
1	S	1640	HIS
1	S	1775	HIS
1	S	1953	HIS
1	S	2125	HIS
1	S	2194	HIS
1	S	2284	ASN
1	S	2441	HIS
1	S	2520	HIS
1	S	2773	ASN
1	S	2780	ASN
1	S	2877	GLN
1	S	2931	GLN
1	S	2991	HIS
1	S	3150	HIS
1	S	3326	ASN
1	S	3449	HIS
1	S	3450	ASN
1	S	3994	HIS
1	S	3998	HIS
1	S	4034	ASN
1	S	4109	GLN
1	S	4997	ASN
2	T	95	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

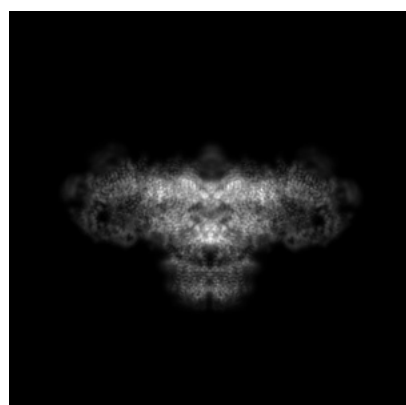
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-70591. These allow visual inspection of the internal detail of the map and identification of artifacts.

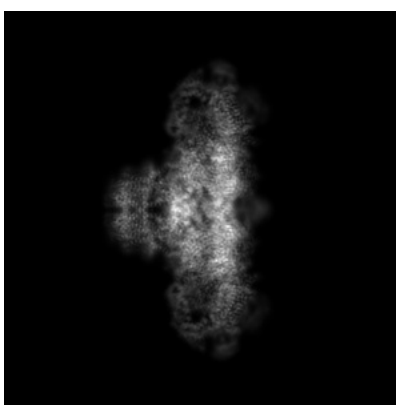
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

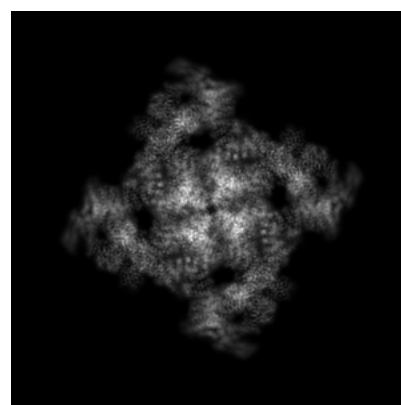
6.1.1 Primary map



X



Y



Z

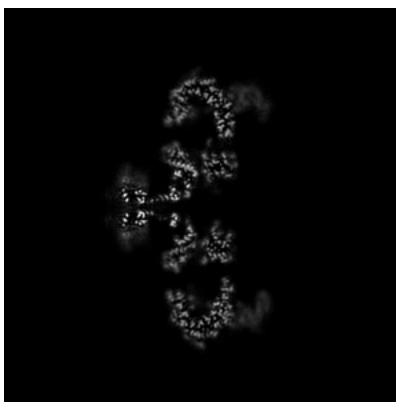
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

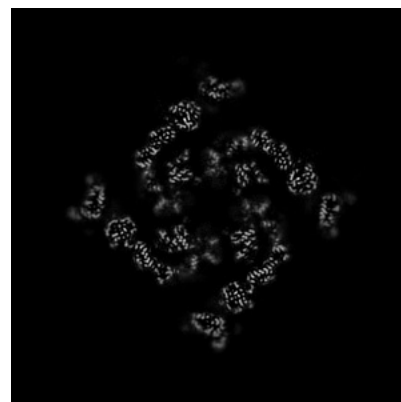
6.2.1 Primary map



X Index: 256



Y Index: 256

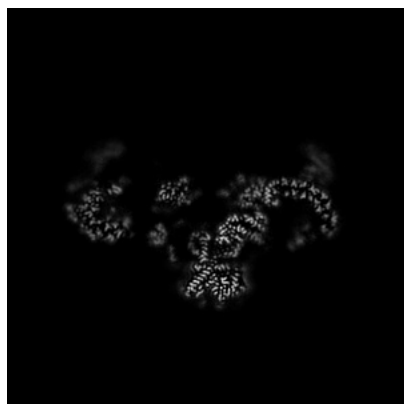


Z Index: 256

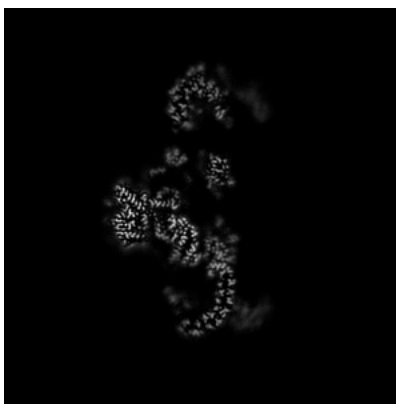
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

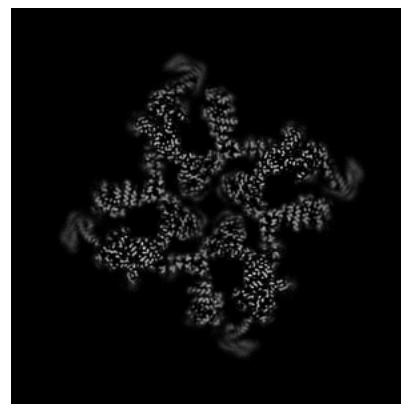
6.3.1 Primary map



X Index: 266



Y Index: 267

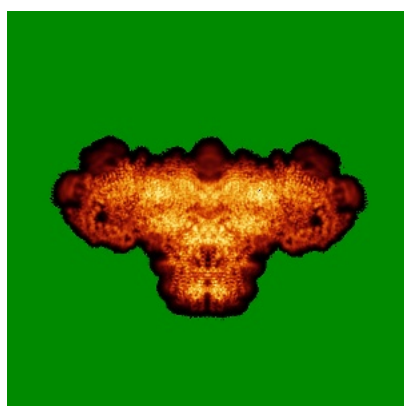


Z Index: 277

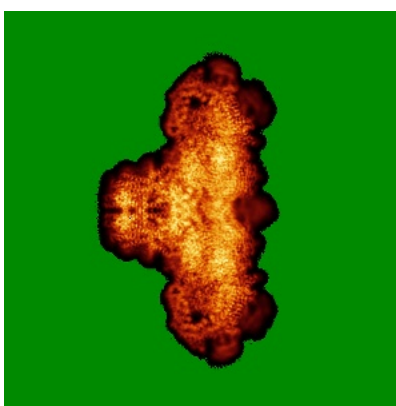
The images above show the largest variance slices of the map in three orthogonal directions.

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

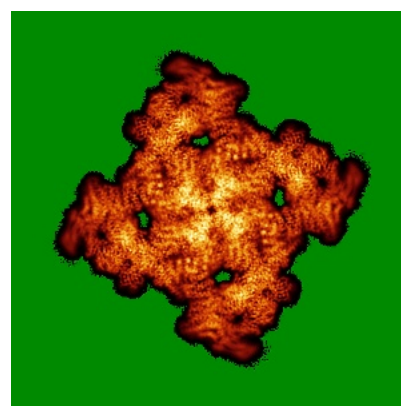
6.4.1 Primary map



X



Y

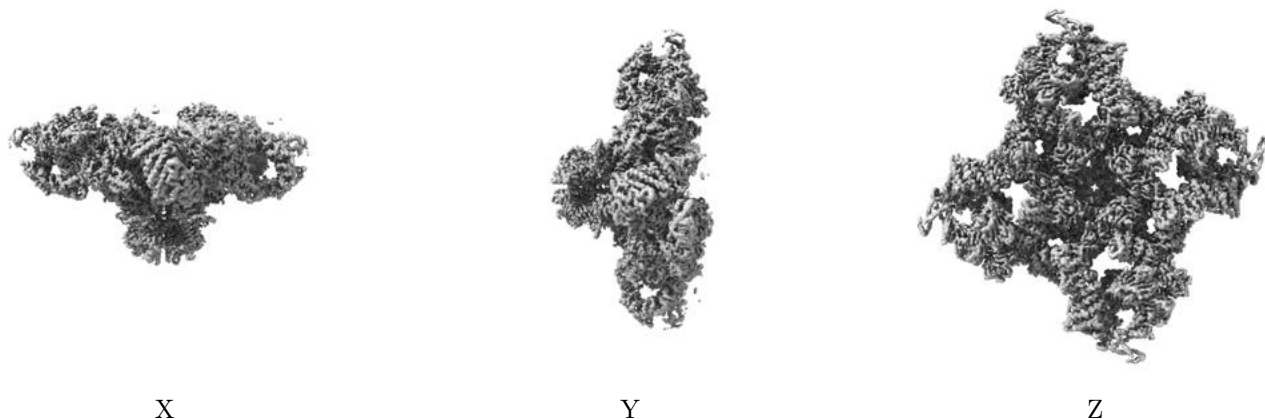


Z

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

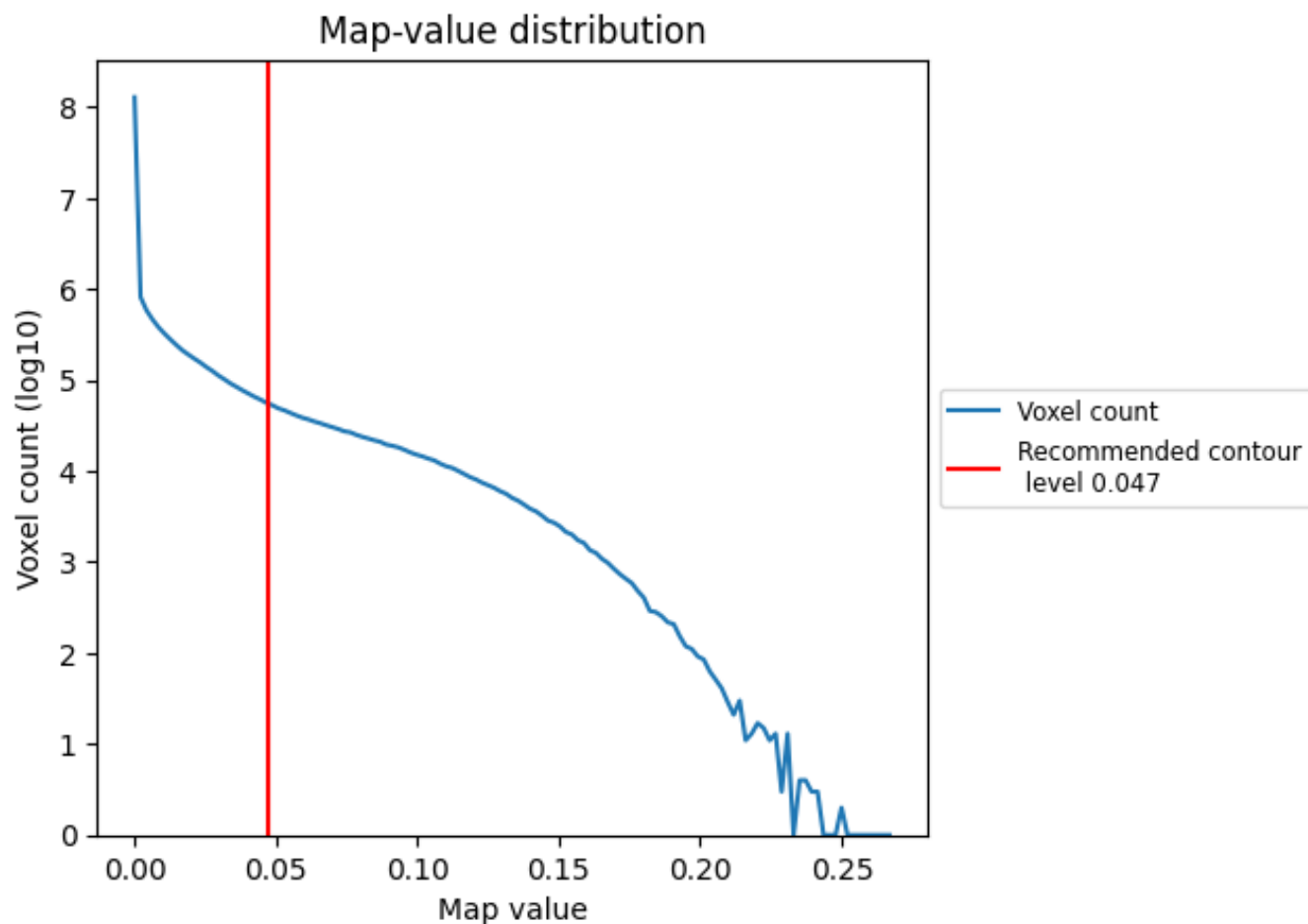
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

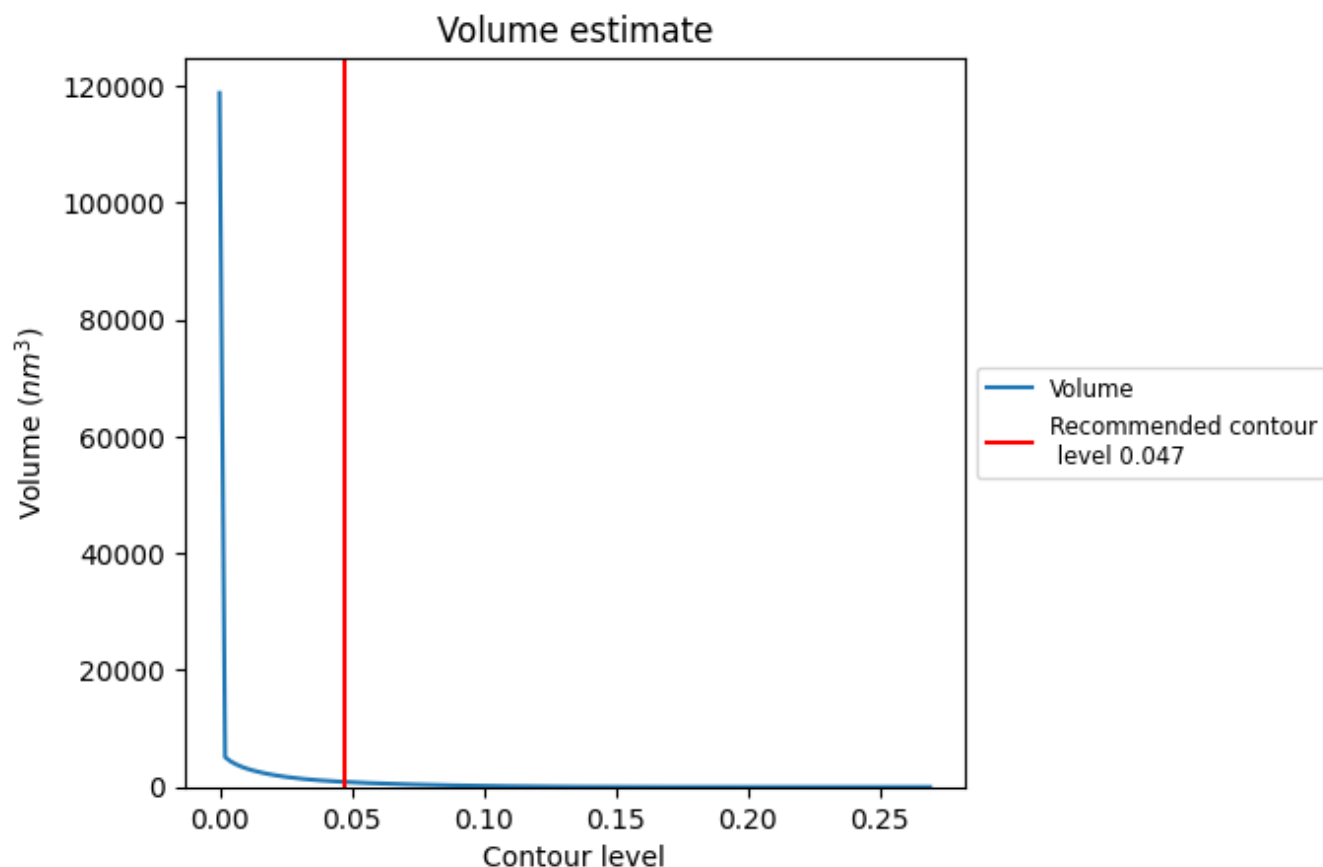
This section contains the results of statistical analysis of the map.

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.

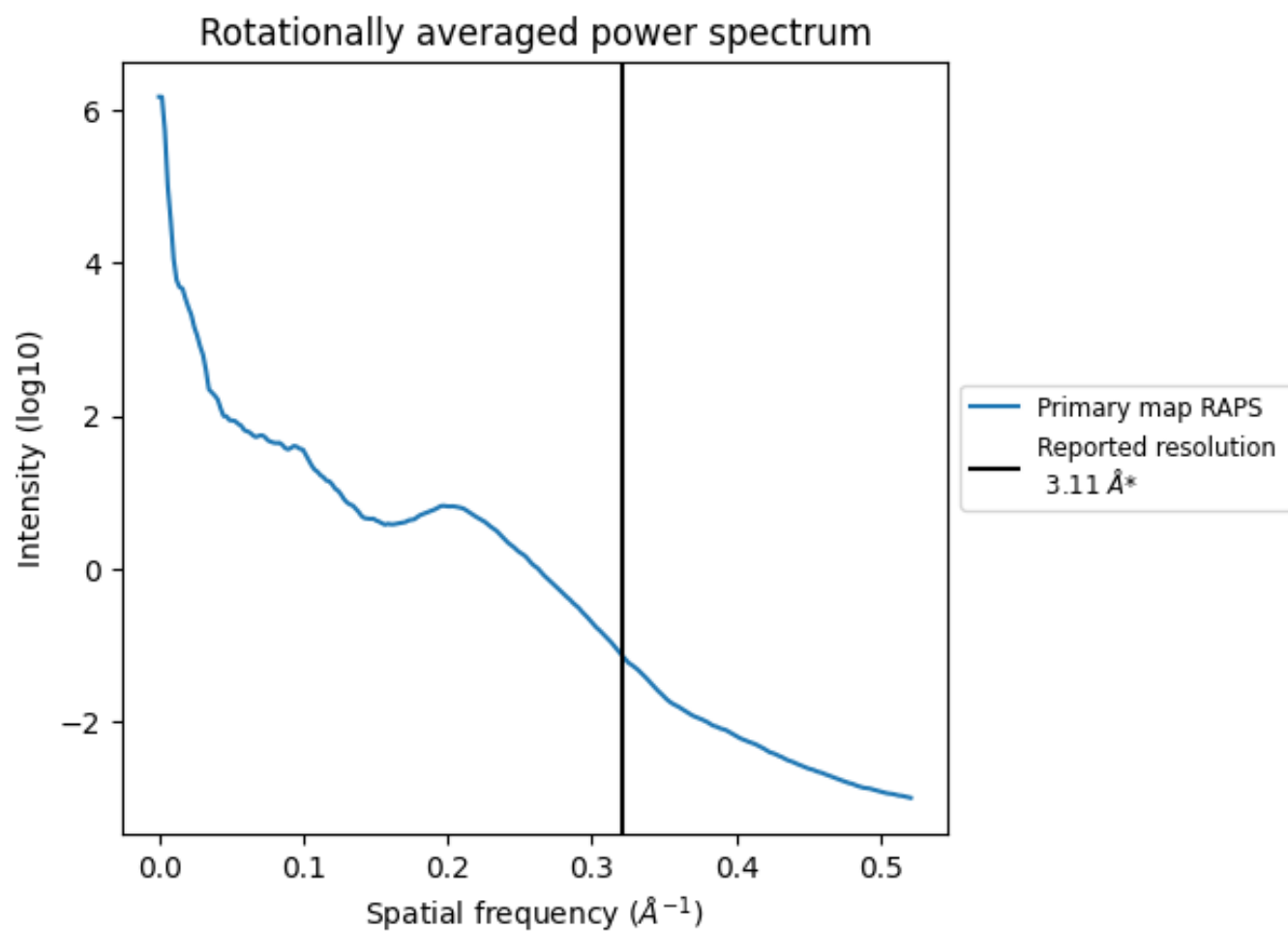
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 871 nm³; this corresponds to an approximate mass of 787 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 0.322 Å⁻¹

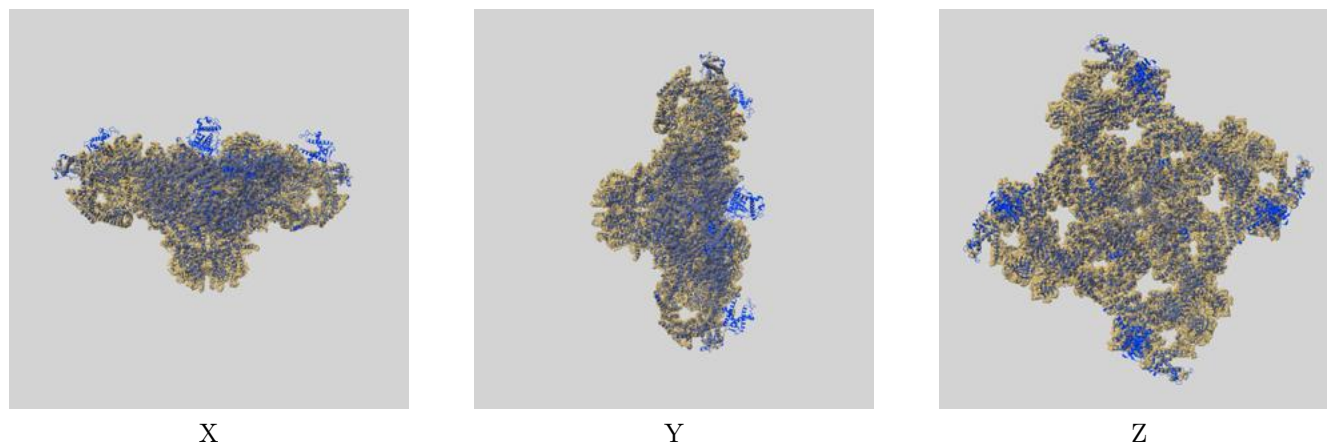
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

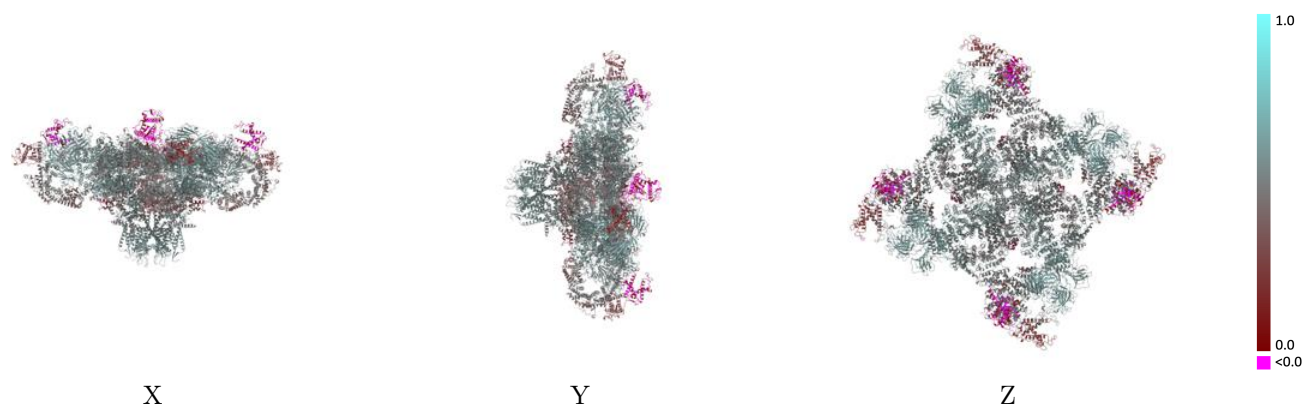
This section contains information regarding the fit between EMDB map EMD-70591 and PDB model 9OL6. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



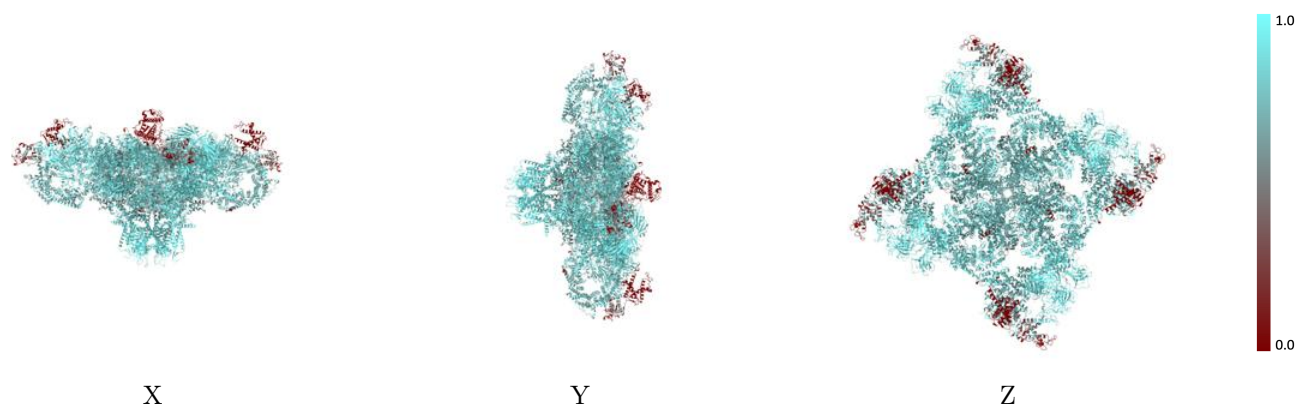
The images above show the 3D surface view of the map at the recommended contour level 0.047 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



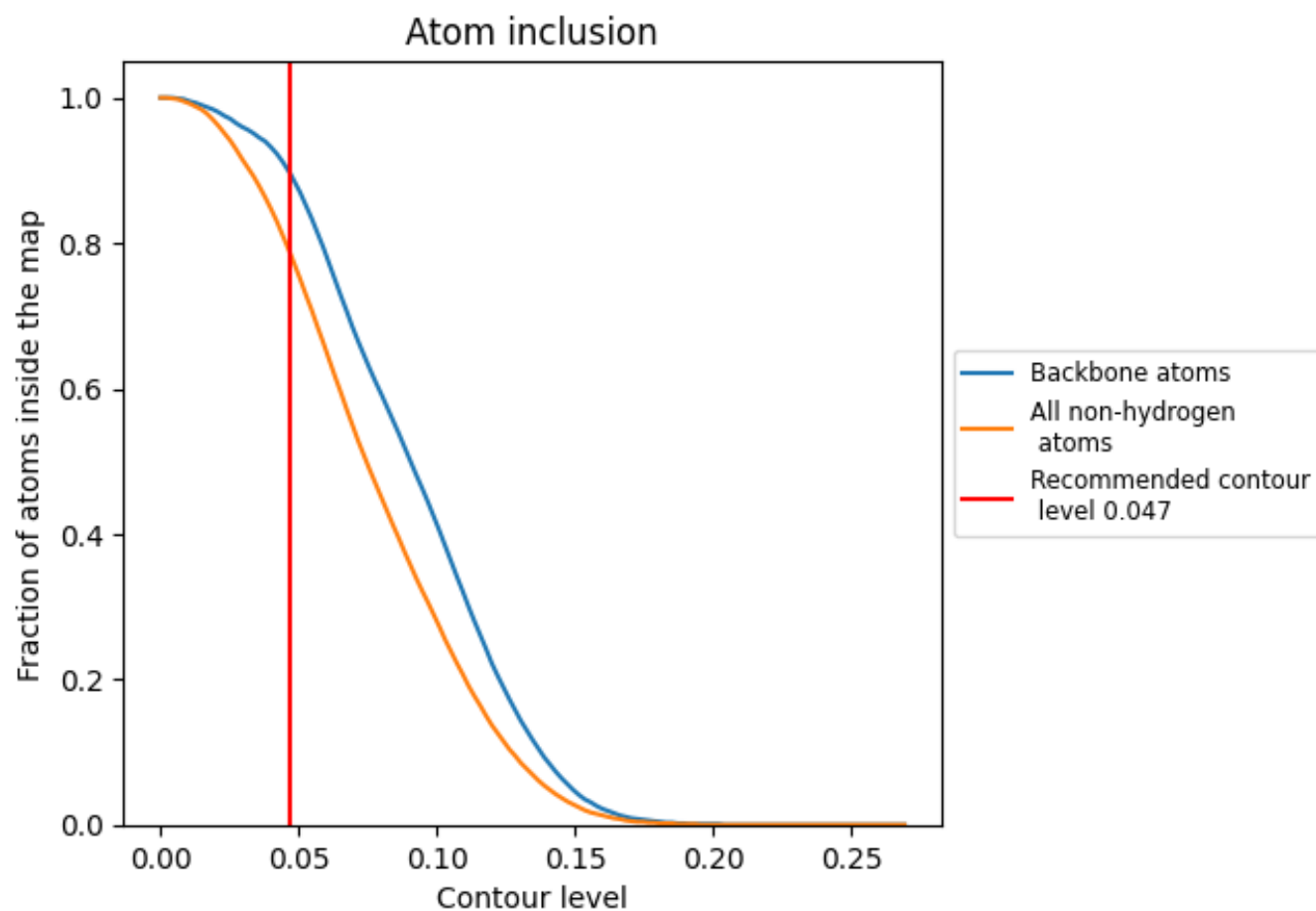
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.047).

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 78% 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 (0.047) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7850	0.4810
A	0.7820	0.4790
B	0.8660	0.5590
G	0.7830	0.4800
H	0.8690	0.5620
M	0.7830	0.4800
N	0.8690	0.5600
S	0.7820	0.4790
T	0.8680	0.5630

1.0

0.0

<0.0