



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:27 PM UTC

PDB ID : 6IRA / pdb_00006ira
EMDB ID : EMD-9714
Title : Structure of the human GluN1/GluN2A NMDA receptor in the glutamate/glutamate-bound state at pH 7.8
Authors : Zhang, J.; Chang, S.; Zhang, X.; Zhu, S.
Deposited on : 2018-11-12
Resolution : 4.50 Å (reported)
Based on initial models : 4PE5, 5TQ0, 5H8F

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

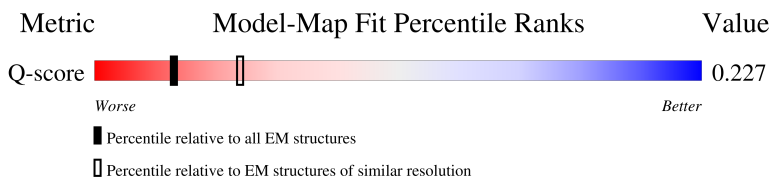
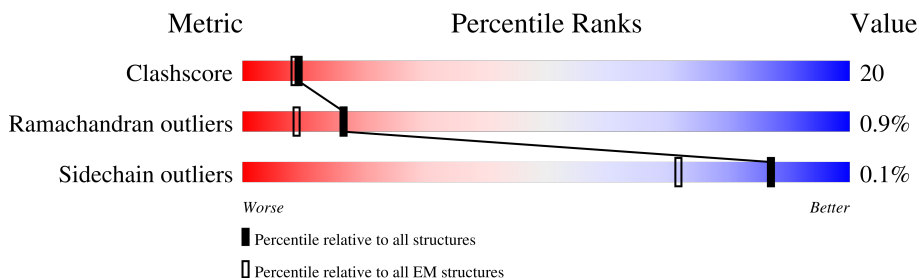
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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

Mol	Chain	Length	Quality of chain
1	B	853	34% 62% 25% 12%
1	D	853	38% 62% 25% 12%
2	A	847	39% 64% 27% 7%
2	C	847	39% 65% 26% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 23932 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 Glutamate receptor ionotropic, NMDA 2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	751	Total	C	N	O	S	1	0
			5791	3744	949	1062	36		
1	B	751	Total	C	N	O	S	1	0
			5791	3744	949	1062	36		

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	656	ARG	GLU	engineered mutation	UNP Q12879
D	657	ARG	GLU	engineered mutation	UNP Q12879
D	843	LYS	-	expression tag	UNP Q12879
D	844	SER	-	expression tag	UNP Q12879
D	845	ARG	-	expression tag	UNP Q12879
D	846	ALA	-	expression tag	UNP Q12879
D	847	GLU	-	expression tag	UNP Q12879
D	848	ALA	-	expression tag	UNP Q12879
D	849	LYS	-	expression tag	UNP Q12879
D	850	ARG	-	expression tag	UNP Q12879
D	851	MET	-	expression tag	UNP Q12879
D	852	LYS	-	expression tag	UNP Q12879
D	853	GLY	-	expression tag	UNP Q12879
B	656	ARG	GLU	engineered mutation	UNP Q12879
B	657	ARG	GLU	engineered mutation	UNP Q12879
B	843	LYS	-	expression tag	UNP Q12879
B	844	SER	-	expression tag	UNP Q12879
B	845	ARG	-	expression tag	UNP Q12879
B	846	ALA	-	expression tag	UNP Q12879
B	847	GLU	-	expression tag	UNP Q12879
B	848	ALA	-	expression tag	UNP Q12879
B	849	LYS	-	expression tag	UNP Q12879
B	850	ARG	-	expression tag	UNP Q12879
B	851	MET	-	expression tag	UNP Q12879
B	852	LYS	-	expression tag	UNP Q12879
B	853	GLY	-	expression tag	UNP Q12879

- Molecule 2 is a protein called Glutamate receptor ionotropic, NMDA 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	789	Total	C	N	O	S	1	0
			6175	3935	1071	1134	35		
2	C	789	Total	C	N	O	S	1	0
			6175	3935	1071	1134	35		

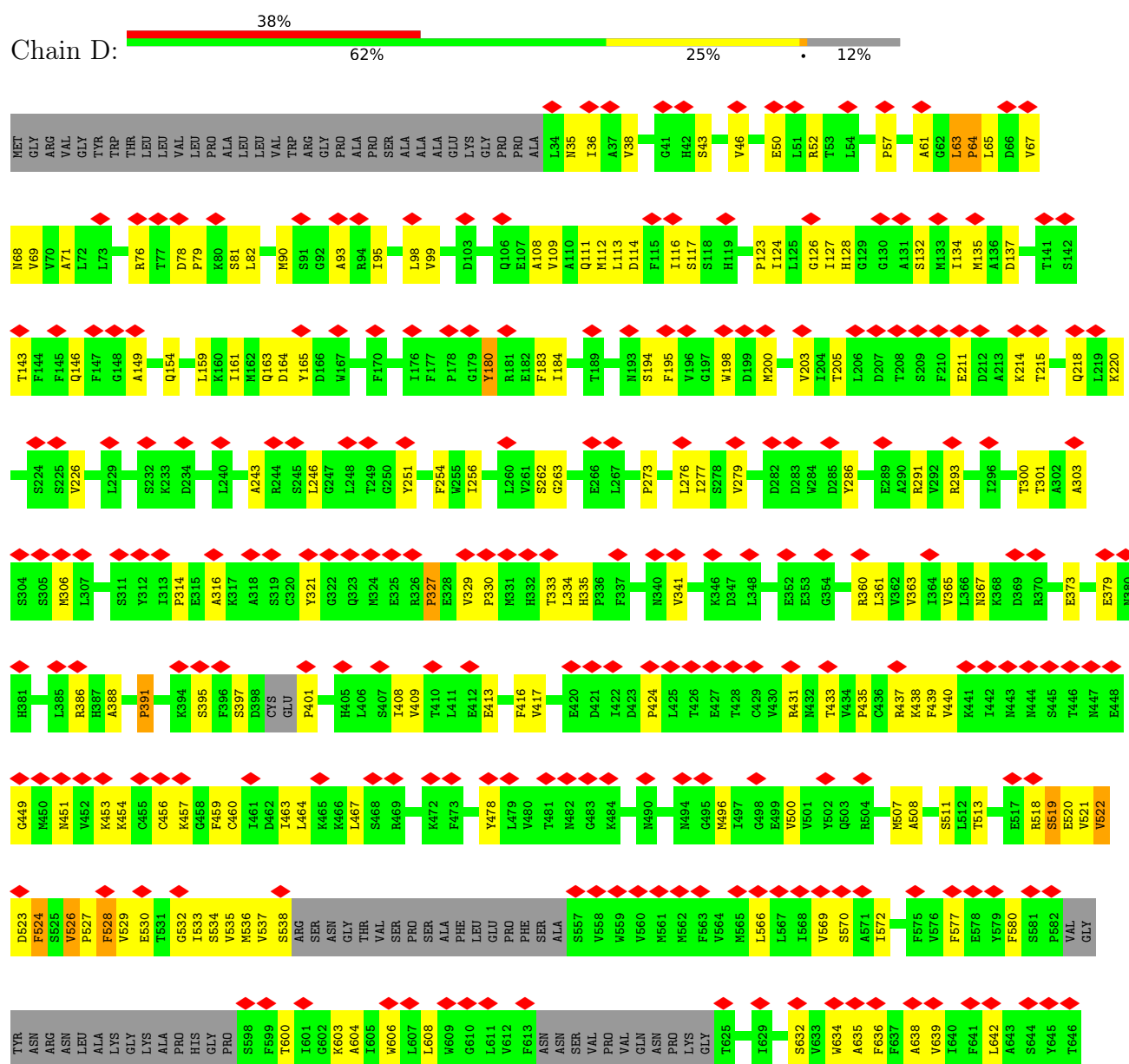
There are 2 discrepancies between the modelled and reference sequences:

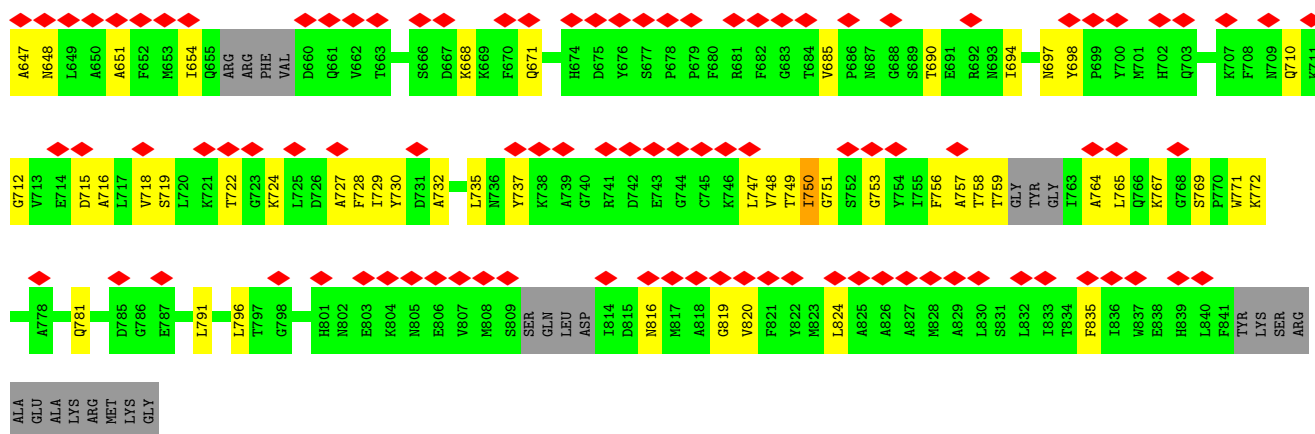
Chain	Residue	Modelled	Actual	Comment	Reference
A	612	ARG	GLY	engineered mutation	UNP Q05586
C	612	ARG	GLY	engineered mutation	UNP Q05586

3 Residue-property plots [i](#)

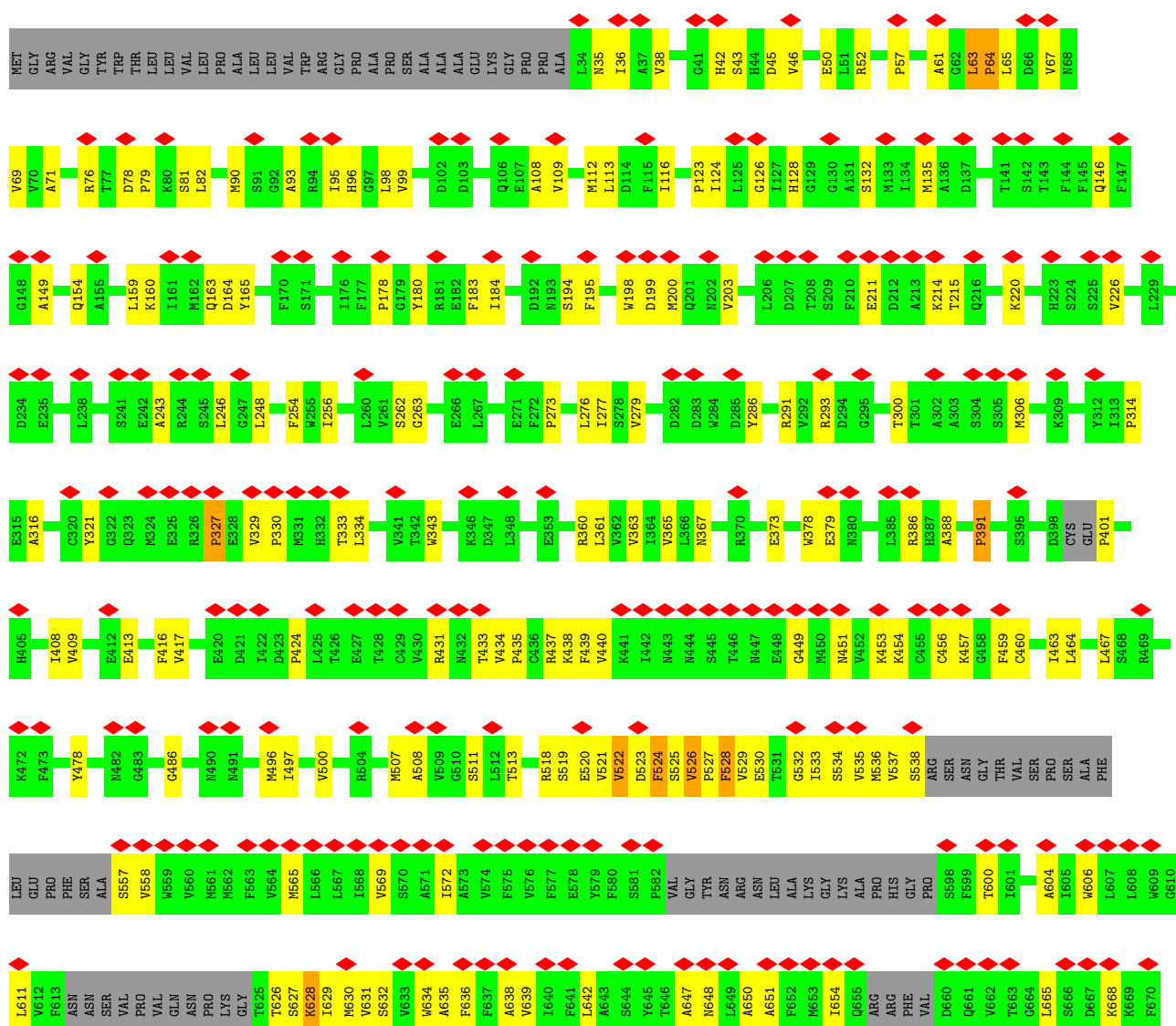
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

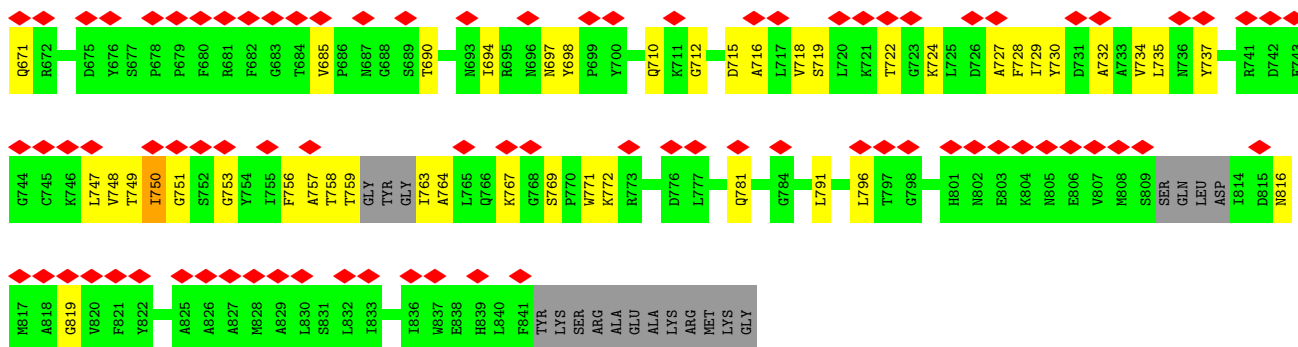
- Molecule 1: Glutamate receptor ionotropic, NMDA 2A



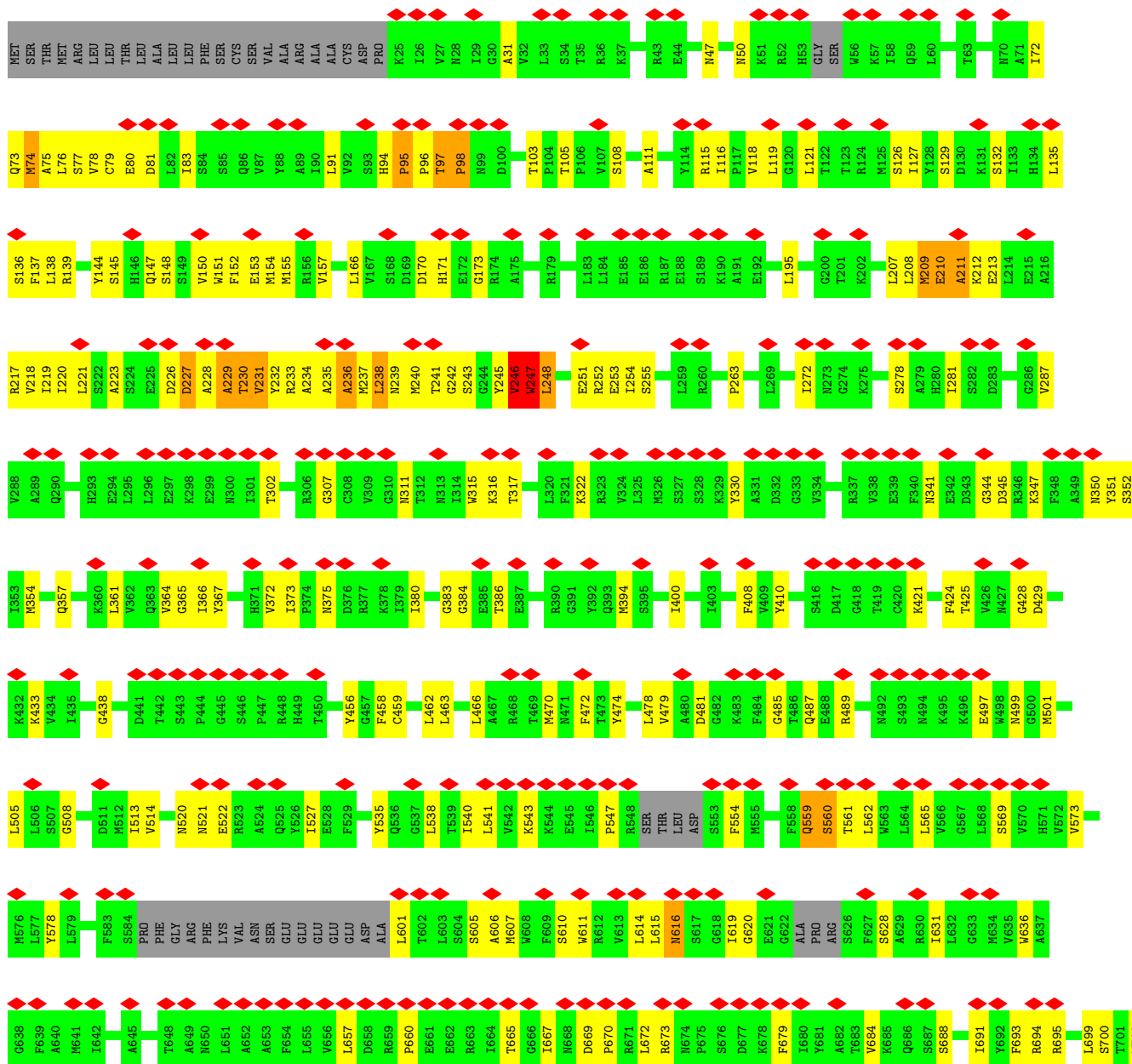
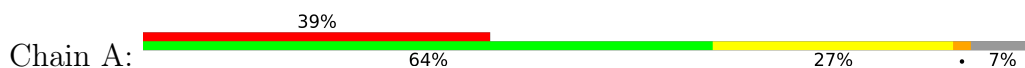


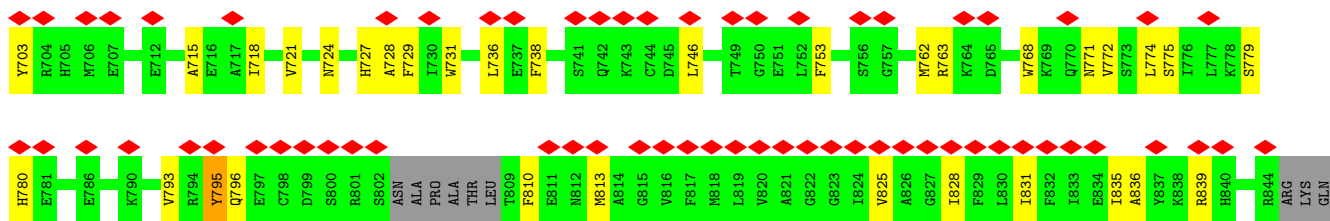
• Molecule 1: Glutamate receptor ionotropic, NMDA 2A



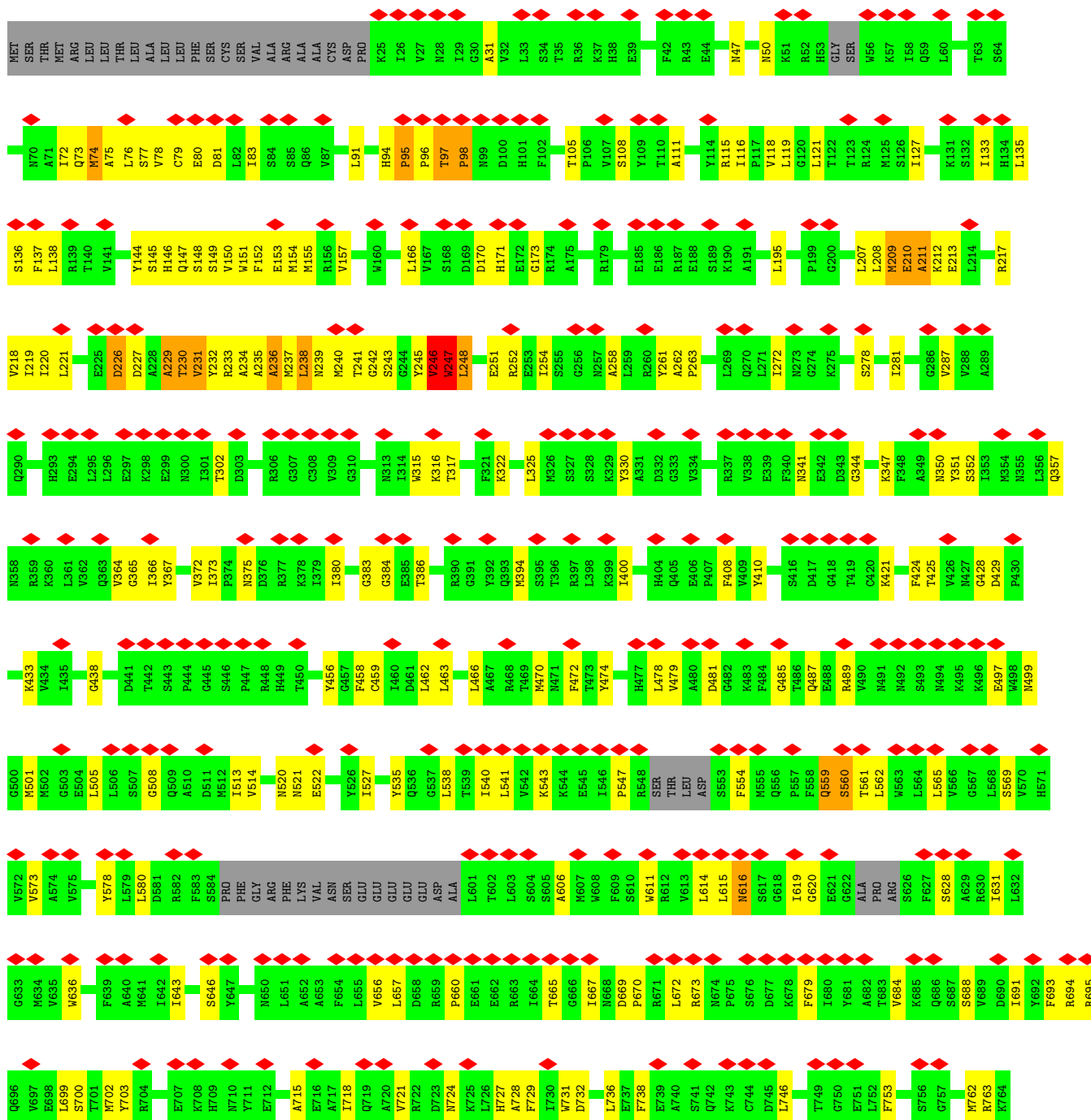


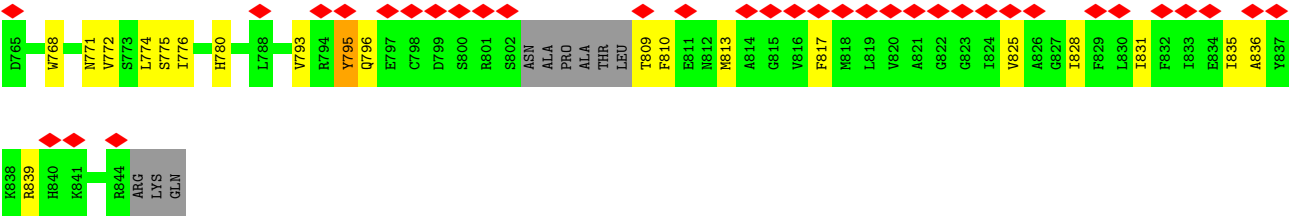
• Molecule 2: Glutamate receptor ionotropic, NMDA 1





• Molecule 2: Glutamate receptor ionotropic, NMDA 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	131990	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 ($e^-/\text{\AA}^2$)	63	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	17.068	Depositor
Minimum map value	-9.414	Depositor
Average map value	0.018	Depositor
Map value standard deviation	1.311	Depositor
Recommended contour level	5.05	Depositor
Map size ($\text{\AA}$)	242.4, 242.4, 242.4	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.01, 1.01, 1.01	Depositor

5 Model quality

5.1 Standard geometry

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	B	0.50	3/5921 (0.1%)	0.93	33/8037 (0.4%)
1	D	0.50	4/5921 (0.1%)	0.92	27/8037 (0.3%)
2	A	0.44	1/6304 (0.0%)	0.93	29/8531 (0.3%)
2	C	0.44	1/6304 (0.0%)	0.92	27/8531 (0.3%)
All	All	0.47	9/24450 (0.0%)	0.93	116/33136 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	7
1	D	0	4
2	A	0	3
2	C	0	3
All	All	0	17

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	628	LYS	C-N	8.54	1.45	1.33
1	B	753	GLY	C-N	7.85	1.44	1.33
1	D	753	GLY	C-N	7.84	1.44	1.33
1	D	519	SER	C-N	-7.76	1.23	1.33
2	A	230	THR	N-CA	-7.04	1.38	1.46
1	D	750	ILE	N-CA	-6.60	1.38	1.46
1	B	750	ILE	N-CA	-6.60	1.38	1.46
2	C	230	THR	N-CA	-5.56	1.39	1.46
1	D	68	ASN	C-N	5.07	1.40	1.33

All (116) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	246	VAL	O-C-N	-24.02	97.69	122.67
2	A	246	VAL	O-C-N	-24.01	97.70	122.67
1	B	64	PRO	N-CA-C	-13.35	94.97	113.53
1	D	64	PRO	N-CA-C	-13.35	94.98	113.53
2	A	559	GLN	N-CA-C	11.79	124.70	110.91
2	C	559	GLN	N-CA-C	11.69	124.58	110.91
1	D	424	PRO	N-CA-CB	11.20	110.26	102.65
1	B	424	PRO	N-CA-CB	11.20	110.26	102.65
2	A	230	THR	N-CA-C	-9.86	99.28	111.11
2	C	247	TRP	O-C-N	-9.69	113.74	123.62
2	A	247	TRP	O-C-N	-9.64	113.78	123.62
2	A	95	PRO	N-CA-CB	9.63	112.42	103.08
2	C	95	PRO	N-CA-CB	9.61	112.40	103.08
1	D	63	LEU	CA-C-N	9.30	129.37	119.05
1	D	63	LEU	C-N-CA	9.30	129.37	119.05
2	C	619	ILE	N-CA-C	-9.27	104.00	112.90
2	A	619	ILE	N-CA-C	-9.26	104.01	112.90
1	B	63	LEU	CA-C-N	9.24	129.31	119.05
1	B	63	LEU	C-N-CA	9.24	129.31	119.05
1	D	753	GLY	O-C-N	-8.86	110.57	122.35
1	B	753	GLY	O-C-N	-8.82	110.61	122.35
1	B	526	VAL	N-CA-C	-8.35	100.77	108.95
1	D	526	VAL	N-CA-C	-8.31	100.80	108.95
2	C	209	MET	O-C-N	8.02	130.75	122.09
2	A	209	MET	O-C-N	7.95	130.68	122.09
1	B	528	PHE	N-CA-C	7.95	119.72	111.14
1	D	528	PHE	N-CA-C	7.92	119.69	111.14
1	D	526	VAL	CA-C-N	7.61	128.07	119.93
1	D	526	VAL	C-N-CA	7.61	128.07	119.93
1	B	526	VAL	CA-C-N	7.45	127.90	119.93
1	B	526	VAL	C-N-CA	7.45	127.90	119.93
1	B	401	PRO	N-CA-CB	7.31	111.04	103.00
1	D	401	PRO	N-CA-CB	7.28	111.00	103.00
1	D	61	ALA	N-CA-C	7.18	121.30	111.17
2	C	96	PRO	N-CA-CB	7.18	110.79	103.25
2	A	96	PRO	N-CA-CB	7.17	110.78	103.25
1	B	61	ALA	N-CA-C	7.17	121.28	111.17
1	D	327	PRO	N-CA-CB	7.13	110.73	103.25
1	D	330	PRO	N-CA-CB	7.11	110.07	103.46
1	B	327	PRO	N-CA-CB	7.06	110.66	103.25
1	B	330	PRO	N-CA-CB	7.05	110.02	103.46
1	B	391	PRO	N-CA-CB	7.01	110.61	103.25
1	D	391	PRO	N-CA-CB	6.97	110.57	103.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	547	PRO	N-CA-CB	6.97	110.70	103.38
2	A	210	GLU	N-CA-C	-6.95	96.00	110.80
2	A	547	PRO	N-CA-CB	6.95	110.67	103.38
2	C	210	GLU	N-CA-C	-6.94	96.01	110.80
2	A	660	PRO	N-CA-CB	6.93	110.53	103.25
2	C	660	PRO	N-CA-CB	6.93	110.53	103.25
2	C	246	VAL	CA-C-N	6.88	130.97	121.33
2	C	246	VAL	C-N-CA	6.88	130.97	121.33
2	A	246	VAL	CA-C-N	6.88	130.96	121.33
2	A	246	VAL	C-N-CA	6.88	130.96	121.33
2	A	246	VAL	CB-CA-C	-6.68	101.97	111.40
2	C	246	VAL	CB-CA-C	-6.68	101.98	111.40
1	D	63	LEU	N-CA-C	-6.61	99.78	109.50
1	B	63	LEU	N-CA-C	-6.61	99.79	109.50
1	D	57	PRO	N-CA-CB	6.60	110.07	102.88
1	D	636	PHE	CB-CA-C	6.60	122.06	110.85
1	B	57	PRO	N-CA-CB	6.59	110.06	102.88
1	B	636	PHE	CB-CA-C	6.57	122.02	110.85
2	A	98	PRO	N-CA-CB	6.40	109.97	103.25
2	C	98	PRO	N-CA-CB	6.37	109.94	103.25
1	B	43	SER	N-CA-C	-6.25	101.31	108.49
2	A	227	ASP	N-CA-CB	-6.06	101.22	110.01
1	B	628	LYS	CA-C-N	-6.06	110.85	120.55
1	B	628	LYS	C-N-CA	-6.06	110.85	120.55
2	A	231	VAL	N-CA-C	5.99	116.77	110.72
2	C	229	ALA	N-CA-C	-5.96	104.78	111.28
1	B	135	MET	N-CA-C	-5.91	104.61	112.94
2	A	229	ALA	N-CA-C	-5.90	104.85	111.28
2	A	234	ALA	CA-C-N	-5.90	112.42	120.44
2	A	234	ALA	C-N-CA	-5.90	112.42	120.44
1	B	628	LYS	O-C-N	5.88	128.91	122.20
2	C	231	VAL	CA-C-N	5.83	128.03	120.44
2	C	231	VAL	C-N-CA	5.83	128.03	120.44
1	D	524	PHE	N-CA-C	5.79	118.20	109.23
1	B	524	PHE	N-CA-C	5.79	118.20	109.23
2	C	231	VAL	CB-CA-C	-5.78	104.25	112.22
1	D	64	PRO	CA-C-O	5.68	128.73	119.86
2	A	236	ALA	CA-C-N	-5.66	113.08	120.44
2	A	236	ALA	C-N-CA	-5.66	113.08	120.44
1	B	64	PRO	CA-C-O	5.66	128.69	119.86
2	C	236	ALA	CA-C-N	-5.66	113.08	120.44
2	C	236	ALA	C-N-CA	-5.66	113.08	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	97	THR	CA-C-N	5.61	126.85	119.84
2	C	97	THR	C-N-CA	5.61	126.85	119.84
2	A	97	THR	CA-C-N	5.60	126.83	119.84
2	A	97	THR	C-N-CA	5.60	126.83	119.84
1	D	43	SER	N-CA-C	-5.56	102.10	108.49
1	D	135	MET	N-CA-C	-5.52	104.80	113.02
2	A	227	ASP	CB-CA-C	-5.47	102.28	110.88
2	A	246	VAL	N-CA-C	5.46	115.51	107.75
2	C	246	VAL	N-CA-C	5.46	115.51	107.75
1	B	520	GLU	CA-C-N	-5.41	116.19	122.63
1	B	520	GLU	C-N-CA	-5.41	116.19	122.63
1	D	520	GLU	CA-C-N	-5.41	116.19	122.63
1	D	520	GLU	C-N-CA	-5.41	116.19	122.63
1	B	819	GLY	CA-C-N	5.39	128.13	120.53
1	B	819	GLY	C-N-CA	5.39	128.13	120.53
2	A	229	ALA	O-C-N	5.33	127.77	122.12
2	C	234	ALA	N-CA-C	5.27	117.02	111.28
1	D	361	LEU	N-CA-C	5.22	117.02	110.91
1	B	45	ASP	N-CA-C	5.20	117.44	109.95
2	C	554	PHE	N-CA-C	5.20	115.24	108.07
2	A	554	PHE	N-CA-C	5.19	115.24	108.07
2	A	620	GLY	N-CA-C	5.18	119.19	112.25
2	C	620	GLY	N-CA-C	5.18	119.19	112.25
2	C	230	THR	N-CA-CB	-5.13	101.82	110.49
1	D	819	GLY	CA-C-N	5.09	127.71	120.53
1	D	819	GLY	C-N-CA	5.09	127.71	120.53
1	D	522	VAL	N-CA-C	5.03	117.06	108.86
1	B	361	LEU	N-CA-C	5.03	116.79	110.91
1	B	522	VAL	N-CA-C	5.03	117.05	108.86
1	B	42	HIS	CA-C-N	5.01	128.98	120.81
1	B	42	HIS	C-N-CA	5.01	128.98	120.81

There are no chirality outliers.

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	247	TRP	Mainchain
2	A	248	LEU	Peptide
2	A	795	TYR	Peptide
1	B	165	TYR	Peptide
1	B	199	ASP	Peptide
1	B	200	MET	Peptide

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Mol	Chain	Res	Type	Group
1	B	333	THR	Peptide
1	B	343	TRP	Peptide
1	B	611	LEU	Peptide
1	B	628	LYS	Mainchain
2	C	247	TRP	Mainchain
2	C	248	LEU	Peptide
2	C	795	TYR	Peptide
1	D	165	TYR	Peptide
1	D	180	TYR	Peptide
1	D	200	MET	Peptide
1	D	333	THR	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	B	5791	0	5617	262	0
1	D	5791	0	5617	259	0
2	A	6175	0	6111	242	0
2	C	6175	0	6110	248	0
All	All	23932	0	23455	967	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 20.

All (967) 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:D:522:VAL:CG1	1:D:765:LEU:O	1.70	1.37
1:B:533:ILE:CG1	1:B:757:ALA:HB3	1.58	1.33
2:A:208:LEU:O	2:A:211:ALA:HB3	1.19	1.33
1:B:63:LEU:HD21	1:B:300:THR:CB	1.58	1.33
2:A:227:ASP:O	2:A:230:THR:HB	1.25	1.32
1:D:63:LEU:HD21	1:D:300:THR:CB	1.57	1.32
1:B:63:LEU:HD11	1:B:300:THR:CG2	1.60	1.31
1:D:533:ILE:CG1	1:D:757:ALA:HB3	1.58	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:63:LEU:HD11	1:D:300:THR:CG2	1.63	1.26
2:A:218:VAL:CA	2:A:246:VAL:HG21	1.64	1.26
2:C:218:VAL:CA	2:C:246:VAL:HG21	1.64	1.25
2:C:208:LEU:O	2:C:211:ALA:HB3	1.19	1.25
2:C:243:SER:HB3	2:C:384:GLY:N	1.51	1.24
2:C:218:VAL:HA	2:C:246:VAL:CG2	1.69	1.22
2:A:243:SER:HB3	2:A:384:GLY:N	1.51	1.22
1:D:63:LEU:CD2	1:D:300:THR:HB	1.69	1.22
1:B:63:LEU:CD2	1:B:300:THR:HB	1.68	1.22
2:A:218:VAL:HA	2:A:246:VAL:CG2	1.69	1.21
1:B:536:MET:O	1:B:727:ALA:HB1	1.08	1.21
2:C:227:ASP:O	2:C:230:THR:HB	1.32	1.21
1:D:536:MET:O	1:D:727:ALA:HB1	1.04	1.19
1:D:63:LEU:CD1	1:D:67:VAL:HG21	1.74	1.18
2:A:217:ARG:O	2:A:246:VAL:HG23	1.44	1.17
1:B:526:VAL:CG1	1:B:527:PRO:HD2	1.74	1.17
1:D:63:LEU:CD1	1:D:300:THR:HG22	1.75	1.17
1:B:63:LEU:CD1	1:B:67:VAL:HG21	1.74	1.17
2:A:207:LEU:O	2:A:210:GLU:HB3	1.45	1.16
1:D:526:VAL:CG1	1:D:527:PRO:HD2	1.75	1.15
1:D:816:ASN:ND2	2:C:559:GLN:HE22	1.45	1.15
2:C:217:ARG:O	2:C:246:VAL:HG23	1.44	1.15
2:A:559:GLN:HE22	1:B:816:ASN:ND2	1.46	1.14
1:D:535:VAL:HG22	1:D:729:ILE:CG1	1.75	1.14
1:D:63:LEU:HD12	1:D:67:VAL:HG21	1.15	1.13
2:A:243:SER:CB	2:A:384:GLY:H	1.61	1.13
2:C:207:LEU:O	2:C:210:GLU:HB3	1.45	1.13
2:C:243:SER:CB	2:C:384:GLY:H	1.62	1.13
1:B:63:LEU:CD1	1:B:300:THR:HG22	1.79	1.12
1:B:535:VAL:HG22	1:B:729:ILE:HG12	1.15	1.12
1:B:536:MET:HA	1:B:749:THR:HA	1.14	1.12
1:B:63:LEU:HD12	1:B:67:VAL:CG2	1.82	1.10
1:D:536:MET:O	1:D:727:ALA:CB	2.00	1.10
1:D:536:MET:HA	1:D:749:THR:HA	1.13	1.10
1:D:522:VAL:HG13	1:D:765:LEU:O	1.33	1.09
2:A:246:VAL:O	2:A:247:TRP:CD1	2.05	1.09
2:C:246:VAL:O	2:C:247:TRP:CD1	2.05	1.09
2:A:223:ALA:HB1	2:A:227:ASP:OD2	1.52	1.09
1:D:63:LEU:HD12	1:D:67:VAL:CG2	1.82	1.09
1:D:533:ILE:CG2	1:D:729:ILE:CG2	2.30	1.09
1:B:63:LEU:HD12	1:B:67:VAL:HG21	1.15	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:533:ILE:HG12	1:B:757:ALA:HB3	1.10	1.08
1:D:535:VAL:HG22	1:D:729:ILE:HG12	1.08	1.07
2:C:243:SER:CA	2:C:383:GLY:HA3	1.84	1.07
1:B:463:ILE:HD13	1:B:528:PHE:CE2	1.90	1.06
2:A:243:SER:CA	2:A:383:GLY:HA3	1.84	1.06
1:B:536:MET:O	1:B:727:ALA:CB	2.03	1.06
2:A:228:ALA:HB1	2:A:232:TYR:CE2	1.91	1.06
2:A:217:ARG:O	2:A:246:VAL:CG2	2.03	1.06
2:C:217:ARG:O	2:C:246:VAL:CG2	2.03	1.05
2:A:243:SER:HA	2:A:383:GLY:HA3	1.37	1.05
1:D:533:ILE:HG12	1:D:757:ALA:HB3	1.10	1.05
2:C:243:SER:HA	2:C:383:GLY:HA3	1.37	1.04
1:D:526:VAL:HG13	1:D:527:PRO:HD2	1.39	1.04
2:C:229:ALA:O	2:C:233:ARG:N	1.91	1.03
1:D:533:ILE:HG12	1:D:757:ALA:CB	1.90	1.02
1:B:529:VAL:CG1	1:B:530:GLU:H	1.71	1.02
1:D:463:ILE:HD13	1:D:528:PHE:CE2	1.94	1.02
2:C:232:TYR:CE2	2:C:262:ALA:N	2.29	1.01
1:D:529:VAL:CG1	1:D:530:GLU:H	1.71	1.01
1:B:521:VAL:O	1:B:767:LYS:HE3	1.60	1.00
2:C:219:ILE:H	2:C:246:VAL:CG1	1.73	1.00
1:D:536:MET:HA	1:D:749:THR:CA	1.91	1.00
1:D:521:VAL:O	1:D:767:LYS:HE3	1.59	1.00
1:B:533:ILE:HG12	1:B:757:ALA:CB	1.90	1.00
1:B:526:VAL:HG13	1:B:527:PRO:HD2	1.38	0.99
1:B:536:MET:HA	1:B:749:THR:CA	1.92	0.99
2:A:226:ASP:O	2:A:230:THR:OG1	1.79	0.99
2:A:219:ILE:H	2:A:246:VAL:CG1	1.74	0.98
1:B:533:ILE:CG2	1:B:729:ILE:CG2	2.40	0.98
2:A:615:LEU:O	2:A:616:ASN:HB2	1.63	0.98
1:B:529:VAL:CG1	1:B:530:GLU:N	2.26	0.98
2:A:218:VAL:HA	2:A:246:VAL:HG21	1.00	0.98
2:A:208:LEU:O	2:A:211:ALA:CB	2.12	0.97
2:C:218:VAL:HA	2:C:246:VAL:HG21	1.00	0.97
2:C:208:LEU:O	2:C:211:ALA:CB	2.12	0.97
2:C:615:LEU:O	2:C:616:ASN:HB2	1.64	0.97
1:B:533:ILE:N	1:B:756:PHE:O	1.97	0.96
1:D:533:ILE:HD11	1:D:690:THR:HG22	1.47	0.96
1:B:535:VAL:HG22	1:B:729:ILE:CG1	1.95	0.96
1:D:533:ILE:N	1:D:756:PHE:O	1.97	0.96
1:D:522:VAL:HG11	1:D:765:LEU:O	1.64	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:246:VAL:O	2:A:247:TRP:CG	2.20	0.95
1:D:537:VAL:O	1:D:748:VAL:O	1.85	0.94
1:D:535:VAL:CG2	1:D:729:ILE:HG12	1.97	0.94
1:D:529:VAL:HG12	1:D:530:GLU:N	1.80	0.94
1:B:533:ILE:CG1	1:B:757:ALA:CB	2.45	0.94
2:C:227:ASP:O	2:C:231:VAL:HG23	1.66	0.94
1:B:529:VAL:HG12	1:B:530:GLU:N	1.80	0.94
1:B:537:VAL:O	1:B:748:VAL:O	1.85	0.93
2:C:243:SER:HB3	2:C:384:GLY:H	1.09	0.93
2:C:232:TYR:CZ	2:C:262:ALA:N	2.27	0.93
1:D:529:VAL:CG1	1:D:530:GLU:N	2.26	0.93
2:C:246:VAL:O	2:C:247:TRP:CG	2.20	0.93
1:B:463:ILE:HD11	1:B:528:PHE:CZ	2.03	0.93
1:D:816:ASN:HD21	2:C:559:GLN:HE22	1.11	0.92
2:A:228:ALA:O	2:A:232:TYR:N	2.03	0.92
2:A:559:GLN:HE22	1:B:816:ASN:HD21	1.04	0.92
1:D:533:ILE:CG1	1:D:757:ALA:CB	2.45	0.91
2:C:219:ILE:H	2:C:246:VAL:HG11	1.30	0.91
2:A:219:ILE:H	2:A:246:VAL:HG11	1.31	0.91
1:D:529:VAL:HG13	1:D:530:GLU:H	1.35	0.91
1:D:533:ILE:HG22	1:D:729:ILE:CG2	2.00	0.91
2:C:615:LEU:O	2:C:616:ASN:CB	2.17	0.91
1:B:536:MET:CB	1:B:749:THR:HG22	2.01	0.91
1:D:536:MET:CB	1:D:749:THR:HG22	2.01	0.90
2:A:227:ASP:O	2:A:230:THR:CB	2.18	0.90
2:A:228:ALA:HB1	2:A:232:TYR:HE2	1.34	0.90
1:B:529:VAL:HG13	1:B:530:GLU:H	1.34	0.90
2:A:615:LEU:O	2:A:616:ASN:CB	2.16	0.89
1:D:63:LEU:CD1	1:D:67:VAL:CG2	2.47	0.89
2:A:218:VAL:HA	2:A:246:VAL:CB	2.03	0.89
2:C:229:ALA:CA	2:C:232:TYR:HB3	2.03	0.89
1:B:533:ILE:HD11	1:B:690:THR:HG22	1.53	0.89
2:C:219:ILE:N	2:C:246:VAL:HG11	1.87	0.89
2:A:227:ASP:O	2:A:231:VAL:HG23	1.74	0.88
1:B:533:ILE:HB	1:B:756:PHE:O	1.74	0.88
1:B:463:ILE:CD1	1:B:528:PHE:CZ	2.57	0.88
2:A:559:GLN:NE2	1:B:816:ASN:HD21	1.71	0.88
1:D:526:VAL:HG12	1:D:527:PRO:HD2	1.55	0.87
1:D:533:ILE:HB	1:D:756:PHE:O	1.73	0.87
2:A:243:SER:HB3	2:A:384:GLY:H	1.09	0.87
1:D:463:ILE:HD11	1:D:528:PHE:CZ	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:500:VAL:HG11	1:B:522:VAL:HG21	1.54	0.87
1:D:533:ILE:HG23	1:D:729:ILE:HG22	1.56	0.87
2:C:218:VAL:HA	2:C:246:VAL:CB	2.03	0.87
2:A:219:ILE:N	2:A:246:VAL:HG11	1.88	0.87
2:A:211:ALA:CB	2:A:240:MET:HE1	2.05	0.86
1:B:63:LEU:CD1	1:B:67:VAL:CG2	2.47	0.86
1:B:526:VAL:HG12	1:B:527:PRO:HD2	1.54	0.86
1:B:64:PRO:CD	1:B:65:LEU:H	1.89	0.86
1:B:534:SER:HB2	1:B:732:ALA:CB	2.05	0.86
1:D:816:ASN:HD21	2:C:559:GLN:NE2	1.71	0.86
2:A:77:SER:O	2:A:81:ASP:HB2	1.77	0.85
1:D:536:MET:CA	1:D:749:THR:HA	2.05	0.85
1:B:535:VAL:HB	1:B:750:ILE:HB	1.57	0.85
1:D:536:MET:HB2	1:D:749:THR:HG22	1.57	0.85
2:C:211:ALA:CB	2:C:240:MET:HE1	2.06	0.85
1:D:535:VAL:HB	1:D:750:ILE:HD13	1.58	0.85
2:A:466:LEU:O	2:A:470:MET:HB2	1.77	0.85
1:D:535:VAL:HB	1:D:750:ILE:HB	1.57	0.85
1:B:535:VAL:HB	1:B:750:ILE:HD13	1.59	0.84
1:B:536:MET:HB2	1:B:749:THR:HG22	1.58	0.84
2:C:77:SER:O	2:C:81:ASP:HB2	1.77	0.84
1:D:533:ILE:CG2	1:D:729:ILE:HG21	2.07	0.84
2:C:466:LEU:O	2:C:470:MET:HB2	1.77	0.84
1:D:463:ILE:CD1	1:D:528:PHE:CZ	2.61	0.84
1:D:534:SER:O	1:D:729:ILE:HA	1.76	0.84
1:B:536:MET:CA	1:B:749:THR:HA	2.06	0.84
1:D:535:VAL:H	1:D:750:ILE:CG2	1.90	0.83
1:D:816:ASN:CG	2:C:559:GLN:HE22	1.84	0.83
1:D:533:ILE:CD1	1:D:690:THR:HG22	2.08	0.83
1:B:63:LEU:HD11	1:B:300:THR:HG22	0.85	0.83
1:D:533:ILE:HG23	1:D:729:ILE:CG2	2.05	0.82
1:B:463:ILE:HD13	1:B:528:PHE:HE2	1.41	0.82
1:B:463:ILE:HD11	1:B:528:PHE:HZ	1.39	0.82
2:C:232:TYR:CE2	2:C:261:TYR:C	2.56	0.82
1:D:816:ASN:ND2	2:C:559:GLN:NE2	2.25	0.82
1:B:535:VAL:H	1:B:750:ILE:CG2	1.92	0.81
1:D:64:PRO:CD	1:D:65:LEU:H	1.89	0.81
2:A:559:GLN:HE22	1:B:816:ASN:CG	1.89	0.81
1:B:519:SER:HA	1:B:524:PHE:HE2	1.45	0.80
1:D:109:VAL:O	1:D:112:MET:HB2	1.80	0.80
1:B:534:SER:O	1:B:729:ILE:HA	1.82	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:565:MET:HG3	2:C:817:PHE:CE1	2.16	0.80
2:A:243:SER:N	2:A:383:GLY:HA3	1.97	0.80
2:A:559:GLN:O	2:A:562:LEU:N	2.15	0.80
1:B:533:ILE:CA	1:B:756:PHE:O	2.30	0.80
1:B:521:VAL:C	1:B:767:LYS:HE3	2.07	0.79
1:D:533:ILE:CB	1:D:756:PHE:O	2.31	0.79
1:B:533:ILE:HG13	1:B:757:ALA:HB3	1.63	0.79
1:D:533:ILE:CA	1:D:756:PHE:O	2.30	0.79
1:D:535:VAL:CA	1:D:750:ILE:HB	2.13	0.78
2:A:235:ALA:O	2:A:238:LEU:N	2.16	0.78
1:B:109:VAL:O	1:B:112:MET:HB2	1.82	0.78
2:C:243:SER:N	2:C:383:GLY:HA3	1.97	0.78
2:A:218:VAL:HA	2:A:246:VAL:HG11	1.66	0.78
1:B:534:SER:HB2	1:B:732:ALA:HB2	1.64	0.78
2:C:235:ALA:O	2:C:238:LEU:N	2.16	0.78
1:B:463:ILE:CD1	1:B:528:PHE:CE2	2.65	0.78
1:B:533:ILE:CB	1:B:756:PHE:O	2.32	0.78
2:C:559:GLN:O	2:C:562:LEU:N	2.15	0.78
1:D:463:ILE:HD11	1:D:528:PHE:HZ	1.47	0.78
1:D:533:ILE:HG13	1:D:757:ALA:HB3	1.63	0.78
1:B:536:MET:HE3	1:B:749:THR:CG2	2.14	0.78
1:B:533:ILE:HG23	1:B:729:ILE:HG22	1.66	0.78
1:B:533:ILE:CD1	1:B:690:THR:HG22	2.14	0.78
1:D:536:MET:HE3	1:D:749:THR:CG2	2.13	0.78
1:D:654:ILE:HG12	2:C:657:LEU:HD11	1.66	0.78
1:B:535:VAL:CA	1:B:750:ILE:HB	2.14	0.78
2:A:559:GLN:NE2	1:B:816:ASN:ND2	2.27	0.77
2:C:227:ASP:C	2:C:230:THR:HB	2.09	0.77
1:B:532:GLY:HA2	1:B:757:ALA:O	1.84	0.77
1:B:533:ILE:HG22	1:B:729:ILE:CG2	2.14	0.77
1:B:533:ILE:HG23	1:B:729:ILE:CG2	2.15	0.77
1:D:532:GLY:HA2	1:D:757:ALA:O	1.84	0.77
1:B:522:VAL:CG1	1:B:523:ASP:N	2.48	0.77
1:D:536:MET:CG	1:D:749:THR:HG22	2.15	0.77
2:A:195:LEU:HD21	2:A:210:GLU:OE2	1.85	0.77
1:B:64:PRO:CG	1:B:65:LEU:H	1.98	0.77
1:D:535:VAL:HG22	1:D:729:ILE:CD1	2.14	0.76
2:C:195:LEU:HD21	2:C:210:GLU:OE2	1.85	0.76
2:C:76:LEU:O	2:C:80:GLU:HB2	1.86	0.76
2:C:226:ASP:O	2:C:230:THR:OG1	2.04	0.76
1:D:522:VAL:CG1	1:D:523:ASP:N	2.48	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:218:VAL:HA	2:C:246:VAL:HG11	1.66	0.76
2:A:235:ALA:O	2:A:236:ALA:C	2.27	0.76
2:C:235:ALA:O	2:C:236:ALA:C	2.27	0.76
1:D:63:LEU:HD21	1:D:300:THR:HB	0.79	0.76
2:C:410:TYR:HB2	2:C:456:TYR:HB2	1.68	0.76
1:D:522:VAL:HG12	1:D:523:ASP:N	2.01	0.75
1:D:64:PRO:CG	1:D:65:LEU:H	1.98	0.75
1:B:536:MET:CG	1:B:749:THR:HG22	2.15	0.75
2:A:410:TYR:HB2	2:A:456:TYR:HB2	1.68	0.75
1:D:535:VAL:HA	1:D:728:PHE:O	1.86	0.75
2:A:223:ALA:CB	2:A:227:ASP:OD2	2.32	0.75
1:B:63:LEU:CD1	1:B:300:THR:CG2	2.53	0.75
1:B:537:VAL:HG12	1:B:727:ALA:CB	2.16	0.75
1:B:537:VAL:HG12	1:B:727:ALA:HB2	1.69	0.75
2:A:352:SER:HA	2:A:365:GLY:O	1.87	0.75
2:C:211:ALA:HB3	2:C:240:MET:HE1	1.69	0.75
1:D:433:THR:HA	1:D:456:CYS:O	1.87	0.74
1:D:500:VAL:HG11	1:D:522:VAL:HG21	1.69	0.74
1:D:463:ILE:CD1	1:D:528:PHE:CE2	2.70	0.74
2:A:76:LEU:O	2:A:80:GLU:HB2	1.86	0.74
1:D:63:LEU:HD11	1:D:300:THR:HG22	0.80	0.74
2:C:352:SER:HA	2:C:365:GLY:O	1.87	0.74
2:A:218:VAL:HA	2:A:246:VAL:CG1	2.17	0.74
2:A:211:ALA:HB3	2:A:240:MET:HE1	1.69	0.74
2:A:540:ILE:HA	2:A:729:PHE:O	1.88	0.73
1:B:522:VAL:O	1:B:524:PHE:CE2	2.41	0.73
1:B:532:GLY:CA	1:B:757:ALA:O	2.36	0.73
2:C:218:VAL:HA	2:C:246:VAL:CG1	2.17	0.73
1:B:533:ILE:HG22	1:B:729:ILE:HG23	1.70	0.73
1:D:533:ILE:HG22	1:D:729:ILE:HG23	1.69	0.73
1:B:522:VAL:HG12	1:B:523:ASP:N	2.01	0.73
1:D:522:VAL:O	1:D:524:PHE:CE2	2.41	0.73
1:D:532:GLY:CA	1:D:757:ALA:O	2.37	0.73
2:A:207:LEU:O	2:A:210:GLU:CB	2.31	0.73
2:C:229:ALA:HA	2:C:232:TYR:HB3	1.69	0.73
1:D:463:ILE:HD13	1:D:528:PHE:HE2	1.49	0.73
1:B:36:ILE:O	1:B:69:VAL:HA	1.87	0.73
1:B:535:VAL:CB	1:B:750:ILE:HB	2.18	0.73
1:D:519:SER:HA	1:D:524:PHE:HE2	1.52	0.73
1:D:535:VAL:CB	1:D:750:ILE:HB	2.17	0.72
1:B:535:VAL:HA	1:B:728:PHE:O	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:535:VAL:CG2	1:B:729:ILE:HG12	2.09	0.72
2:C:540:ILE:HA	2:C:729:PHE:O	1.88	0.72
2:C:195:LEU:CD2	2:C:210:GLU:OE2	2.39	0.71
1:D:534:SER:O	1:D:729:ILE:HG23	1.90	0.71
1:D:408:ILE:HG12	1:D:507:MET:HB2	1.71	0.71
1:D:36:ILE:O	1:D:69:VAL:HA	1.90	0.70
1:D:534:SER:HB2	1:D:732:ALA:CB	2.21	0.70
1:D:600:THR:O	1:D:604:ALA:HB3	1.91	0.70
1:D:211:GLU:HB2	1:D:215:THR:HG23	1.71	0.70
2:A:657:LEU:HD11	1:B:654:ILE:HG12	1.74	0.70
2:C:218:VAL:CG2	2:C:246:VAL:HG21	2.21	0.70
2:A:218:VAL:CB	2:A:246:VAL:HG21	2.21	0.70
1:B:433:THR:HA	1:B:456:CYS:O	1.92	0.70
2:C:170:ASP:HB2	2:C:173:GLY:H	1.56	0.70
2:A:195:LEU:CD2	2:A:210:GLU:OE2	2.39	0.70
1:B:435:PRO:HA	1:B:454:LYS:O	1.92	0.70
2:C:218:VAL:CA	2:C:246:VAL:HG11	2.21	0.70
2:C:479:VAL:HG12	2:C:481:ASP:H	1.57	0.70
1:D:220:LYS:HE2	1:B:220:LYS:HE2	1.73	0.70
1:B:408:ILE:HG12	1:B:507:MET:HB2	1.73	0.70
1:D:537:VAL:HG12	1:D:727:ALA:CB	2.21	0.70
2:C:211:ALA:HB1	2:C:240:MET:HE1	1.73	0.70
2:A:211:ALA:HB1	2:A:240:MET:HE1	1.72	0.69
2:C:229:ALA:O	2:C:233:ARG:CB	2.39	0.69
2:A:218:VAL:CA	2:A:246:VAL:HG11	2.21	0.69
2:C:218:VAL:CB	2:C:246:VAL:HG21	2.21	0.69
2:C:229:ALA:C	2:C:232:TYR:HB3	2.16	0.69
2:C:207:LEU:O	2:C:210:GLU:CB	2.31	0.69
2:A:170:ASP:HB2	2:A:173:GLY:H	1.56	0.69
1:B:113:LEU:O	1:B:116:ILE:HB	1.92	0.69
1:D:211:GLU:HB3	1:D:214:LYS:HB2	1.73	0.69
1:B:211:GLU:HB2	1:B:215:THR:HG23	1.73	0.68
1:B:521:VAL:O	1:B:767:LYS:CE	2.39	0.68
2:A:218:VAL:CG2	2:A:246:VAL:HG21	2.21	0.68
2:C:220:ILE:HG12	2:C:248:LEU:HB2	1.75	0.68
1:D:321:TYR:HE1	2:C:73:GLN:HE21	1.42	0.68
2:A:479:VAL:HG12	2:A:481:ASP:H	1.57	0.68
1:B:211:GLU:HB3	1:B:214:LYS:HB2	1.75	0.68
1:D:526:VAL:CG1	1:D:527:PRO:CD	2.66	0.67
2:A:541:LEU:HD22	2:A:746:LEU:HD22	1.75	0.67
1:B:526:VAL:CG1	1:B:527:PRO:CD	2.66	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:541:LEU:HD22	2:C:746:LEU:HD22	1.75	0.67
2:A:220:ILE:HG12	2:A:248:LEU:HB2	1.75	0.67
1:B:534:SER:CB	1:B:732:ALA:CB	2.72	0.67
2:A:218:VAL:HG22	2:A:246:VAL:CG2	2.25	0.67
1:D:535:VAL:HB	1:D:750:ILE:CD1	2.25	0.67
2:C:218:VAL:HG22	2:C:246:VAL:CG2	2.25	0.67
1:B:306:MET:HE2	1:B:314:PRO:HD3	1.76	0.66
1:D:409:VAL:HG22	1:D:478:TYR:HB2	1.77	0.66
1:B:569:VAL:HG11	1:B:631:VAL:HG13	1.78	0.66
1:D:306:MET:HE2	1:D:314:PRO:HD3	1.76	0.66
2:C:208:LEU:C	2:C:211:ALA:HB3	2.15	0.66
2:A:615:LEU:O	2:A:616:ASN:ND2	2.28	0.66
1:D:438:LYS:O	1:D:451:ASN:HA	1.95	0.65
2:A:119:LEU:HA	2:A:138:LEU:O	1.96	0.65
2:A:242:GLY:O	2:A:245:TYR:HD2	1.79	0.65
2:A:219:ILE:H	2:A:246:VAL:HG12	1.61	0.65
1:B:535:VAL:HB	1:B:750:ILE:CD1	2.26	0.65
2:A:232:TYR:OH	2:A:253:GLU:HB3	1.96	0.65
2:C:242:GLY:O	2:C:245:TYR:HD2	1.80	0.65
1:B:409:VAL:HG22	1:B:478:TYR:HB2	1.78	0.65
1:D:113:LEU:O	1:D:116:ILE:HB	1.97	0.65
2:A:208:LEU:CD1	2:A:238:LEU:HD12	2.27	0.65
1:B:534:SER:HB2	1:B:732:ALA:HB1	1.78	0.65
2:C:119:LEU:HA	2:C:138:LEU:O	1.96	0.65
2:C:144:TYR:O	2:C:147:GLN:HB2	1.96	0.65
2:A:208:LEU:C	2:A:211:ALA:HB3	2.16	0.65
2:C:208:LEU:HB2	2:C:238:LEU:HD13	1.79	0.65
1:D:435:PRO:HA	1:D:454:LYS:O	1.98	0.64
2:C:218:VAL:HG22	2:C:246:VAL:HG21	1.80	0.64
2:A:144:TYR:O	2:A:147:GLN:HB2	1.96	0.64
1:D:648:ASN:O	1:D:651:ALA:HB3	1.97	0.64
2:A:615:LEU:O	2:A:616:ASN:CG	2.40	0.64
1:B:63:LEU:HD21	1:B:300:THR:HB	0.75	0.64
1:B:648:ASN:O	1:B:651:ALA:HB3	1.97	0.64
2:A:218:VAL:HG22	2:A:246:VAL:HG21	1.79	0.64
2:C:208:LEU:CD1	2:C:238:LEU:HD12	2.27	0.64
2:C:611:TRP:HE3	2:C:615:LEU:HD11	1.64	0.64
2:C:615:LEU:O	2:C:616:ASN:ND2	2.30	0.63
1:D:63:LEU:HD21	1:D:300:THR:CA	2.28	0.63
2:C:219:ILE:H	2:C:246:VAL:HG12	1.61	0.63
2:A:208:LEU:HB2	2:A:238:LEU:HD13	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:229:ALA:HA	2:C:232:TYR:CD2	2.33	0.63
1:B:533:ILE:CB	1:B:757:ALA:HB3	2.28	0.63
1:D:64:PRO:CG	1:D:65:LEU:N	2.57	0.63
1:B:64:PRO:CG	1:B:65:LEU:N	2.57	0.63
1:D:64:PRO:HG2	1:D:65:LEU:H	1.63	0.63
1:B:536:MET:HG3	1:B:749:THR:HG22	1.81	0.63
2:C:615:LEU:O	2:C:616:ASN:CG	2.42	0.63
2:A:211:ALA:O	2:A:213:GLU:N	2.32	0.62
1:B:533:ILE:HG13	1:B:757:ALA:CB	2.25	0.62
2:A:243:SER:HB2	2:A:384:GLY:H	1.62	0.62
1:D:367:ASN:ND2	1:D:373:GLU:OE1	2.32	0.62
1:B:98:LEU:HB2	1:B:124:ILE:HG12	1.80	0.62
1:B:533:ILE:CG2	1:B:729:ILE:HG21	2.27	0.62
1:D:496:MET:HE3	1:D:508:ALA:HB1	1.82	0.62
1:B:367:ASN:ND2	1:B:373:GLU:OE1	2.31	0.62
2:A:211:ALA:C	2:A:213:GLU:H	2.08	0.62
2:A:228:ALA:CB	2:A:232:TYR:HE2	2.12	0.62
1:B:64:PRO:HG2	1:B:65:LEU:H	1.63	0.62
2:C:211:ALA:C	2:C:213:GLU:H	2.08	0.62
2:C:836:ALA:HA	2:C:839:ARG:HD2	1.80	0.62
1:B:535:VAL:HB	1:B:750:ILE:CB	2.29	0.62
1:B:639:VAL:O	1:B:642:LEU:HB2	1.98	0.62
2:A:836:ALA:HA	2:A:839:ARG:HD2	1.80	0.62
1:D:38:VAL:HA	1:D:99:VAL:HB	1.81	0.62
1:D:533:ILE:CD1	1:D:690:THR:CG2	2.76	0.62
2:C:810:PHE:H	2:C:813:MET:HB2	1.65	0.62
1:B:534:SER:CB	1:B:732:ALA:HB1	2.30	0.61
1:D:533:ILE:CB	1:D:757:ALA:HB3	2.28	0.61
1:D:536:MET:HG3	1:D:749:THR:HG22	1.81	0.61
2:A:229:ALA:O	2:A:230:THR:C	2.43	0.61
1:B:164:ASP:O	1:B:453:LYS:NZ	2.33	0.61
2:A:611:TRP:HE3	2:A:615:LEU:HD11	1.65	0.61
2:C:211:ALA:O	2:C:213:GLU:N	2.32	0.61
1:D:440:VAL:O	1:D:449:GLY:HA2	2.00	0.61
1:B:440:VAL:O	1:B:449:GLY:HA2	2.01	0.61
1:D:164:ASP:O	1:D:453:LYS:NZ	2.33	0.61
1:D:431:ARG:NH2	2:C:694:ARG:O	2.34	0.60
2:A:380:ILE:HA	2:A:386:THR:HG22	1.83	0.60
2:A:810:PHE:H	2:A:813:MET:HB2	1.65	0.60
1:D:537:VAL:HG12	1:D:727:ALA:HB2	1.82	0.60
2:C:380:ILE:HA	2:C:386:THR:HG22	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:523:ASP:HB3	1:D:772:LYS:HE2	1.83	0.60
2:C:237:MET:C	2:C:239:ASN:H	2.09	0.60
1:D:36:ILE:HB	1:D:69:VAL:HG22	1.84	0.60
1:B:535:VAL:N	1:B:750:ILE:HB	2.17	0.60
1:D:273:PRO:HG2	1:D:276:LEU:HD21	1.83	0.60
1:D:533:ILE:HG13	1:D:757:ALA:CB	2.25	0.60
2:A:240:MET:HA	2:A:245:TYR:CE1	2.37	0.60
1:B:530:GLU:CD	2:C:535:TYR:HB3	2.27	0.60
2:C:350:ASN:HA	2:C:367:TYR:O	2.02	0.60
2:C:543:LYS:NZ	2:C:724:ASN:OD1	2.34	0.60
2:A:543:LYS:NZ	2:A:724:ASN:OD1	2.34	0.60
1:B:534:SER:CB	1:B:732:ALA:HB2	2.30	0.60
1:D:534:SER:HB2	1:D:732:ALA:HB2	1.84	0.60
2:A:350:ASN:HA	2:A:367:TYR:O	2.02	0.60
2:C:243:SER:HB2	2:C:384:GLY:H	1.62	0.60
1:B:256:ILE:HG12	1:B:277:ILE:HB	1.84	0.59
1:D:535:VAL:H	1:D:750:ILE:HG21	1.68	0.59
2:A:438:GLY:HA3	2:A:478:LEU:HD12	1.84	0.59
1:D:63:LEU:HB2	1:D:65:LEU:O	2.03	0.59
1:D:535:VAL:N	1:D:750:ILE:HB	2.16	0.59
2:C:240:MET:HA	2:C:245:TYR:CE1	2.36	0.59
1:D:535:VAL:HB	1:D:750:ILE:CB	2.29	0.59
2:A:208:LEU:HB2	2:A:238:LEU:CD1	2.33	0.59
1:D:63:LEU:HD21	1:D:300:THR:CG2	2.30	0.59
1:D:570:SER:HB3	1:D:608:LEU:HD11	1.83	0.59
2:A:237:MET:C	2:A:239:ASN:H	2.09	0.59
1:D:63:LEU:CD1	1:D:300:THR:CG2	2.55	0.58
1:D:536:MET:CE	1:D:749:THR:CG2	2.81	0.58
1:B:647:ALA:O	1:B:651:ALA:N	2.37	0.58
2:C:438:GLY:HA3	2:C:478:LEU:HD12	1.84	0.58
1:B:64:PRO:HG2	1:B:65:LEU:N	2.18	0.58
1:D:639:VAL:O	1:D:642:LEU:HB2	2.03	0.58
1:B:36:ILE:HB	1:B:69:VAL:HG22	1.85	0.58
1:B:496:MET:HE3	1:B:508:ALA:HB1	1.83	0.58
1:D:536:MET:HA	1:D:749:THR:CB	2.33	0.58
1:B:63:LEU:HB2	1:B:65:LEU:O	2.03	0.58
2:C:208:LEU:HB2	2:C:238:LEU:CD1	2.33	0.58
1:D:46:VAL:O	1:D:50:GLU:N	2.34	0.58
2:A:207:LEU:HA	2:A:210:GLU:OE1	2.03	0.58
2:C:487:GLN:HA	2:C:497:GLU:O	2.04	0.58
2:A:508:GLY:HA2	2:A:763:ARG:HH22	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:694:ARG:O	1:B:431:ARG:NH2	2.36	0.58
1:B:35:ASN:ND2	1:B:93:ALA:O	2.36	0.58
1:B:38:VAL:HA	1:B:99:VAL:HB	1.85	0.58
2:A:157:VAL:HG21	2:A:372:VAL:HG11	1.85	0.58
2:A:233:ARG:CZ	2:A:233:ARG:HB3	2.33	0.58
1:B:536:MET:CE	1:B:749:THR:CG2	2.81	0.58
2:C:521:ASN:H	2:C:695:ARG:HH12	1.52	0.57
1:D:769:SER:HB2	1:D:771:TRP:HD1	1.69	0.57
1:B:46:VAL:O	1:B:50:GLU:N	2.35	0.57
1:B:523:ASP:HB3	1:B:772:LYS:HE2	1.86	0.57
2:C:152:PHE:O	2:C:155:MET:HB2	2.04	0.57
2:C:207:LEU:HA	2:C:210:GLU:OE1	2.03	0.57
2:A:521:ASN:H	2:A:695:ARG:HH12	1.52	0.57
2:A:831:ILE:HG23	2:A:835:ILE:HD12	1.86	0.57
1:B:464:LEU:HD23	1:B:467:LEU:HD12	1.86	0.57
2:A:487:GLN:HA	2:A:497:GLU:O	2.04	0.57
1:D:35:ASN:ND2	1:D:93:ALA:O	2.37	0.57
2:A:218:VAL:C	2:A:246:VAL:HG11	2.29	0.57
2:C:218:VAL:C	2:C:246:VAL:HG11	2.29	0.57
2:A:520:ASN:HB3	2:A:695:ARG:HH22	1.69	0.57
1:B:273:PRO:HG2	1:B:276:LEU:HD21	1.86	0.57
1:B:638:ALA:O	1:B:642:LEU:N	2.37	0.57
1:D:64:PRO:HG2	1:D:65:LEU:N	2.18	0.57
1:D:98:LEU:HB2	1:D:124:ILE:HG12	1.86	0.57
1:D:535:VAL:H	1:D:750:ILE:HB	1.70	0.57
1:D:149:ALA:HB1	1:D:154:GLN:HE21	1.70	0.57
2:C:227:ASP:O	2:C:230:THR:CB	2.28	0.57
1:B:533:ILE:CD1	1:B:690:THR:CG2	2.83	0.56
2:C:157:VAL:HG21	2:C:372:VAL:HG11	1.86	0.56
2:C:508:GLY:HA2	2:C:763:ARG:HH22	1.68	0.56
1:D:535:VAL:CB	1:D:750:ILE:HD13	2.33	0.56
2:C:520:ASN:HB3	2:C:695:ARG:HH22	1.69	0.56
1:B:533:ILE:O	1:B:756:PHE:O	2.23	0.56
1:B:535:VAL:H	1:B:750:ILE:HG21	1.69	0.56
2:C:424:PHE:HB3	2:C:428:GLY:HA2	1.87	0.56
2:A:233:ARG:NH1	2:A:233:ARG:HB2	2.21	0.56
1:B:63:LEU:HD13	1:B:67:VAL:CG2	2.35	0.56
1:B:149:ALA:HB1	1:B:154:GLN:HE21	1.71	0.56
1:B:536:MET:HA	1:B:749:THR:CB	2.34	0.56
2:A:217:ARG:C	2:A:246:VAL:CG2	2.79	0.56
2:A:227:ASP:O	2:A:231:VAL:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:535:VAL:C	1:D:750:ILE:HB	2.27	0.56
1:D:647:ALA:O	1:D:651:ALA:N	2.38	0.56
2:C:831:ILE:HG23	2:C:835:ILE:HD12	1.86	0.56
1:D:63:LEU:HD13	1:D:67:VAL:CG2	2.35	0.56
2:C:243:SER:CB	2:C:384:GLY:N	2.32	0.56
1:B:439:PHE:HB3	1:B:449:GLY:HA3	1.88	0.56
1:B:632:SER:O	1:B:635:ALA:HB3	2.06	0.56
2:A:152:PHE:O	2:A:155:MET:HB2	2.04	0.56
1:B:63:LEU:HD21	1:B:300:THR:CG2	2.31	0.56
1:B:694:ILE:HA	1:B:697:ASN:HB2	1.88	0.56
2:A:91:LEU:HB3	2:A:121:LEU:HD11	1.88	0.55
2:A:115:ARG:HG2	2:A:135:LEU:HD13	1.88	0.55
2:C:115:ARG:HG2	2:C:135:LEU:HD13	1.88	0.55
1:D:632:SER:O	1:D:635:ALA:HB3	2.06	0.55
2:C:628:SER:HA	2:C:631:ILE:HD12	1.89	0.55
1:D:52:ARG:HA	1:D:293:ARG:HH21	1.70	0.55
1:B:535:VAL:H	1:B:750:ILE:HB	1.71	0.55
2:C:232:TYR:HE2	2:C:261:TYR:C	2.10	0.55
1:D:35:ASN:HB3	1:D:95:ILE:HG12	1.88	0.55
1:D:256:ILE:HG12	1:D:277:ILE:HB	1.88	0.55
1:D:533:ILE:O	1:D:756:PHE:O	2.24	0.55
2:A:243:SER:N	2:A:383:GLY:CA	2.68	0.55
1:B:438:LYS:O	1:B:451:ASN:HA	2.05	0.55
1:B:668:LYS:HA	1:B:671:GLN:HB2	1.89	0.55
1:B:750:ILE:HG23	1:B:750:ILE:O	2.07	0.55
2:C:226:ASP:O	2:C:227:ASP:C	2.50	0.55
2:C:217:ARG:C	2:C:246:VAL:CG2	2.79	0.55
1:D:464:LEU:HD23	1:D:467:LEU:HD12	1.88	0.55
2:A:424:PHE:HB3	2:A:428:GLY:HA2	1.87	0.55
2:A:208:LEU:HD13	2:A:238:LEU:HD12	1.89	0.55
1:B:600:THR:O	1:B:604:ALA:HB3	2.06	0.55
2:C:91:LEU:HB3	2:C:121:LEU:HD11	1.88	0.55
1:D:38:VAL:O	1:D:71:ALA:HA	2.06	0.55
1:D:321:TYR:HA	2:C:72:ILE:HD13	1.89	0.55
1:D:535:VAL:H	1:D:750:ILE:CB	2.19	0.55
2:A:628:SER:HA	2:A:631:ILE:HD12	1.88	0.55
2:A:715:ALA:HA	2:A:718:ILE:HD12	1.89	0.55
1:B:35:ASN:HB3	1:B:95:ILE:HG12	1.88	0.55
2:C:243:SER:N	2:C:383:GLY:CA	2.68	0.55
1:B:63:LEU:HD12	1:B:67:VAL:HG23	1.85	0.54
1:B:665:LEU:O	1:B:671:GLN:NE2	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:233:ARG:CZ	2:A:233:ARG:CB	2.85	0.54
1:B:277:ILE:HG12	1:B:365:VAL:HG22	1.88	0.54
1:D:694:ILE:HA	1:D:697:ASN:HB2	1.89	0.54
2:A:665:THR:N	2:A:669:ASP:OD2	2.36	0.54
2:C:302:THR:HG21	2:C:316:LYS:HB2	1.90	0.54
1:D:246:LEU:HA	1:B:220:LYS:HZ2	1.72	0.54
2:C:208:LEU:HD13	2:C:238:LEU:HD12	1.89	0.54
1:D:522:VAL:HG12	1:D:523:ASP:O	2.08	0.54
2:A:302:THR:HG21	2:A:316:LYS:HB2	1.89	0.54
1:B:513:THR:OG1	1:B:518:ARG:NH1	2.40	0.54
1:B:522:VAL:CG1	1:B:523:ASP:H	2.21	0.54
1:B:535:VAL:CB	1:B:750:ILE:HD13	2.34	0.54
1:B:569:VAL:HG13	1:B:631:VAL:HG22	1.90	0.54
1:B:769:SER:HB2	1:B:771:TRP:HD1	1.72	0.54
1:B:38:VAL:O	1:B:71:ALA:HA	2.08	0.54
1:B:522:VAL:HG12	1:B:523:ASP:O	2.08	0.54
1:D:750:ILE:HG23	1:D:750:ILE:O	2.07	0.54
2:A:211:ALA:C	2:A:213:GLU:N	2.66	0.54
2:C:505:LEU:O	2:C:763:ARG:NH2	2.41	0.54
1:D:528:PHE:CD1	1:D:528:PHE:C	2.86	0.54
1:B:532:GLY:HA3	1:B:758:THR:HA	1.90	0.54
2:C:243:SER:HB3	2:C:383:GLY:C	2.28	0.54
2:C:715:ALA:HA	2:C:718:ILE:HD12	1.89	0.54
1:B:535:VAL:H	1:B:750:ILE:CB	2.20	0.53
1:B:533:ILE:CG2	1:B:729:ILE:HG23	2.27	0.53
1:B:528:PHE:CD1	1:B:528:PHE:C	2.86	0.53
1:D:534:SER:CB	1:D:732:ALA:CB	2.86	0.53
1:B:534:SER:O	1:B:729:ILE:HG23	2.09	0.53
1:D:521:VAL:C	1:D:767:LYS:HE3	2.32	0.53
1:D:522:VAL:CG1	1:D:523:ASP:H	2.21	0.53
1:D:439:PHE:HB3	1:D:449:GLY:HA3	1.90	0.53
1:D:538:SER:HA	1:D:747:LEU:HD23	1.91	0.53
2:A:79:CYS:HA	2:A:83:ILE:HB	1.90	0.53
1:B:184:ILE:HG23	1:B:203:VAL:HG21	1.90	0.53
2:C:665:THR:N	2:C:669:ASP:OD2	2.35	0.53
1:B:626:THR:O	1:B:629:ILE:HB	2.09	0.53
2:C:208:LEU:HD12	2:C:238:LEU:CD1	2.39	0.53
2:A:145:SER:O	2:A:148:SER:OG	2.23	0.53
2:C:208:LEU:O	2:C:240:MET:HE1	2.08	0.53
2:A:208:LEU:O	2:A:240:MET:HE1	2.08	0.53
2:C:145:SER:O	2:C:148:SER:OG	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:233:ARG:NH1	2:A:233:ARG:CB	2.72	0.52
1:D:530:GLU:CD	2:A:535:TYR:HB3	2.34	0.52
1:D:534:SER:HB2	1:D:732:ALA:HB1	1.89	0.52
1:D:532:GLY:HA3	1:D:758:THR:HA	1.90	0.52
1:D:638:ALA:O	1:D:642:LEU:N	2.41	0.52
2:C:364:VAL:O	2:C:375:ASN:N	2.42	0.52
2:C:562:LEU:HD23	2:C:565:LEU:HD12	1.92	0.52
1:D:668:LYS:HA	1:D:671:GLN:HB2	1.91	0.52
2:A:208:LEU:HD12	2:A:238:LEU:CD1	2.39	0.52
2:A:472:PHE:HB2	2:A:474:TYR:CZ	2.44	0.52
2:A:505:LEU:O	2:A:763:ARG:NH2	2.41	0.52
1:B:52:ARG:HA	1:B:293:ARG:HH21	1.74	0.52
2:C:79:CYS:HA	2:C:83:ILE:HB	1.90	0.52
2:C:278:SER:HA	2:C:281:ILE:HD12	1.92	0.52
1:D:534:SER:CB	1:D:732:ALA:HB1	2.40	0.52
2:A:278:SER:HA	2:A:281:ILE:HD12	1.92	0.52
2:C:366:ILE:HB	2:C:373:ILE:HB	1.92	0.52
1:D:513:THR:OG1	1:D:518:ARG:NH1	2.42	0.52
2:A:364:VAL:O	2:A:375:ASN:N	2.42	0.52
2:C:522:GLU:H	2:C:695:ARG:NH2	2.08	0.52
2:A:118:VAL:O	2:A:137:PHE:HA	2.10	0.52
2:A:209:MET:O	2:A:210:GLU:C	2.51	0.52
2:A:147:GLN:O	2:A:150:VAL:HB	2.10	0.52
1:B:538:SER:HA	1:B:747:LEU:HD23	1.90	0.52
2:A:351:TYR:HB2	2:A:367:TYR:HB2	1.92	0.51
2:A:559:GLN:O	2:A:561:THR:N	2.43	0.51
1:B:46:VAL:HG13	1:B:71:ALA:HB3	1.92	0.51
1:B:279:VAL:HG22	1:B:363:VAL:HG22	1.92	0.51
2:C:433:LYS:HE2	2:C:456:TYR:HE1	1.76	0.51
1:D:279:VAL:HG22	1:D:363:VAL:HG22	1.92	0.51
2:A:522:GLU:H	2:A:695:ARG:NH2	2.08	0.51
1:B:108:ALA:O	1:B:112:MET:N	2.39	0.51
2:C:472:PHE:HB2	2:C:474:TYR:CZ	2.44	0.51
2:C:559:GLN:O	2:C:561:THR:N	2.44	0.51
1:B:413:GLU:OE1	1:B:511:SER:OG	2.25	0.51
2:A:366:ILE:HB	2:A:373:ILE:HB	1.92	0.51
2:A:721:VAL:HG11	2:A:746:LEU:HD21	1.93	0.51
1:D:526:VAL:HG13	1:D:527:PRO:CD	2.27	0.51
2:A:208:LEU:CB	2:A:238:LEU:HD13	2.40	0.51
2:A:243:SER:HB3	2:A:383:GLY:C	2.28	0.51
2:C:147:GLN:O	2:C:150:VAL:HB	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:251:GLU:HA	2:C:254:ILE:HD12	1.92	0.51
2:C:721:VAL:HG11	2:C:746:LEU:HD21	1.93	0.51
1:D:226:VAL:HG22	1:D:254:PHE:HB2	1.92	0.51
2:A:144:TYR:OH	2:A:252:ARG:NE	2.44	0.51
2:A:228:ALA:O	2:A:232:TYR:CD2	2.63	0.51
2:A:562:LEU:HD23	2:A:565:LEU:HD12	1.92	0.51
2:C:229:ALA:O	2:C:233:ARG:HB2	2.09	0.51
1:D:220:LYS:HZ2	1:B:246:LEU:HA	1.76	0.51
1:B:63:LEU:HD11	1:B:300:THR:HG21	1.78	0.51
2:A:237:MET:O	2:A:239:ASN:N	2.44	0.51
2:A:501:MET:HE3	2:A:513:ILE:HG12	1.92	0.51
2:C:232:TYR:OH	2:C:258:ALA:O	2.28	0.51
2:C:351:TYR:HB2	2:C:367:TYR:HB2	1.92	0.51
1:D:536:MET:N	1:D:728:PHE:O	2.37	0.50
2:A:251:GLU:HA	2:A:254:ILE:HD12	1.92	0.50
2:C:118:VAL:O	2:C:137:PHE:HA	2.10	0.50
2:C:211:ALA:C	2:C:213:GLU:N	2.66	0.50
1:D:108:ALA:O	1:D:112:MET:N	2.40	0.50
1:D:277:ILE:HG12	1:D:365:VAL:HG22	1.92	0.50
1:D:730:TYR:HB2	1:D:735:LEU:HD11	1.93	0.50
2:C:237:MET:O	2:C:239:ASN:N	2.44	0.50
2:A:243:SER:CB	2:A:384:GLY:N	2.32	0.50
1:B:759:THR:HG21	2:C:780:HIS:CE1	2.47	0.50
2:C:209:MET:O	2:C:210:GLU:C	2.51	0.50
2:C:501:MET:HE3	2:C:513:ILE:HG12	1.92	0.50
2:C:795:TYR:HB2	2:C:796:GLN:HG3	1.93	0.50
2:A:433:LYS:HE2	2:A:456:TYR:HE1	1.76	0.50
2:A:485:GLY:HA2	2:A:499:ASN:HB2	1.93	0.50
2:C:208:LEU:CB	2:C:238:LEU:HD13	2.40	0.50
2:C:226:ASP:C	2:C:230:THR:HG1	2.15	0.50
2:C:485:GLY:HA2	2:C:499:ASN:HB2	1.93	0.50
2:C:144:TYR:OH	2:C:252:ARG:NE	2.44	0.50
1:B:558:VAL:HG22	2:C:809:THR:HG23	1.93	0.50
1:D:535:VAL:HB	1:D:750:ILE:CG1	2.42	0.50
1:B:63:LEU:HB3	1:B:65:LEU:HB2	1.94	0.50
2:C:693:PHE:O	2:C:703:TYR:OH	2.26	0.50
1:D:460:CYS:HA	1:D:463:ILE:HD12	1.94	0.50
2:A:208:LEU:HD12	2:A:238:LEU:HD12	1.94	0.50
1:B:460:CYS:HA	1:B:463:ILE:HD12	1.93	0.50
1:B:526:VAL:HG13	1:B:527:PRO:CD	2.27	0.50
1:B:730:TYR:HB2	1:B:735:LEU:HD11	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:795:TYR:HB2	2:A:796:GLN:HG3	1.93	0.49
1:D:63:LEU:HB3	1:D:65:LEU:HB2	1.94	0.49
1:D:538:SER:HA	1:D:747:LEU:HA	1.95	0.49
2:A:394:MET:HG3	2:A:768:TRP:HZ2	1.77	0.49
2:A:489:ARG:HH21	1:B:195:PHE:H	1.59	0.49
1:B:527:PRO:O	1:B:527:PRO:HG2	2.12	0.49
2:C:237:MET:C	2:C:239:ASN:N	2.70	0.49
1:D:527:PRO:HG2	1:D:527:PRO:O	2.12	0.49
1:B:486:GLY:HA3	1:B:497:ILE:HD12	1.94	0.49
1:D:459:PHE:HE1	1:D:791:LEU:HB3	1.76	0.49
1:B:78:ASP:O	1:B:81:SER:OG	2.25	0.49
1:B:459:PHE:HE1	1:B:791:LEU:HB3	1.78	0.49
1:B:500:VAL:CG1	1:B:522:VAL:HG21	2.35	0.49
1:B:535:VAL:HB	1:B:750:ILE:CG1	2.43	0.49
2:C:105:THR:O	2:C:108:SER:OG	2.26	0.49
2:C:505:LEU:HD12	2:C:527:ILE:HD13	1.95	0.49
1:B:536:MET:N	1:B:728:PHE:O	2.42	0.49
2:A:73:GLN:O	2:A:75:ALA:N	2.46	0.49
2:A:111:ALA:HA	2:A:116:ILE:HD12	1.95	0.49
2:A:227:ASP:C	2:A:231:VAL:HG23	2.37	0.49
1:B:537:VAL:O	1:B:748:VAL:N	2.46	0.49
1:B:759:THR:HG21	2:C:780:HIS:ND1	2.28	0.49
2:C:232:TYR:CZ	2:C:258:ALA:O	2.66	0.49
1:D:759:THR:HG22	2:A:535:TYR:HE2	1.78	0.48
2:A:738:PHE:CZ	2:A:793:VAL:HA	2.48	0.48
2:C:218:VAL:N	2:C:246:VAL:HG21	2.22	0.48
2:C:394:MET:HG3	2:C:768:TRP:HZ2	1.77	0.48
2:A:693:PHE:O	2:A:703:TYR:OH	2.26	0.48
2:C:111:ALA:HA	2:C:116:ILE:HD12	1.95	0.48
2:C:217:ARG:O	2:C:246:VAL:CB	2.61	0.48
2:A:463:LEU:HD21	2:A:514:VAL:HG21	1.96	0.48
2:A:541:LEU:O	2:A:728:ALA:HA	2.13	0.48
2:C:463:LEU:HD21	2:C:514:VAL:HG21	1.96	0.48
1:D:134:ILE:HD11	1:D:146:GLN:HB2	1.95	0.48
1:D:537:VAL:O	1:D:748:VAL:N	2.46	0.48
2:A:217:ARG:O	2:A:246:VAL:CB	2.61	0.48
2:A:459:CYS:HA	2:A:462:LEU:HD12	1.96	0.48
2:C:541:LEU:O	2:C:728:ALA:HA	2.13	0.48
2:C:559:GLN:HB2	2:C:562:LEU:HD12	1.95	0.48
1:B:538:SER:HA	1:B:747:LEU:HA	1.94	0.48
1:B:508:ALA:HB3	1:B:764:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:533:ILE:HD12	1:D:690:THR:CG2	2.43	0.48
2:C:272:ILE:HD12	2:C:350:ASN:HB3	1.96	0.48
2:C:738:PHE:CZ	2:C:793:VAL:HA	2.48	0.48
1:B:712:GLY:N	1:B:715:ASP:OD2	2.47	0.48
1:D:111:GLN:O	1:D:114:ASP:HB2	2.14	0.48
1:D:710:GLN:HE22	1:D:716:ALA:HA	1.79	0.48
2:C:73:GLN:O	2:C:75:ALA:N	2.46	0.48
2:C:111:ALA:HB1	2:C:116:ILE:HB	1.96	0.48
2:C:538:LEU:HB2	2:C:753:PHE:HB2	1.96	0.48
1:D:46:VAL:HG13	1:D:71:ALA:HB3	1.96	0.47
2:A:559:GLN:O	2:A:560:SER:C	2.57	0.47
1:B:627:SER:HA	1:B:630:MET:HG2	1.96	0.47
2:A:538:LEU:HB2	2:A:753:PHE:HB2	1.96	0.47
2:A:601:LEU:O	2:A:605:SER:OG	2.30	0.47
2:C:229:ALA:HA	2:C:232:TYR:CB	2.40	0.47
2:C:341:ASN:HA	2:C:347:LYS:HE3	1.97	0.47
2:A:505:LEU:HD12	2:A:527:ILE:HD13	1.95	0.47
2:A:559:GLN:HB2	2:A:562:LEU:HD12	1.95	0.47
2:C:459:CYS:HA	2:C:462:LEU:HD12	1.96	0.47
1:D:128:HIS:HA	1:D:132:SER:HB3	1.95	0.47
1:B:719:SER:O	1:B:724:LYS:N	2.46	0.47
2:A:72:ILE:HD13	1:B:321:TYR:HA	1.96	0.47
1:B:565:MET:HG3	2:C:817:PHE:HE1	1.77	0.47
2:A:341:ASN:HA	2:A:347:LYS:HE3	1.97	0.47
1:B:291:ARG:HE	1:B:360:ARG:HH11	1.62	0.47
1:B:537:VAL:CG1	1:B:727:ALA:CB	2.91	0.47
2:C:559:GLN:O	2:C:560:SER:C	2.58	0.47
1:D:719:SER:O	1:D:724:LYS:N	2.45	0.47
2:A:272:ILE:HD12	2:A:350:ASN:HB3	1.96	0.47
1:B:286:TYR:OH	1:B:379:GLU:OE2	2.29	0.47
1:B:565:MET:HG3	2:C:817:PHE:CD1	2.48	0.47
1:B:627:SER:C	1:B:629:ILE:N	2.72	0.47
1:B:388:ALA:O	1:B:437:ARG:NH1	2.48	0.47
1:B:535:VAL:HG22	1:B:729:ILE:CD1	2.44	0.47
1:B:535:VAL:C	1:B:750:ILE:HB	2.28	0.47
2:C:208:LEU:CD1	2:C:238:LEU:CD1	2.93	0.47
1:D:537:VAL:HA	1:D:727:ALA:HB2	1.97	0.46
1:D:634:TRP:O	1:D:638:ALA:N	2.46	0.46
2:A:75:ALA:HA	2:A:78:VAL:HB	1.98	0.46
2:A:111:ALA:HB1	2:A:116:ILE:HB	1.96	0.46
1:D:413:GLU:OE1	1:D:511:SER:OG	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:820:VAL:O	1:D:824:LEU:N	2.35	0.46
2:A:150:VAL:O	2:A:153:GLU:HB2	2.15	0.46
2:A:195:LEU:HD22	2:A:210:GLU:OE2	2.16	0.46
2:A:218:VAL:N	2:A:246:VAL:HG21	2.22	0.46
2:C:219:ILE:N	2:C:246:VAL:CG1	2.53	0.46
2:C:235:ALA:O	2:C:237:MET:N	2.48	0.46
1:B:63:LEU:C	1:B:65:LEU:N	2.63	0.46
1:B:128:HIS:HA	1:B:132:SER:HB3	1.97	0.46
2:C:150:VAL:O	2:C:153:GLU:HB2	2.16	0.46
2:C:825:VAL:HA	2:C:828:ILE:HD12	1.97	0.46
1:D:123:PRO:HG3	1:D:334:LEU:HD12	1.96	0.46
1:B:434:VAL:O	1:B:456:CYS:HB2	2.16	0.46
1:D:78:ASP:O	1:D:81:SER:OG	2.25	0.46
1:D:577:PHE:HA	1:D:580:PHE:HB2	1.96	0.46
2:A:237:MET:C	2:A:239:ASN:N	2.70	0.46
2:A:315:TRP:HB3	2:A:317:THR:H	1.81	0.46
1:B:522:VAL:HG13	1:B:523:ASP:H	1.81	0.46
1:B:710:GLN:HE22	1:B:716:ALA:HA	1.81	0.46
2:C:74:MET:O	2:C:77:SER:OG	2.29	0.46
2:C:151:TRP:O	2:C:154:MET:HB2	2.16	0.46
1:D:90:MET:HE1	1:D:316:ALA:HB1	1.96	0.46
2:A:825:VAL:HA	2:A:828:ILE:HD12	1.97	0.46
1:B:694:ILE:O	1:B:698:TYR:N	2.35	0.46
2:C:217:ARG:C	2:C:246:VAL:HG21	2.40	0.46
1:D:533:ILE:HG22	1:D:729:ILE:HG21	1.79	0.46
2:C:208:LEU:HD12	2:C:238:LEU:HD12	1.94	0.46
1:D:262:SER:OG	1:D:263:GLY:N	2.49	0.46
2:A:228:ALA:C	2:A:232:TYR:HD2	2.24	0.46
2:A:607:MET:O	2:A:610:SER:OG	2.33	0.46
1:B:226:VAL:HG22	1:B:254:PHE:HB2	1.97	0.46
2:A:235:ALA:O	2:A:237:MET:N	2.48	0.46
2:C:315:TRP:HB3	2:C:317:THR:H	1.81	0.46
2:A:151:TRP:O	2:A:154:MET:HB2	2.15	0.45
1:D:137:ASP:H	2:C:133:ILE:HD11	1.82	0.45
1:D:569:VAL:HA	1:D:572:ILE:HD12	1.99	0.45
1:D:694:ILE:O	1:D:698:TYR:N	2.35	0.45
2:A:208:LEU:CD1	2:A:238:LEU:CD1	2.93	0.45
2:A:578:TYR:OH	2:A:606:ALA:N	2.49	0.45
1:B:163:GLN:HA	1:B:198:TRP:HH2	1.81	0.45
2:C:75:ALA:HA	2:C:78:VAL:HB	1.98	0.45
2:C:521:ASN:H	2:C:695:ARG:NH1	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:63:LEU:HD12	1:D:67:VAL:HG23	1.85	0.45
2:A:357:GLN:HE22	2:A:380:ILE:H	1.64	0.45
2:A:421:LYS:O	2:A:433:LYS:NZ	2.48	0.45
1:D:533:ILE:CG2	1:D:729:ILE:HG23	2.29	0.45
1:B:533:ILE:CG2	1:B:729:ILE:HG22	2.27	0.45
2:C:208:LEU:CB	2:C:238:LEU:CD1	2.94	0.45
2:C:394:MET:HE2	2:C:768:TRP:HE1	1.80	0.45
2:C:731:TRP:HB3	2:C:732:ASP:H	1.62	0.45
1:D:522:VAL:HG13	1:D:523:ASP:H	1.81	0.45
2:A:138:LEU:HD22	2:A:344:GLY:HA3	1.99	0.45
1:B:126:GLY:HA3	1:B:146:GLN:HG2	1.98	0.45
1:B:534:SER:OG	1:B:732:ALA:CB	2.65	0.45
2:C:578:TYR:OH	2:C:606:ALA:N	2.49	0.45
1:D:535:VAL:HG22	1:D:729:ILE:HD11	1.96	0.45
2:A:521:ASN:H	2:A:695:ARG:NH1	2.14	0.45
1:D:416:PHE:HA	1:D:459:PHE:HB2	1.99	0.45
2:A:208:LEU:CB	2:A:238:LEU:CD1	2.94	0.45
2:A:394:MET:HE2	2:A:768:TRP:HE1	1.80	0.45
1:B:417:VAL:HA	1:B:457:LYS:O	2.16	0.45
2:C:611:TRP:CE3	2:C:615:LEU:HD11	2.49	0.45
2:A:611:TRP:CE3	2:A:615:LEU:HD11	2.49	0.45
2:C:226:ASP:C	2:C:230:THR:OG1	2.59	0.45
1:D:127:ILE:HG22	1:D:128:HIS:CD2	2.52	0.45
2:A:136:SER:HB3	2:A:322:LYS:HE2	1.99	0.45
2:A:228:ALA:O	2:A:231:VAL:N	2.49	0.45
1:B:123:PRO:HG3	1:B:334:LEU:HD12	1.99	0.45
2:C:738:PHE:HZ	2:C:793:VAL:HA	1.81	0.45
2:A:73:GLN:HE21	1:B:321:TYR:HE1	1.65	0.44
2:A:738:PHE:HZ	2:A:793:VAL:HA	1.81	0.44
2:C:210:GLU:HB3	2:C:211:ALA:H	1.55	0.44
2:C:772:VAL:O	2:C:775:SER:OG	2.31	0.44
2:A:74:MET:O	2:A:77:SER:OG	2.30	0.44
2:A:688:SER:HA	2:A:691:ILE:HD12	1.99	0.44
1:B:416:PHE:HA	1:B:459:PHE:HB2	2.00	0.44
1:B:513:THR:O	1:B:518:ARG:NH1	2.47	0.44
1:B:536:MET:HG3	1:B:749:THR:CG2	2.47	0.44
1:B:536:MET:C	1:B:727:ALA:HB1	2.16	0.44
1:B:654:ILE:HD12	2:C:656:VAL:HG21	1.99	0.44
2:C:195:LEU:HD22	2:C:210:GLU:OE2	2.15	0.44
1:D:194:SER:HA	2:C:489:ARG:HH21	1.83	0.44
2:A:217:ARG:C	2:A:246:VAL:HG21	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:227:ASP:C	2:A:230:THR:HB	2.23	0.44
2:A:228:ALA:CB	2:A:232:TYR:CE2	2.81	0.44
2:C:357:GLN:HE22	2:C:380:ILE:H	1.64	0.44
2:C:463:LEU:HD23	2:C:466:LEU:HD12	2.00	0.44
2:A:218:VAL:HG22	2:A:246:VAL:HG22	1.99	0.44
2:C:241:THR:HB	2:C:263:PRO:HG3	2.00	0.44
1:D:163:GLN:HA	1:D:198:TRP:HH2	1.82	0.44
1:D:835:PHE:CE2	2:C:580:LEU:HD13	2.52	0.44
2:A:367:TYR:HE1	2:A:372:VAL:HG22	1.82	0.44
1:B:246:LEU:HD13	1:B:248:LEU:HD12	2.00	0.44
2:C:118:VAL:HB	2:C:137:PHE:HD1	1.83	0.44
2:C:138:LEU:HD22	2:C:344:GLY:HA3	1.99	0.44
2:C:688:SER:HA	2:C:691:ILE:HD12	1.99	0.44
1:D:533:ILE:HG21	1:D:729:ILE:HG21	1.96	0.44
1:D:737:TYR:CE1	1:D:796:LEU:HA	2.53	0.44
2:A:241:THR:HB	2:A:263:PRO:HG3	2.00	0.44
2:A:615:LEU:C	2:A:616:ASN:CG	2.86	0.44
1:B:557:SER:OG	2:C:809:THR:HG21	2.17	0.44
2:C:367:TYR:HE1	2:C:372:VAL:HG22	1.82	0.44
1:D:126:GLY:HA3	1:D:146:GLN:HG2	1.99	0.44
1:D:536:MET:HE3	1:D:749:THR:HG22	1.98	0.44
2:A:31:ALA:HA	2:A:91:LEU:H	1.83	0.44
1:B:291:ARG:HE	1:B:360:ARG:NH1	2.16	0.44
2:C:208:LEU:HA	2:C:211:ALA:HB2	2.00	0.44
1:D:534:SER:CB	1:D:732:ALA:HB2	2.47	0.43
1:D:603:LYS:HA	1:D:606:TRP:HD1	1.83	0.43
2:A:670:PRO:HA	2:A:673:ARG:HB2	2.00	0.43
2:C:421:LYS:O	2:C:433:LYS:NZ	2.48	0.43
2:A:463:LEU:HD23	2:A:466:LEU:HD12	2.00	0.43
1:D:63:LEU:C	1:D:65:LEU:N	2.63	0.43
1:D:184:ILE:HG23	1:D:203:VAL:HG21	2.00	0.43
1:D:536:MET:HG3	1:D:749:THR:CG2	2.47	0.43
1:D:781:GLN:HA	2:A:521:ASN:HD21	1.83	0.43
2:A:210:GLU:HB3	2:A:211:ALA:H	1.55	0.43
2:C:227:ASP:O	2:C:231:VAL:N	2.37	0.43
2:A:211:ALA:HB1	2:A:240:MET:CE	2.47	0.43
1:B:534:SER:OG	1:B:732:ALA:HB1	2.18	0.43
2:C:425:THR:OG1	2:C:429:ASP:N	2.37	0.43
1:D:291:ARG:HE	1:D:360:ARG:NH1	2.16	0.43
1:D:737:TYR:HE1	1:D:796:LEU:HA	1.84	0.43
1:B:113:LEU:HA	1:B:116:ILE:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:737:TYR:CE1	1:B:796:LEU:HA	2.54	0.43
2:C:31:ALA:HA	2:C:91:LEU:H	1.83	0.43
2:C:235:ALA:C	2:C:237:MET:N	2.76	0.43
2:C:643:ILE:O	2:C:646:SER:OG	2.29	0.43
1:D:523:ASP:HB3	1:D:772:LYS:CE	2.47	0.43
1:B:63:LEU:HD13	1:B:67:VAL:HG21	1.83	0.43
1:B:533:ILE:C	1:B:756:PHE:O	2.61	0.43
2:C:136:SER:HB3	2:C:322:LYS:HE2	1.99	0.43
2:C:667:ILE:HA	2:C:672:LEU:HD12	2.01	0.43
2:C:670:PRO:HA	2:C:673:ARG:HB2	2.00	0.43
1:D:534:SER:OG	1:D:732:ALA:HB1	2.18	0.43
2:A:118:VAL:HB	2:A:137:PHE:HD1	1.83	0.43
2:A:208:LEU:HA	2:A:211:ALA:HB2	2.01	0.43
2:C:166:LEU:HB2	2:C:221:LEU:HD23	2.00	0.43
1:D:388:ALA:O	1:D:437:ARG:NH1	2.52	0.43
1:B:718:VAL:O	1:B:722:THR:N	2.47	0.43
1:B:781:GLN:HA	2:C:521:ASN:HD21	1.84	0.43
1:D:63:LEU:CB	1:D:65:LEU:O	2.67	0.43
1:D:536:MET:CE	1:D:749:THR:HG23	2.48	0.43
2:A:287:VAL:HA	2:A:330:TYR:CZ	2.54	0.43
1:D:508:ALA:HB3	1:D:764:ALA:HB3	2.00	0.43
1:D:718:VAL:O	1:D:722:THR:N	2.48	0.43
1:D:750:ILE:O	1:D:751:GLY:C	2.62	0.43
1:B:79:PRO:HA	1:B:82:LEU:HD12	2.01	0.43
2:C:47:ASN:HA	2:C:50:ASN:HD22	1.84	0.43
1:D:712:GLY:N	1:D:715:ASP:OD2	2.52	0.42
1:D:759:THR:HG21	2:A:780:HIS:CE1	2.54	0.42
2:A:233:ARG:HB2	2:A:233:ARG:HH11	1.83	0.42
2:A:679:PHE:HA	2:A:727:HIS:CD2	2.54	0.42
1:B:76:ARG:HD3	1:B:78:ASP:HB2	2.00	0.42
1:B:750:ILE:O	1:B:751:GLY:C	2.62	0.42
2:C:700:SER:HA	2:C:703:TYR:CE2	2.54	0.42
1:D:533:ILE:C	1:D:756:PHE:O	2.61	0.42
2:A:700:SER:HA	2:A:703:TYR:CE2	2.54	0.42
1:B:569:VAL:HA	1:B:572:ILE:HD12	2.01	0.42
2:A:425:THR:OG1	2:A:429:ASP:N	2.37	0.42
2:A:520:ASN:HB3	2:A:695:ARG:NH2	2.34	0.42
2:C:146:HIS:O	2:C:149:SER:OG	2.30	0.42
2:C:229:ALA:O	2:C:232:TYR:HB3	2.18	0.42
2:C:229:ALA:O	2:C:233:ARG:HB3	2.18	0.42
2:C:679:PHE:HA	2:C:727:HIS:CD2	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:143:THR:HA	1:D:335:HIS:HE1	1.84	0.42
1:D:164:ASP:HB2	1:D:386:ARG:NH1	2.34	0.42
2:A:235:ALA:C	2:A:237:MET:N	2.76	0.42
1:B:63:LEU:CD2	1:B:300:THR:CB	2.55	0.42
2:C:127:ILE:HG12	2:C:171:HIS:HB2	2.02	0.42
2:C:287:VAL:HA	2:C:330:TYR:CZ	2.54	0.42
1:D:65:LEU:HD12	1:D:303:ALA:HB1	2.01	0.42
1:D:159:LEU:HD23	1:D:159:LEU:HA	1.89	0.42
2:A:771:ASN:HA	2:A:774:LEU:HD12	2.02	0.42
2:C:771:ASN:HA	2:C:774:LEU:HD12	2.02	0.42
1:D:205:THR:O	1:D:218:GLN:NE2	2.36	0.42
1:D:534:SER:O	1:D:729:ILE:CA	2.59	0.42
2:A:47:ASN:HA	2:A:50:ASN:HD22	1.84	0.42
2:A:132:SER:HB3	1:B:178:PRO:HG2	2.01	0.42
2:A:166:LEU:HB2	2:A:221:LEU:HD23	2.00	0.42
1:B:536:MET:HE3	1:B:749:THR:HG22	1.98	0.42
1:B:734:VAL:HA	1:B:737:TYR:HD2	1.83	0.42
1:D:749:THR:O	1:D:750:ILE:C	2.63	0.42
2:A:126:SER:O	2:A:129:SER:OG	2.29	0.42
2:A:614:LEU:HD21	2:A:636:TRP:HB3	2.02	0.42
1:B:63:LEU:CB	1:B:65:LEU:O	2.67	0.42
1:B:159:LEU:HD23	1:B:159:LEU:HA	1.89	0.42
1:B:536:MET:CE	1:B:749:THR:HG23	2.49	0.42
1:D:114:ASP:O	1:D:117:SER:OG	2.21	0.42
1:D:500:VAL:CG1	1:D:522:VAL:HG21	2.47	0.42
2:A:127:ILE:HG12	2:A:171:HIS:HB2	2.02	0.42
2:A:252:ARG:O	2:A:255:SER:OG	2.33	0.42
2:A:667:ILE:HA	2:A:672:LEU:HD12	2.01	0.42
2:A:684:VAL:H	2:A:731:TRP:HZ2	1.68	0.42
1:B:164:ASP:HB2	1:B:386:ARG:NH1	2.35	0.42
1:D:417:VAL:HA	1:D:457:LYS:O	2.20	0.41
2:A:103:THR:O	2:A:105:THR:N	2.51	0.41
2:A:522:GLU:H	2:A:695:ARG:HH22	1.68	0.41
2:A:541:LEU:HD21	2:A:736:LEU:HD22	2.02	0.41
1:B:634:TRP:O	1:B:638:ALA:N	2.51	0.41
2:C:615:LEU:C	2:C:616:ASN:CG	2.87	0.41
1:D:180:TYR:HA	1:D:183:PHE:CD2	2.55	0.41
1:D:286:TYR:OH	1:D:379:GLU:OE2	2.30	0.41
2:A:105:THR:O	2:A:108:SER:OG	2.26	0.41
2:A:772:VAL:O	2:A:775:SER:OG	2.31	0.41
2:C:684:VAL:H	2:C:731:TRP:HZ2	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:699:LEU:O	2:A:702:MET:HB2	2.20	0.41
2:C:520:ASN:HB3	2:C:695:ARG:NH2	2.34	0.41
2:A:307:GLY:O	2:A:311:ASN:ND2	2.41	0.41
2:C:541:LEU:HD21	2:C:736:LEU:HD22	2.02	0.41
2:C:614:LEU:HD21	2:C:636:TRP:HB3	2.02	0.41
1:D:301:THR:HG21	1:D:341:VAL:HG13	2.03	0.41
2:A:228:ALA:C	2:A:232:TYR:CD2	2.99	0.41
2:A:400:ILE:HD13	2:A:463:LEU:HD13	2.02	0.41
2:A:489:ARG:HH21	1:B:194:SER:HA	1.86	0.41
1:D:79:PRO:HA	1:D:82:LEU:HD12	2.02	0.41
2:A:139:ARG:N	2:A:345:ASP:OD1	2.47	0.41
1:B:90:MET:HE1	1:B:316:ALA:HB1	2.02	0.41
1:B:180:TYR:HA	1:B:183:PHE:CD2	2.56	0.41
1:D:161:ILE:HA	1:D:386:ARG:HH12	1.85	0.41
2:A:631:ILE:HG13	1:B:606:TRP:HH2	1.85	0.41
1:B:759:THR:HG22	2:C:535:TYR:HE2	1.86	0.41
2:C:569:SER:O	2:C:573:VAL:HG23	2.21	0.41
2:A:354:MET:HB3	2:A:361:LEU:HD22	2.03	0.41
2:A:408:PHE:HA	2:A:458:PHE:HD2	1.86	0.41
1:B:96:HIS:HE1	1:B:316:ALA:N	2.19	0.41
1:B:525:SER:OG	1:B:763:ILE:HB	2.20	0.41
2:C:408:PHE:HA	2:C:458:PHE:HD2	1.86	0.41
1:D:251:TYR:OH	1:D:397:SER:N	2.51	0.41
1:D:735:LEU:HB3	1:D:749:THR:HG21	2.02	0.41
2:A:762:MET:HE2	2:A:768:TRP:HB2	2.03	0.41
1:B:243:ALA:HA	1:B:246:LEU:HD12	2.03	0.41
1:B:533:ILE:HD12	1:B:690:THR:CG2	2.50	0.41
2:C:210:GLU:O	2:C:213:GLU:HG3	2.21	0.41
2:C:522:GLU:H	2:C:695:ARG:HH22	1.68	0.41
2:C:699:LEU:O	2:C:702:MET:HB2	2.20	0.41
1:D:195:PHE:H	2:C:489:ARG:HH21	1.69	0.41
1:D:251:TYR:CE2	1:D:395:SER:HA	2.56	0.41
1:B:63:LEU:HD21	1:B:300:THR:CA	2.38	0.41
1:B:65:LEU:HD23	1:B:65:LEU:HA	1.92	0.41
2:C:229:ALA:O	2:C:233:ARG:CA	2.64	0.41
2:C:400:ILE:HD13	2:C:463:LEU:HD13	2.02	0.41
1:D:750:ILE:CG2	1:D:750:ILE:O	2.69	0.40
1:D:76:ARG:HD3	1:D:78:ASP:HB2	2.04	0.40
1:D:286:TYR:CZ	1:D:360:ARG:HD3	2.57	0.40
2:A:569:SER:O	2:A:573:VAL:HG23	2.21	0.40
1:D:243:ALA:HA	1:D:246:LEU:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:566:LEU:HD22	1:D:608:LEU:HD22	2.04	0.40
1:D:685:VAL:H	1:D:730:TYR:HE1	1.69	0.40
1:B:262:SER:OG	1:B:263:GLY:N	2.48	0.40
2:C:207:LEU:CA	2:C:210:GLU:OE1	2.69	0.40
2:C:762:MET:HE2	2:C:768:TRP:HB2	2.03	0.40
1:D:64:PRO:HG2	1:D:65:LEU:HG	2.02	0.40
2:A:228:ALA:O	2:A:232:TYR:HD2	2.03	0.40
1:B:685:VAL:H	1:B:730:TYR:HE1	1.69	0.40
2:C:325:LEU:HD23	2:C:325:LEU:HA	1.90	0.40
2:C:615:LEU:HD23	2:C:615:LEU:HA	1.86	0.40
1:B:64:PRO:HG2	1:B:65:LEU:HG	2.02	0.40
1:B:160:LYS:HD2	1:B:378:TRP:HH2	1.86	0.40
1:B:647:ALA:HA	1:B:650:ALA:HB3	2.03	0.40
2:C:210:GLU:O	2:C:213:GLU:CG	2.70	0.40
2:C:776[B]:ILE:HD13	2:C:776[B]:ILE:HA	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	736/853 (86%)	656 (89%)	77 (10%)	3 (0%)	30	67
1	D	736/853 (86%)	658 (89%)	75 (10%)	3 (0%)	30	67
2	A	778/847 (92%)	693 (89%)	75 (10%)	10 (1%)	9	41
2	C	778/847 (92%)	692 (89%)	76 (10%)	10 (1%)	9	41
All	All	3028/3400 (89%)	2699 (89%)	303 (10%)	26 (1%)	16	49

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	327	PRO
1	D	329	VAL
2	A	95	PRO
2	A	98	PRO
2	A	212	LYS
2	A	616	ASN
1	B	327	PRO
1	B	329	VAL
2	C	95	PRO
2	C	98	PRO
2	C	212	LYS
2	C	616	ASN
2	A	97	THR
2	A	211	ALA
2	A	560	SER
2	C	97	THR
2	C	211	ALA
2	C	560	SER
2	A	74	MET
2	C	74	MET
2	A	238	LEU
2	C	238	LEU
1	D	391	PRO
2	A	94	HIS
1	B	391	PRO
2	C	94	HIS

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	B	612/738 (83%)	612 (100%)	0	100	100
1	D	612/738 (83%)	612 (100%)	0	100	100
2	A	660/731 (90%)	659 (100%)	1 (0%)	87	85
2	C	660/731 (90%)	658 (100%)	2 (0%)	86	84
All	All	2544/2938 (87%)	2541 (100%)	3 (0%)	87	88

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

Mol	Chain	Res	Type
2	A	246	VAL
2	C	226	ASP
2	C	246	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	42	HIS
1	D	96	HIS
1	D	128	HIS
1	D	216	GLN
1	D	223	HIS
1	D	358	HIS
1	D	380	ASN
1	D	405	HIS
2	A	38	HIS
2	A	61	ASN
2	A	134	HIS
2	A	161	ASN
2	A	162	HIS
2	A	357	GLN
2	A	404	HIS
2	A	440	ASN
2	A	559	GLN
1	B	42	HIS
1	B	96	HIS
1	B	128	HIS
1	B	358	HIS
1	B	380	ASN
1	B	387	HIS
1	B	405	HIS
2	C	38	HIS
2	C	61	ASN
2	C	161	ASN
2	C	162	HIS
2	C	404	HIS
2	C	440	ASN
2	C	525	GLN
2	C	559	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

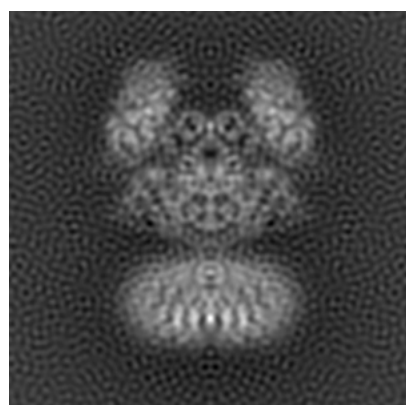
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9714. These allow visual inspection of the internal detail of the map and identification of artifacts.

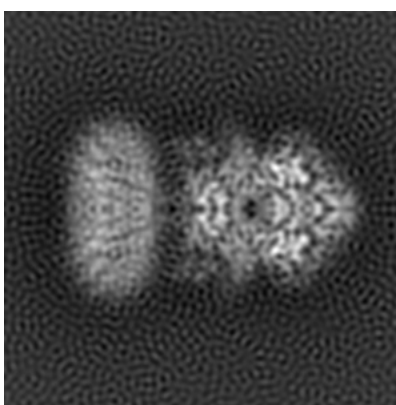
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

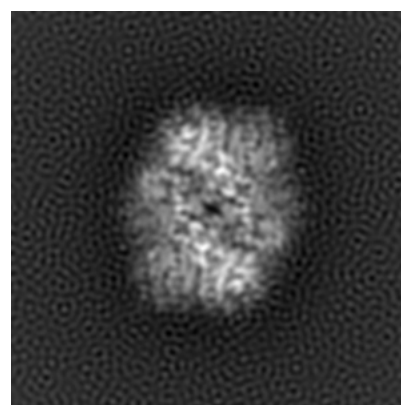
6.1.1 Primary map



X



Y

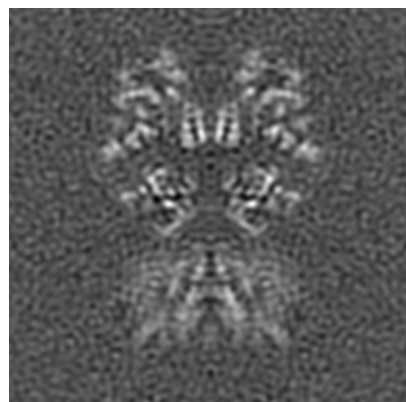


Z

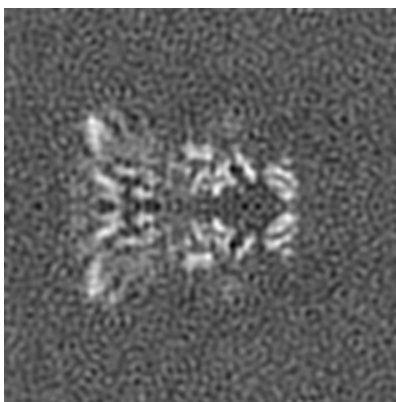
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

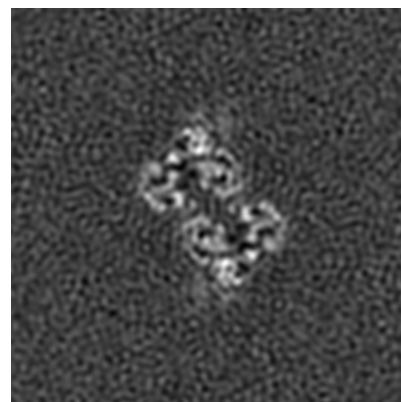
6.2.1 Primary map



X Index: 120



Y Index: 120

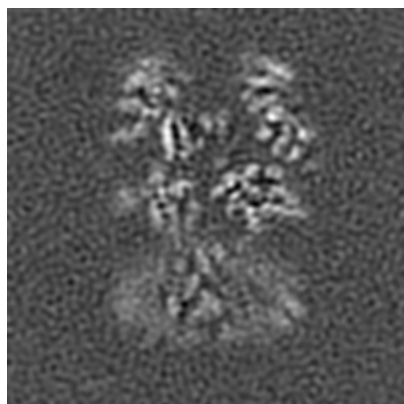


Z Index: 120

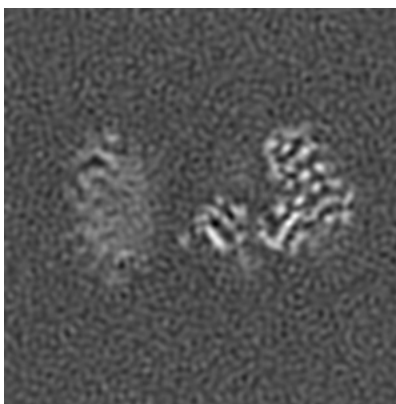
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

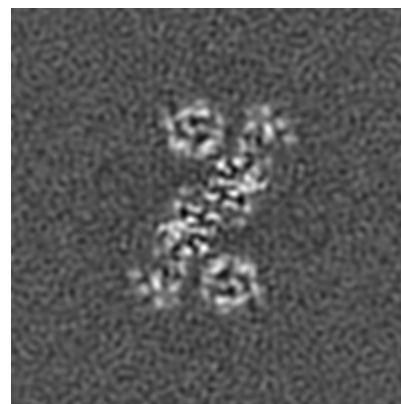
6.3.1 Primary map



X Index: 115



Y Index: 158

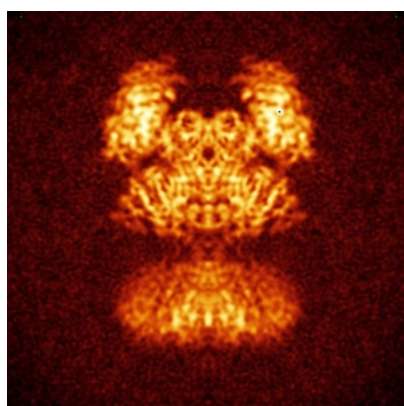


Z Index: 165

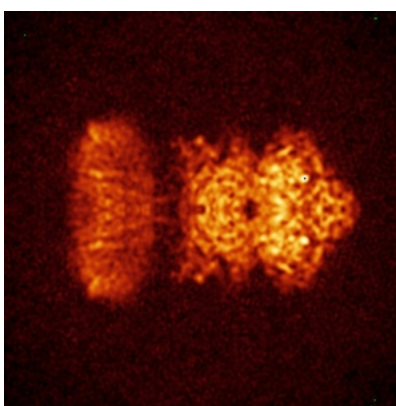
The images above show the largest variance slices of the map in three orthogonal directions.

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

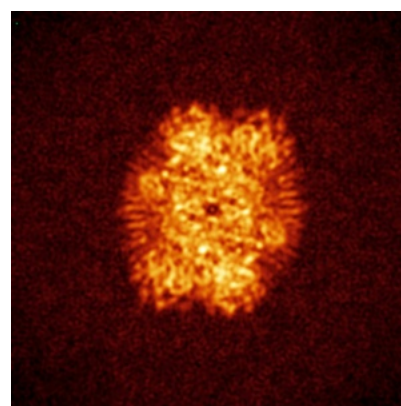
6.4.1 Primary map



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

This section was not generated.

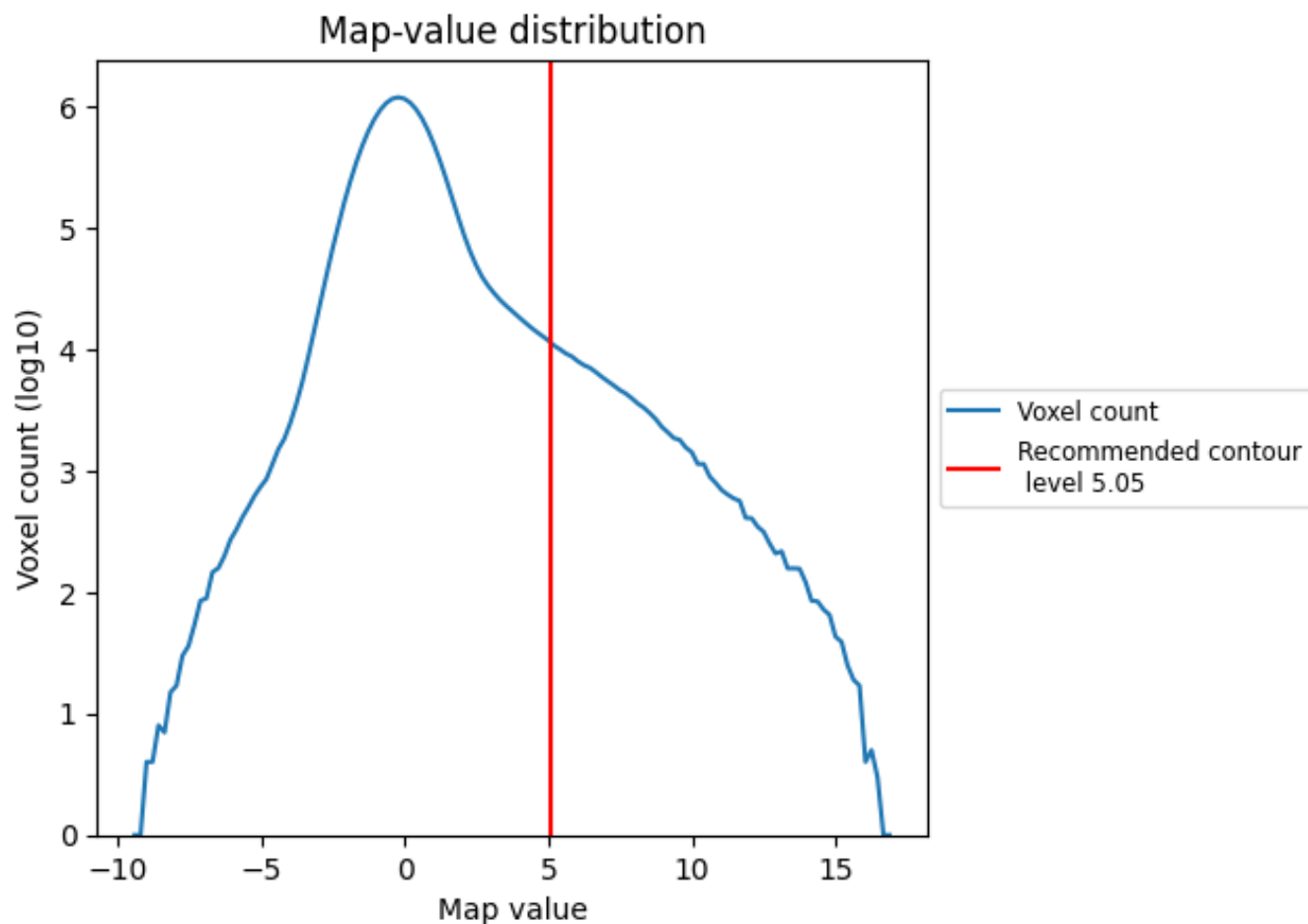
6.6 Mask visualisation

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

7 Map analysis [i](#)

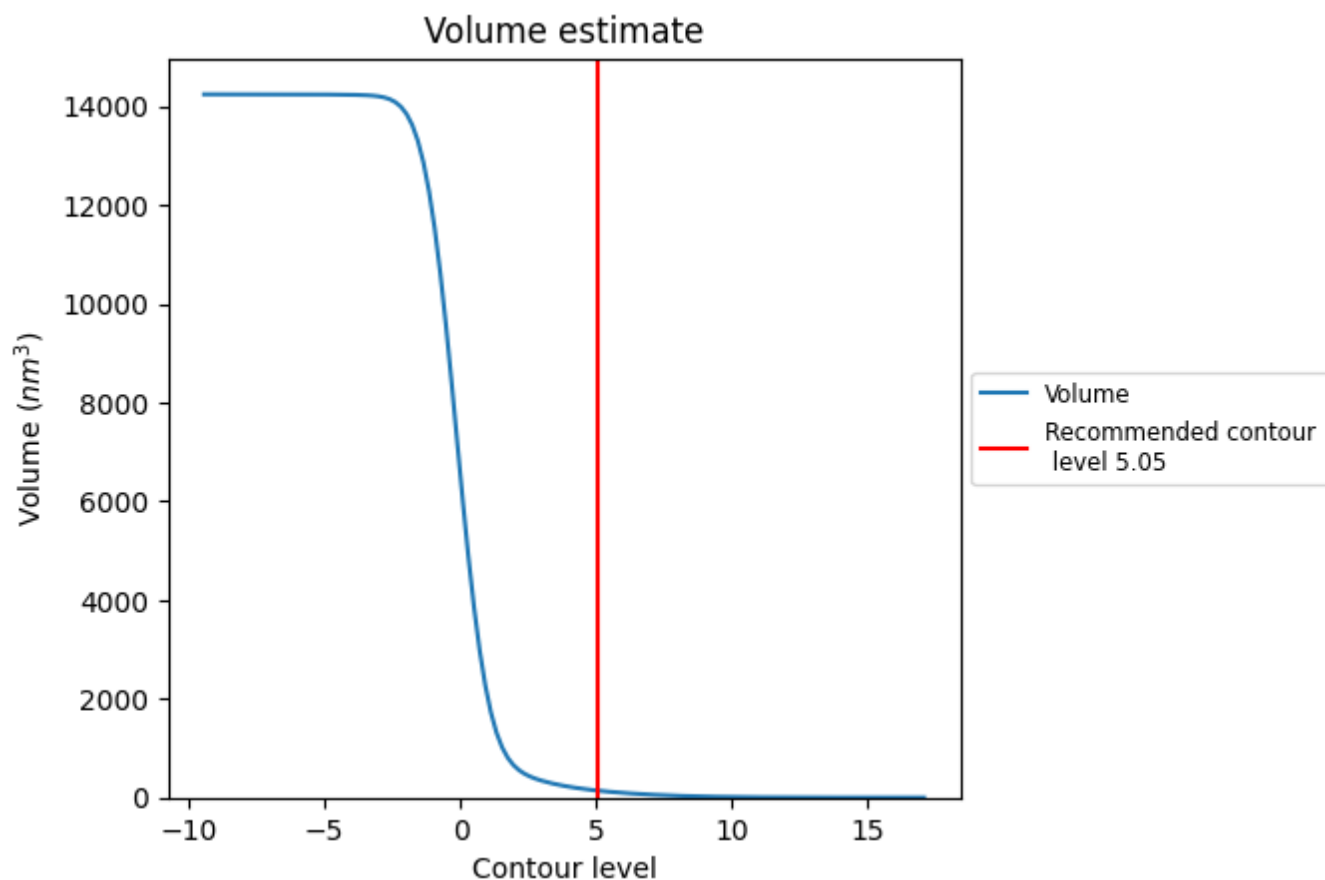
This section contains the results of statistical analysis of the map.

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.

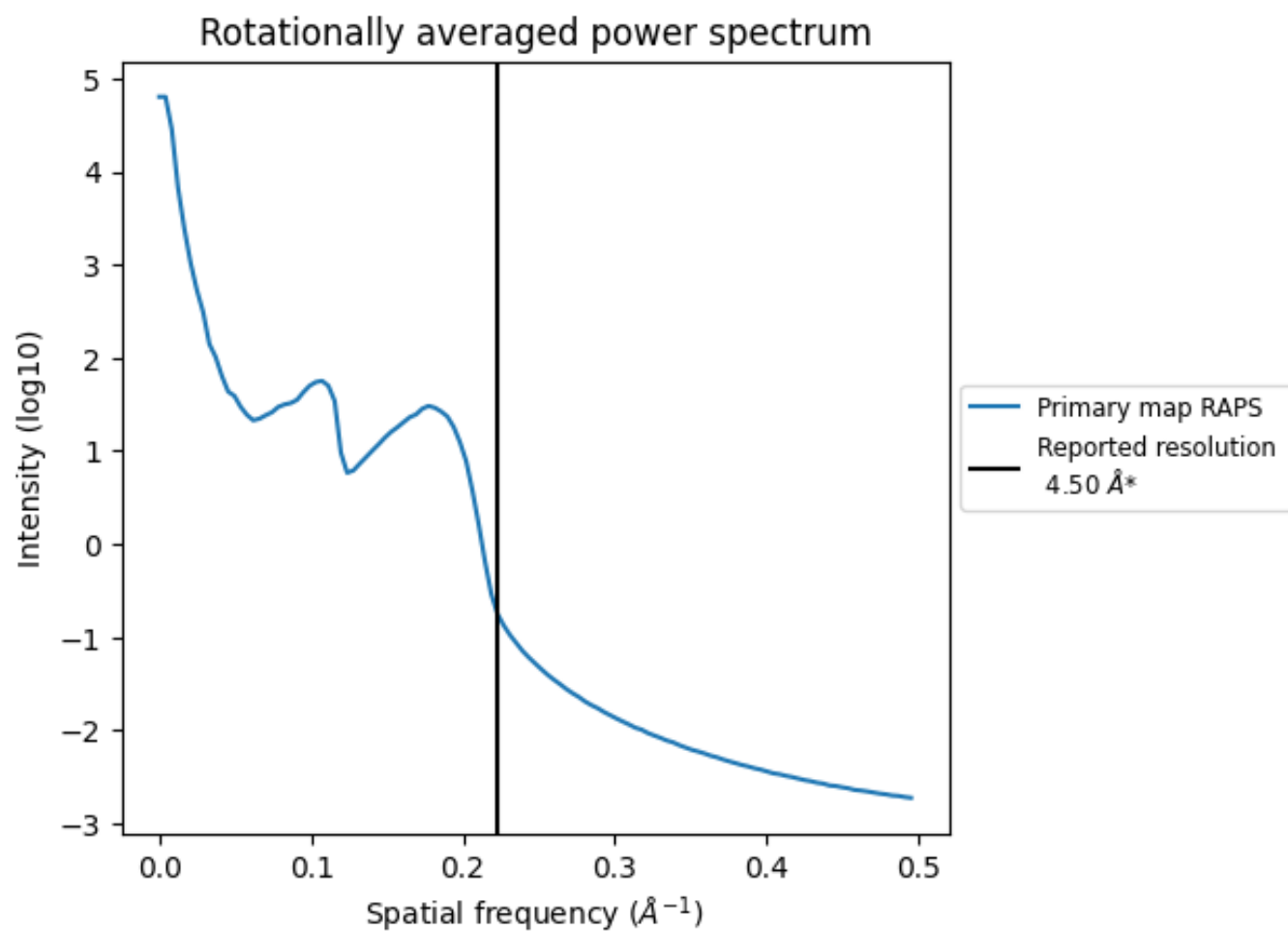
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 142 nm³; this corresponds to an approximate mass of 128 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



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

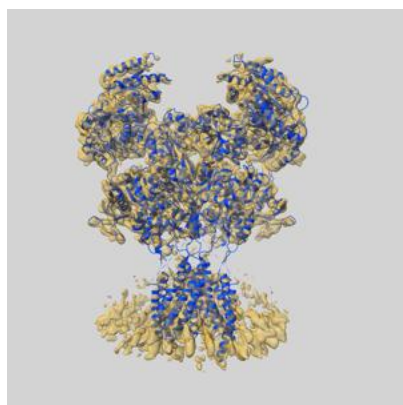
8 Fourier-Shell correlation ⓘ

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

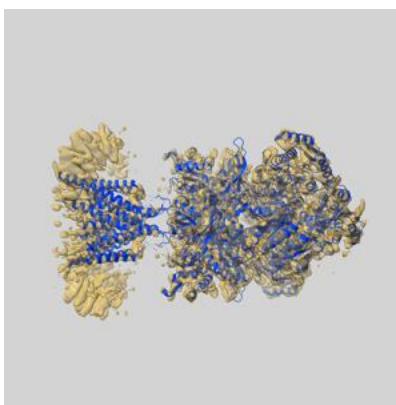
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9714 and PDB model 6IRA. Per-residue inclusion information can be found in [section 3](#) on [page 5](#).

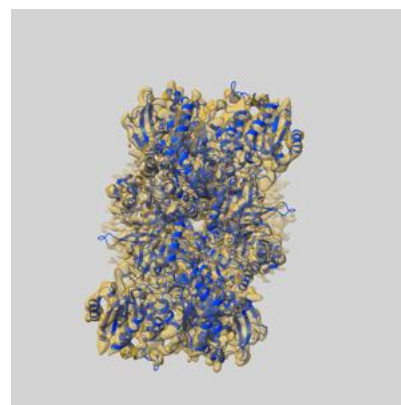
9.1 Map-model overlay [i](#)



X



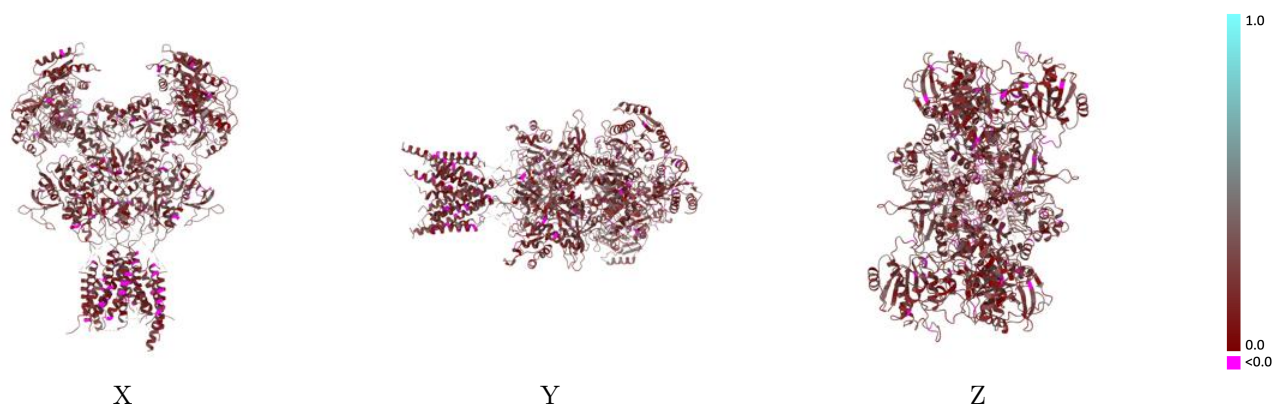
Y



Z

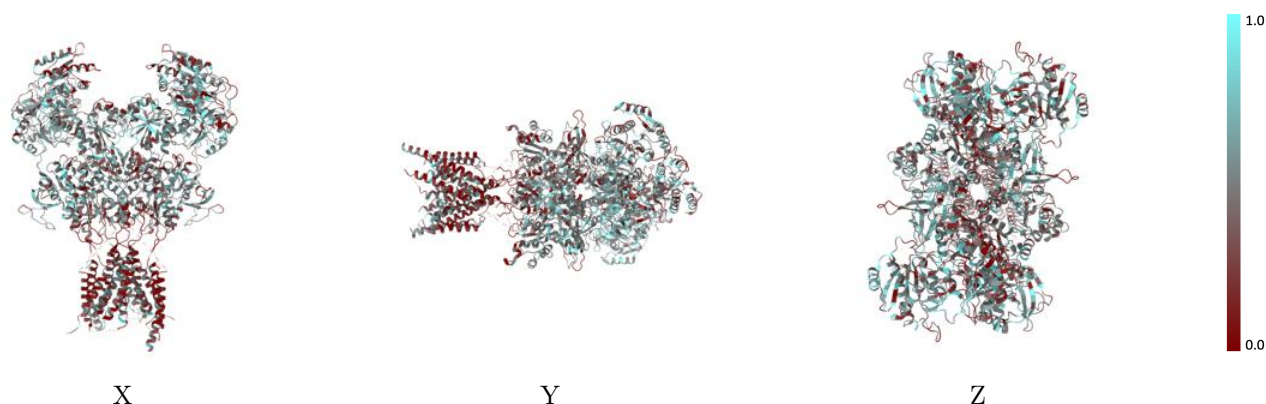
The images above show the 3D surface view of the map at the recommended contour level 5.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



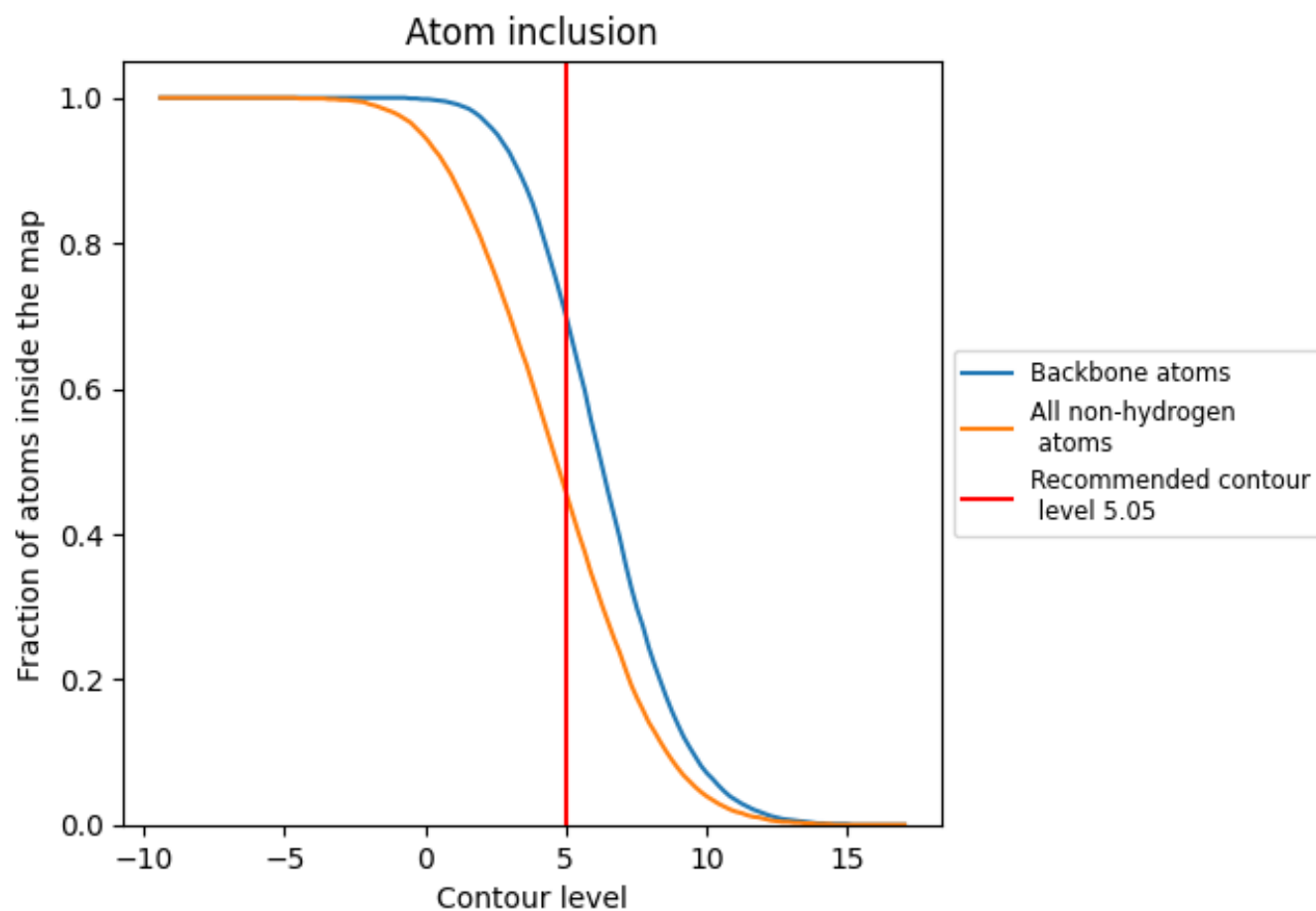
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 45% 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 (5.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4520	0.2270
A	0.4500	0.2330
B	0.4630	0.2330
C	0.4500	0.2250
D	0.4480	0.2180

