Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2023 – 04:08 PM EDT

PDB ID	:	2Q48
Title	:	Ensemble refinement of the protein crystal structure of gene product from Arabidopsis thaliana At5g48480
Authors	:	Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on	:	2007-05-31
Resolution	:	1.80 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp
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:

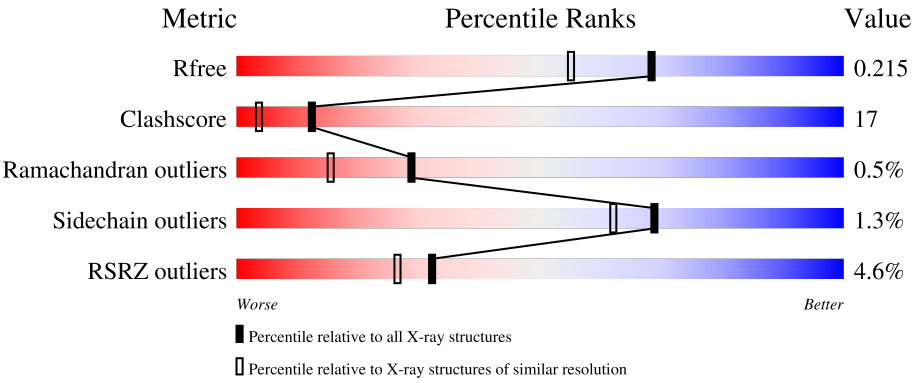
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1-A	166	2% 52% 20% 28%
1	1-B	166	6% 54% 19% 27%
1	2-A	166	2% 54% 17% • 28%
1	2-B	166	6% 52% 20% • 27%
1	3-A	166	2% 43% 27% • 28%

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Mol	Chain	Length	Quality of chain
1	3-B	166	6% 54% 20% 27%
1	4-A	166	2% 55% 17% 28%
1	4-B	166	6% 52% 20% 27%
1	5-A	166	2% 61% 11% 28%
1	5-B	166	6% 58% 15% 27%
1	6-A	166	2% 52% 20% 28%
1	6-B	166	6% 49% 25% 27%
1	7-A	166	2% 48% 25% 28%
1	7-B	166	6% 51% 22% 27%
1	8-A	166	2% 54% 17% 28%
1	8-B	166	6% 48% 24% 27%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 16272 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Protein At5g48480.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	1-A	120	Total	C	N	O	S	Se	0	0	0
			886	572	137	175	1	1			
1	2-A	120	Total	C	N	O	S	Se	0	0	0
			886	572	137	175	1	1			
1	3-A	120	Total	C	N	O	S	Se	0	0	0
			886	572	137	175	1	1			
1	4-A	120	Total	C	N	O	S	Se	0	0	0
			886	572	137	175	1	1			
1	5-A	120	Total	C	N	O	S	Se	0	0	0
			886	572	137	175	1	1			
1	6-A	120	Total	C	N	O	S	Se	0	0	0
			886	572	137	175	1	1			
1	7-A	120	Total	C	N	O	S	Se	0	0	0
			886	572	137	175	1	1			
1	8-A	120	Total	C	N	O	S	Se	0	0	0
			886	572	137	175	1	1			
1	1-B	122	Total	C	N	O	S	Se	0	0	0
			896	577	139	178	1	1			
1	2-B	122	Total	C	N	O	S	Se	0	0	0
			896	577	139	178	1	1			
1	3-B	122	Total	C	N	O	S	Se	0	0	0
			896	577	139	178	1	1			
1	4-B	122	Total	C	N	O	S	Se	0	0	0
			896	577	139	178	1	1			
1	5-B	122	Total	C	N	O	S	Se	0	0	0
			896	577	139	178	1	1			
1	6-B	122	Total	C	N	O	S	Se	0	0	0
			896	577	139	178	1	1			
1	7-B	122	Total	C	N	O	S	Se	0	0	0
			896	577	139	178	1	1			
1	8-B	122	Total	C	N	O	S	Se	0	0	0
			896	577	139	178	1	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q9LV66
A	29	MSE	MET	modified residue	UNP Q9LV66
B	1	MSE	MET	modified residue	UNP Q9LV66
B	29	MSE	MET	modified residue	UNP Q9LV66

- Molecule 2 is water.

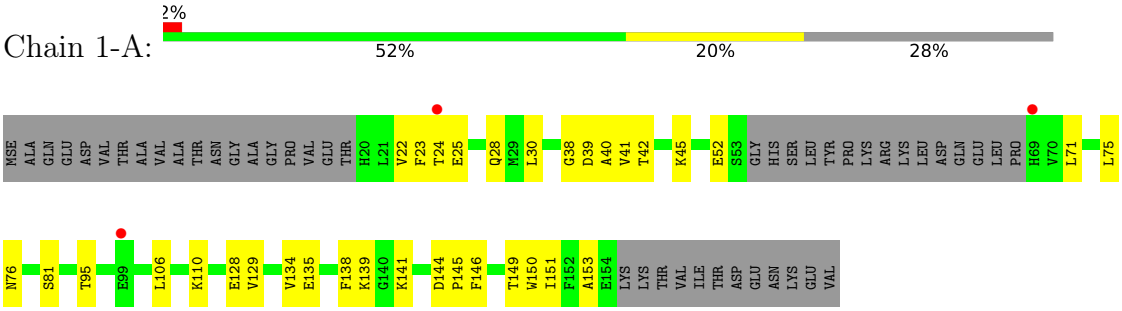
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	1-A	134	Total O 134 134	0	0
2	2-A	131	Total O 131 131	0	0
2	3-A	130	Total O 130 130	0	0
2	4-A	131	Total O 131 131	0	0
2	5-A	131	Total O 131 131	0	0
2	6-A	131	Total O 131 131	0	0
2	7-A	125	Total O 125 125	0	0
2	8-A	133	Total O 133 133	0	0
2	1-B	118	Total O 118 118	0	0
2	2-B	121	Total O 121 121	0	0
2	3-B	122	Total O 122 122	0	0
2	4-B	121	Total O 121 121	0	0
2	5-B	121	Total O 121 121	0	0
2	6-B	121	Total O 121 121	0	0
2	7-B	127	Total O 127 127	0	0
2	8-B	119	Total O 119 119	0	0

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 electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

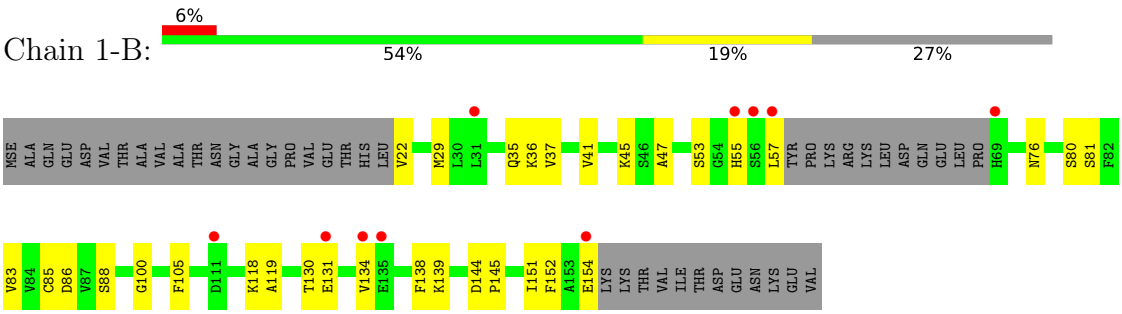
• Molecule 1: Protein At5g48480

Chain 1-A:



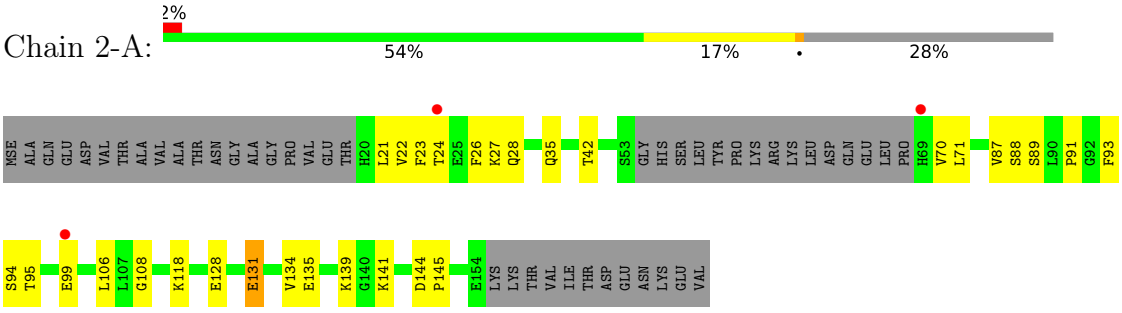
• Molecule 1: Protein At5g48480

Chain 1-B:



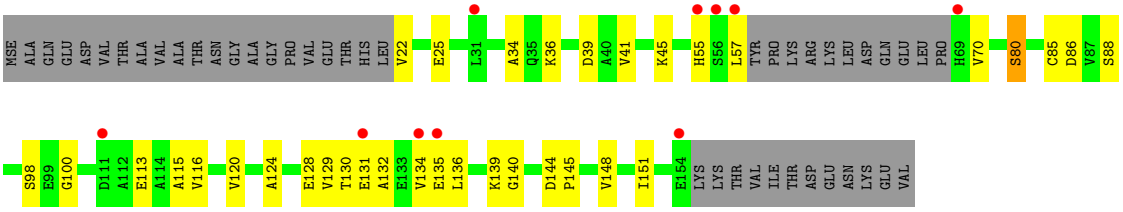
• Molecule 1: Protein At5g48480

Chain 2-A:



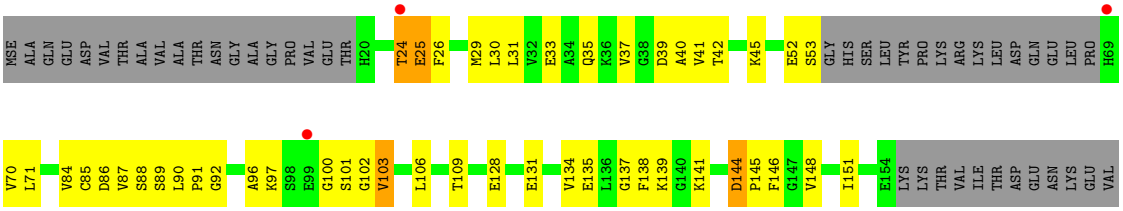
• Molecule 1: Protein At5g48480

Chain 2-B:



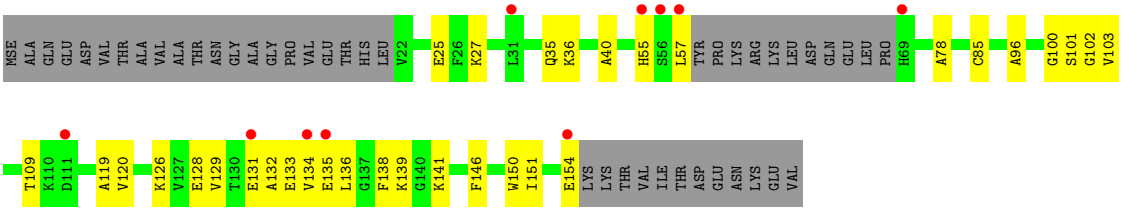
• Molecule 1: Protein At5g48480

Chain 3-A:



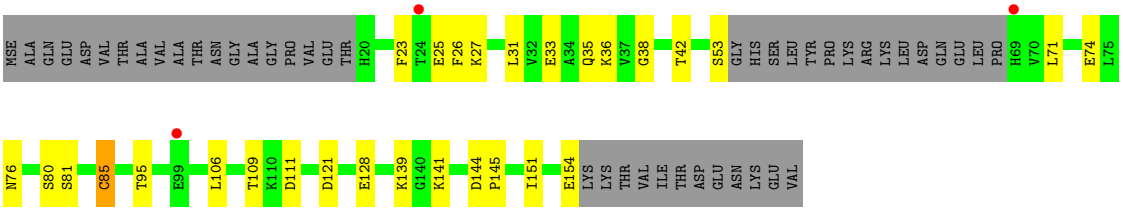
• Molecule 1: Protein At5g48480

Chain 3-B:



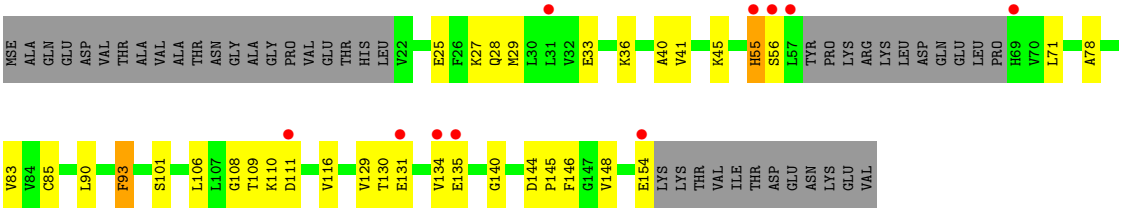
• Molecule 1: Protein At5g48480

Chain 4-A:



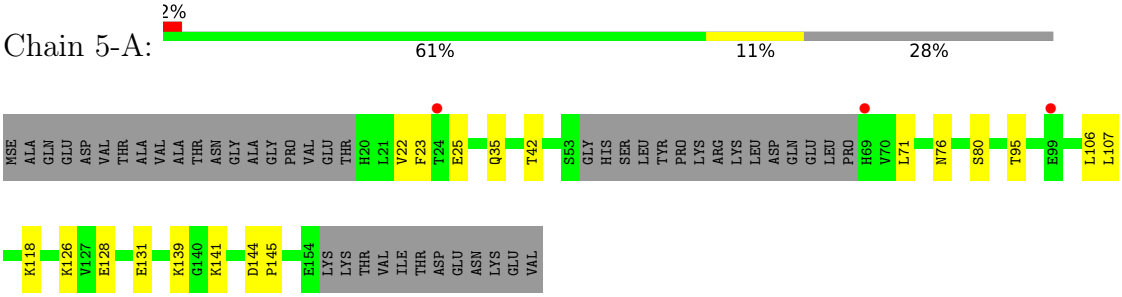
• Molecule 1: Protein At5g48480

Chain 4-B:



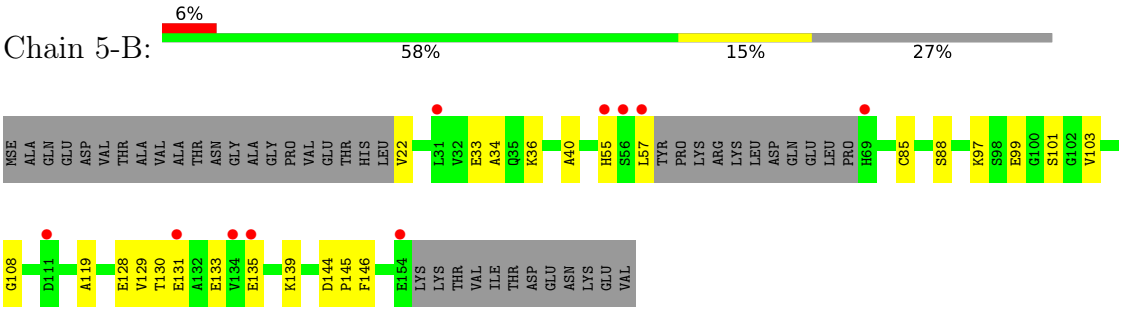
• Molecule 1: Protein At5g48480

Chain 5-A:



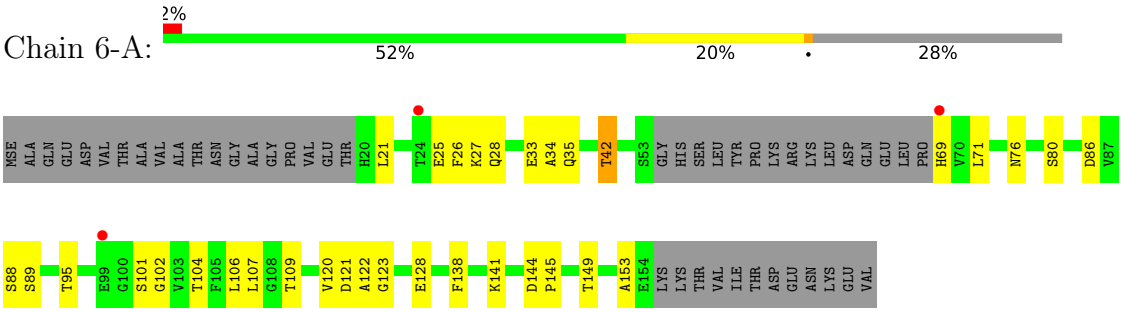
• Molecule 1: Protein At5g48480

Chain 5-B:



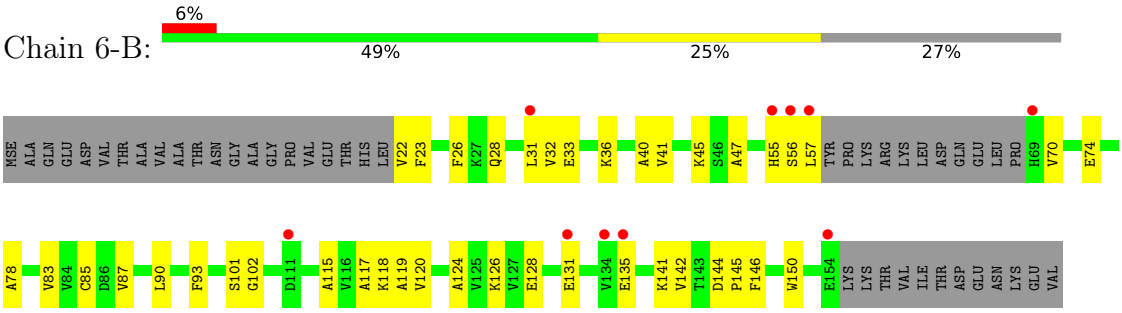
• Molecule 1: Protein At5g48480

Chain 6-A:



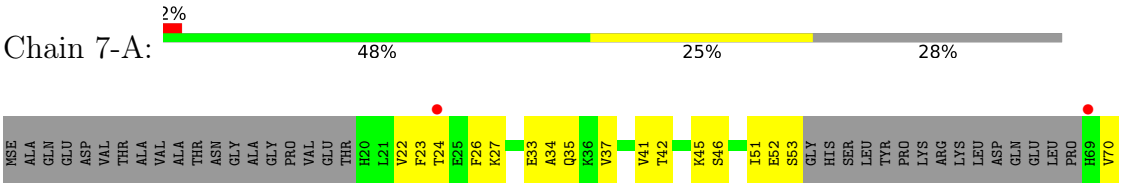
• Molecule 1: Protein At5g48480

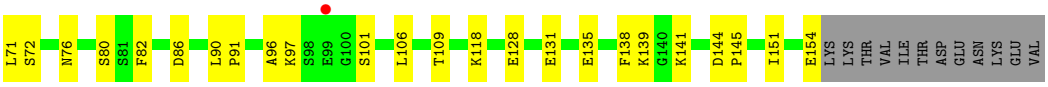
Chain 6-B:



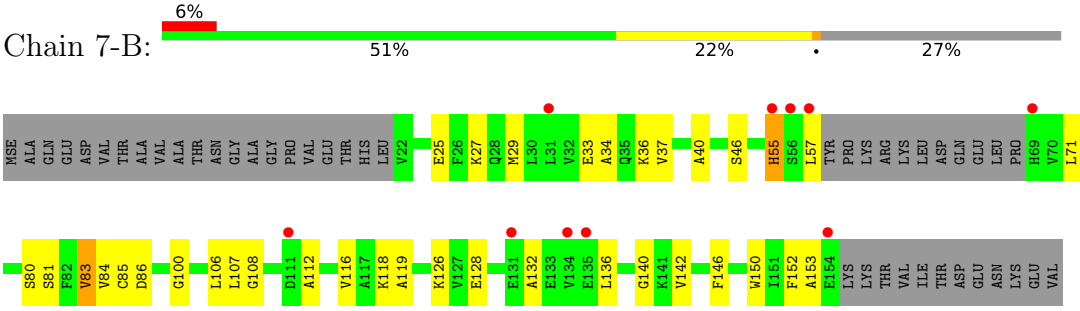
• Molecule 1: Protein At5g48480

Chain 7-A:

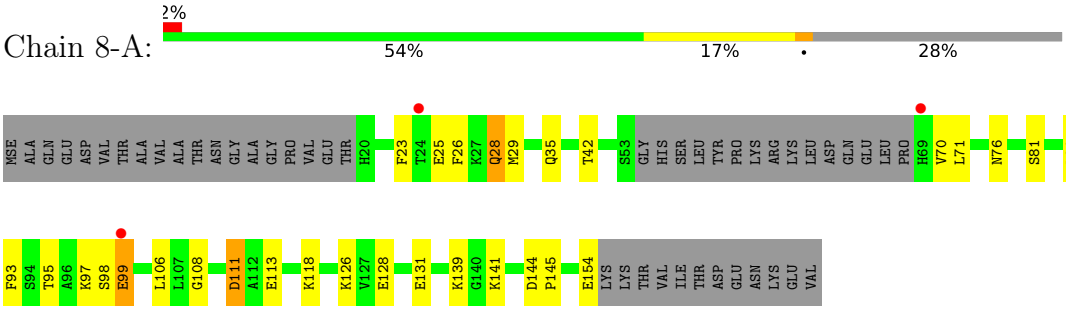




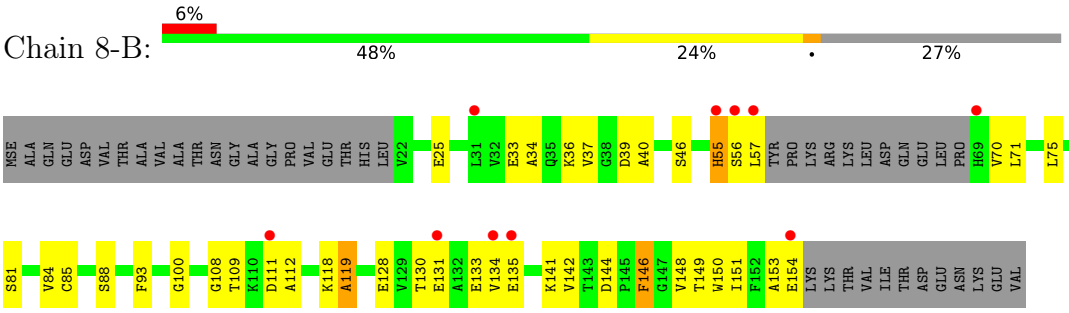
• Molecule 1: Protein At5g48480



• Molecule 1: Protein At5g48480



• Molecule 1: Protein At5g48480



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	55.87Å 55.87Å 147.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	27.45 – 1.80 27.45 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.6 (27.45-1.80) 98.7 (27.45-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	11.61 (at 1.80Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.167 , 0.214 0.173 , 0.215	Depositor DCC
R_{free} test set	1282 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	21.5	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 69.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	16272	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	1-A	0.94	0/900	0.90	0/1215
1	1-B	0.91	1/910 (0.1%)	0.84	0/1228
1	2-A	0.93	0/900	0.86	0/1215
1	2-B	0.89	0/910	0.82	0/1228
1	3-A	1.01	0/900	0.95	1/1215 (0.1%)
1	3-B	0.87	1/910 (0.1%)	0.83	0/1228
1	4-A	0.93	1/900 (0.1%)	0.91	0/1215
1	4-B	0.91	0/910	0.87	0/1228
1	5-A	1.00	0/900	0.92	0/1215
1	5-B	0.95	1/910 (0.1%)	0.84	0/1228
1	6-A	0.99	0/900	0.95	0/1215
1	6-B	0.97	1/910 (0.1%)	0.93	2/1228 (0.2%)
1	7-A	1.02	1/900 (0.1%)	0.91	0/1215
1	7-B	0.97	1/910 (0.1%)	0.89	0/1228
1	8-A	1.00	0/900	0.93	0/1215
1	8-B	1.01	2/910 (0.2%)	0.86	0/1228
All	All	0.96	9/14480 (0.1%)	0.89	3/19544 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	8-B	0	1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	7-A	80	SER	CB-OG	-6.50	1.33	1.42
1	7-B	119	ALA	CA-CB	6.24	1.65	1.52
1	5-B	119	ALA	CA-CB	6.02	1.65	1.52
1	8-B	119	ALA	CA-CB	5.90	1.64	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1-B	119	ALA	CA-CB	5.34	1.63	1.52
1	6-B	119	ALA	CA-CB	5.31	1.63	1.52
1	4-A	85	CYS	CB-SG	-5.12	1.73	1.81
1	3-B	119	ALA	CA-CB	5.06	1.63	1.52
1	8-B	84	VAL	CB-CG1	5.03	1.63	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	3-A	103	VAL	N-CA-C	7.15	130.30	111.00
1	6-B	101	SER	C-N-CA	-6.00	109.70	122.30
1	6-B	26	PHE	N-CA-C	-5.44	96.30	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	8-B	146	PHE	Sidechain

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	1-A	886	0	878	38	0
1	1-B	896	0	886	21	0
1	2-A	886	0	878	39	0
1	2-B	896	0	886	27	0
1	3-A	886	0	878	59	0
1	3-B	896	0	886	34	0
1	4-A	886	0	878	26	0
1	4-B	896	0	886	30	0
1	5-A	886	0	878	19	0
1	5-B	896	0	886	21	0
1	6-A	886	0	878	35	0
1	6-B	896	0	886	29	0
1	7-A	886	0	878	42	0
1	7-B	896	0	886	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	8-A	886	0	878	34	0
1	8-B	896	0	886	36	0
2	1-A	134	0	0	12	0
2	1-B	118	0	0	3	0
2	2-A	131	0	0	18	0
2	2-B	121	0	0	8	0
2	3-A	130	0	0	13	0
2	3-B	122	0	0	8	0
2	4-A	131	0	0	10	0
2	4-B	121	0	0	5	0
2	5-A	131	0	0	13	0
2	5-B	121	0	0	9	0
2	6-A	131	0	0	14	0
2	6-B	121	0	0	6	0
2	7-A	125	0	0	15	0
2	7-B	127	0	0	5	0
2	8-A	133	0	0	15	0
2	8-B	119	0	0	7	0
All	All	16272	0	14112	479	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 17.

All (479) 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:25:GLU:HA	2:B:200:HOH:O	1.53	1.07
1:A:39:ASP:OD2	2:A:253:HOH:O	1.75	1.05
1:B:142:VAL:HG23	1:B:150:TRP:HB2	1.44	0.99
1:A:25:GLU:HA	2:B:202:HOH:O	1.63	0.96
1:A:38:GLY:O	1:A:42:THR:HG23	1.68	0.93
1:A:25:GLU:HA	2:A:202:HOH:O	1.69	0.91
1:A:121:ASP:OD2	2:A:201:HOH:O	1.87	0.91
1:A:102:GLY:H	1:B:102:GLY:H	1.15	0.90
1:B:33:GLU:HG2	1:B:36:LYS:HG3	1.50	0.90
1:A:25:GLU:HA	2:B:201:HOH:O	1.72	0.89
1:A:21:LEU:HD21	1:B:115:ALA:HA	1.54	0.88
1:B:85:CYS:HB3	2:B:190:HOH:O	1.71	0.88
1:A:102:GLY:HA3	1:B:103:VAL:HG23	1.58	0.86
1:A:141:LYS:NZ	2:A:287:HOH:O	1.98	0.85
1:A:139:LYS:HE3	2:A:245:HOH:O	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:VAL:HG13	1:A:139:LYS:HE2	1.58	0.85
1:A:31:LEU:HD23	1:A:87:VAL:HG23	1.59	0.84
1:A:139:LYS:HE3	2:A:244:HOH:O	1.76	0.84
1:A:139:LYS:HE3	2:A:243:HOH:O	1.76	0.84
1:B:22:VAL:HG13	2:B:247:HOH:O	1.77	0.84
1:A:139:LYS:HE3	2:A:244:HOH:O	1.77	0.84
1:B:29:MSE:HA	1:B:83:VAL:HG22	1.60	0.83
1:A:42:THR:HG22	2:A:229:HOH:O	1.78	0.83
1:A:35:GLN:HG3	2:A:273:HOH:O	1.79	0.83
1:B:85:CYS:HB2	2:B:192:HOH:O	1.77	0.83
1:B:85:CYS:HB3	2:B:191:HOH:O	1.78	0.82
1:A:139:LYS:HE3	2:A:245:HOH:O	1.78	0.81
1:A:111:ASP:OD1	1:A:113:GLU:HB3	1.80	0.81
1:B:85:CYS:HB3	2:B:189:HOH:O	1.79	0.81
1:A:70:VAL:HB	1:A:89:SER:OG	1.80	0.80
1:A:35:GLN:HG3	2:A:272:HOH:O	1.79	0.80
1:A:70:VAL:HG11	1:A:90:LEU:HD23	1.62	0.80
1:B:33:GLU:HG2	2:B:176:HOH:O	1.82	0.80
1:A:42:THR:HG21	2:A:209:HOH:O	1.82	0.79
1:A:121:ASP:OD2	2:A:202:HOH:O	1.99	0.79
1:A:151:ILE:HD12	1:B:29:MSE:SE	2.31	0.79
1:A:42:THR:HG21	2:A:208:HOH:O	1.83	0.79
1:A:42:THR:HG22	2:A:230:HOH:O	1.83	0.78
1:B:85:CYS:HB3	2:B:191:HOH:O	1.82	0.78
1:A:42:THR:HG21	2:A:206:HOH:O	1.84	0.78
1:B:22:VAL:HG13	2:B:246:HOH:O	1.83	0.78
1:B:131:GLU:O	1:B:135:GLU:HG3	1.83	0.77
1:A:35:GLN:HG3	2:A:267:HOH:O	1.82	0.77
1:A:70:VAL:HG12	1:A:89:SER:O	1.84	0.77
1:B:29:MSE:HA	1:B:83:VAL:HG22	1.66	0.76
1:B:85:CYS:HB3	2:B:191:HOH:O	1.84	0.76
1:A:41:VAL:O	1:A:45:LYS:HG3	1.86	0.76
1:A:95:THR:HB	2:A:254:HOH:O	1.87	0.74
1:A:141:LYS:HG3	1:A:151:ILE:CD1	2.18	0.74
1:B:25:GLU:OE1	1:B:27:LYS:HE2	1.87	0.74
1:A:95:THR:HB	2:A:255:HOH:O	1.87	0.74
1:B:29:MSE:HE3	1:B:85:CYS:SG	2.29	0.73
1:A:106:LEU:HD21	1:A:153:ALA:HB3	1.71	0.73
1:B:33:GLU:HG3	2:B:168:HOH:O	1.89	0.73
1:B:144:ASP:OD1	1:B:148:VAL:N	2.20	0.72
1:A:141:LYS:HG3	1:A:151:ILE:HD12	1.72	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:ALA:O	1:B:118:LYS:HD3	1.89	0.72
1:A:38:GLY:O	1:A:42:THR:OG1	2.05	0.72
1:B:85:CYS:HB3	2:B:191:HOH:O	1.89	0.72
1:A:134:VAL:HG13	1:A:139:LYS:HE2	1.72	0.71
1:A:25:GLU:HG2	1:B:108:GLY:HA3	1.71	0.71
1:A:71:LEU:HB2	2:A:262:HOH:O	1.90	0.71
1:A:141:LYS:NZ	2:A:282:HOH:O	1.95	0.71
1:B:101:SER:HB3	2:B:221:HOH:O	1.90	0.70
1:A:22:VAL:HG22	1:A:23:PHE:H	1.57	0.70
1:A:25:GLU:HG2	1:B:108:GLY:HA3	1.74	0.70
1:A:27:LYS:HB2	1:B:106:LEU:HB3	1.73	0.70
1:B:85:CYS:HB3	2:B:188:HOH:O	1.90	0.70
1:A:134:VAL:HG13	1:A:139:LYS:HE2	1.72	0.70
1:A:118:LYS:HE3	2:A:292:HOH:O	1.91	0.69
1:A:95:THR:HB	2:A:255:HOH:O	1.92	0.69
1:B:29:MSE:HA	1:B:83:VAL:HG23	1.75	0.69
1:B:22:VAL:HG13	2:B:246:HOH:O	1.92	0.69
1:A:33:GLU:OE2	2:A:254:HOH:O	2.10	0.68
1:A:42:THR:HG21	2:A:207:HOH:O	1.92	0.68
1:A:109:THR:O	1:A:154:GLU:HA	1.94	0.68
1:B:132:ALA:HB1	2:B:243:HOH:O	1.94	0.68
1:A:149:THR:HG22	1:A:151:ILE:HD11	1.75	0.68
1:A:33:GLU:OE1	2:A:221:HOH:O	2.12	0.67
1:A:35:GLN:NE2	2:A:285:HOH:O	2.27	0.67
1:B:33:GLU:HG3	2:B:168:HOH:O	1.93	0.67
1:A:24:THR:O	2:A:202:HOH:O	2.13	0.67
1:B:39:ASP:OD2	2:B:195:HOH:O	2.11	0.67
1:B:133:GLU:HB3	1:B:138:PHE:O	1.95	0.66
1:B:134:VAL:HG22	1:B:139:LYS:HG2	1.76	0.66
1:A:28:GLN:OE1	2:A:180:HOH:O	2.14	0.66
1:A:23:PHE:CD1	1:B:109:THR:HB	2.31	0.66
1:A:71:LEU:HB2	2:A:259:HOH:O	1.94	0.66
1:B:33:GLU:HG2	1:B:36:LYS:CG	2.24	0.66
1:A:71:LEU:HB2	2:A:262:HOH:O	1.96	0.65
1:A:128:GLU:HG2	2:A:291:HOH:O	1.97	0.65
1:A:31:LEU:HD23	1:A:85:CYS:SG	2.35	0.65
1:B:55:HIS:ND1	2:B:255:HOH:O	2.29	0.65
1:A:135:GLU:HG2	2:A:300:HOH:O	1.95	0.65
1:A:35:GLN:O	2:A:262:HOH:O	2.14	0.65
1:B:151:ILE:HD12	1:B:151:ILE:N	2.11	0.65
1:B:130:THR:O	1:B:134:VAL:HG23	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:GLN:O	2:A:267:HOH:O	2.15	0.64
1:A:141:LYS:CE	2:A:282:HOH:O	2.41	0.63
1:B:25:GLU:OE1	1:B:27:LYS:HE2	1.99	0.63
1:A:128:GLU:HG2	2:A:287:HOH:O	1.97	0.63
1:A:107:LEU:HD22	1:B:23:PHE:CG	2.34	0.63
1:A:71:LEU:HB2	2:A:265:HOH:O	1.97	0.62
1:A:141:LYS:NZ	2:A:229:HOH:O	2.31	0.62
1:A:135:GLU:HG2	2:A:297:HOH:O	1.99	0.62
1:B:128:GLU:HG2	2:B:283:HOH:O	1.99	0.62
1:A:141:LYS:CE	2:A:287:HOH:O	2.44	0.62
1:A:35:GLN:NE2	2:A:291:HOH:O	2.33	0.62
1:B:116:VAL:HG22	1:B:142:VAL:HG13	1.81	0.61
1:A:128:GLU:HG2	2:A:295:HOH:O	2.00	0.61
1:B:116:VAL:HG21	1:B:140:GLY:HA3	1.82	0.61
1:A:126:LYS:HE2	1:A:128:GLU:OE2	2.00	0.61
1:B:129:VAL:HG22	2:B:232:HOH:O	2.00	0.61
1:B:142:VAL:CG2	1:B:150:TRP:HB2	2.27	0.61
1:A:42:THR:HG23	2:A:228:HOH:O	1.99	0.61
1:B:107:LEU:O	1:B:152:PHE:HA	2.01	0.61
1:A:118:LYS:HE3	2:A:291:HOH:O	2.01	0.60
1:A:35:GLN:NE2	2:A:290:HOH:O	2.34	0.60
1:B:144:ASP:HB2	1:B:145:PRO:CD	2.32	0.60
1:B:129:VAL:HG22	2:B:233:HOH:O	2.01	0.60
1:B:33:GLU:OE1	1:B:97:LYS:HD3	2.01	0.60
1:B:144:ASP:HB2	1:B:145:PRO:CD	2.31	0.60
1:A:128:GLU:HG2	2:A:292:HOH:O	2.00	0.60
1:A:102:GLY:HA3	1:B:101:SER:HB2	1.84	0.59
1:B:33:GLU:HB3	1:B:36:LYS:HG3	1.83	0.59
1:B:134:VAL:HG13	1:B:139:LYS:HE2	1.83	0.59
1:B:113:GLU:HB2	2:B:235:HOH:O	2.01	0.59
1:A:95:THR:HB	2:A:256:HOH:O	2.02	0.59
1:A:42:THR:HG23	2:A:230:HOH:O	2.02	0.59
1:B:117:ALA:HB3	2:B:214:HOH:O	2.02	0.59
1:A:141:LYS:HG3	1:A:151:ILE:CD1	2.33	0.59
1:B:100:GLY:HA3	2:B:244:HOH:O	2.03	0.58
1:A:71:LEU:HB2	2:A:263:HOH:O	2.03	0.58
1:A:22:VAL:HG22	1:A:23:PHE:N	2.17	0.58
1:B:109:THR:C	1:B:111:ASP:H	2.06	0.58
1:A:70:VAL:HG12	1:A:70:VAL:O	2.03	0.58
1:A:35:GLN:HG3	2:A:271:HOH:O	2.02	0.58
1:A:42:THR:HG23	2:A:231:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:GLN:NE2	2:A:183:HOH:O	2.34	0.58
1:A:30:LEU:HD13	1:A:103:VAL:HG11	1.84	0.58
1:B:144:ASP:HB2	1:B:145:PRO:CD	2.34	0.58
1:A:108:GLY:HA3	1:B:25:GLU:HG2	1.86	0.58
1:B:100:GLY:HA3	2:B:248:HOH:O	2.04	0.58
1:B:36:LYS:HE2	2:B:236:HOH:O	2.03	0.58
1:A:23:PHE:CD1	1:B:109:THR:HB	2.38	0.57
1:B:36:LYS:HE2	2:B:237:HOH:O	2.04	0.57
1:A:111:ASP:HB3	2:A:243:HOH:O	2.04	0.57
1:A:35:GLN:NE2	2:A:290:HOH:O	2.36	0.57
1:A:28:GLN:HB3	1:B:28:GLN:OE1	2.04	0.57
1:B:131:GLU:O	1:B:135:GLU:HG3	2.04	0.57
1:A:131:GLU:O	1:A:135:GLU:HG3	2.05	0.57
1:A:106:LEU:C	1:A:106:LEU:HD23	2.24	0.57
1:A:134:VAL:HG13	1:A:139:LYS:CE	2.35	0.57
1:A:102:GLY:CA	1:B:101:SER:HB2	2.35	0.57
1:B:111:ASP:HA	1:B:154:GLU:OE1	2.05	0.56
1:A:95:THR:HA	2:A:256:HOH:O	2.05	0.56
1:A:134:VAL:HG13	1:A:139:LYS:CE	2.36	0.56
1:B:109:THR:O	1:B:111:ASP:N	2.38	0.56
2:A:251:HOH:O	1:B:100:GLY:HA3	2.05	0.56
1:A:71:LEU:HB2	2:A:264:HOH:O	2.04	0.56
1:B:130:THR:O	1:B:134:VAL:HG23	2.05	0.56
1:A:71:LEU:HB2	2:A:263:HOH:O	2.06	0.56
1:A:135:GLU:HG2	2:A:291:HOH:O	2.05	0.56
1:B:131:GLU:O	1:B:135:GLU:HG3	2.05	0.56
1:B:96:ALA:O	1:B:101:SER:HB3	2.05	0.56
1:A:71:LEU:HB2	2:A:263:HOH:O	2.06	0.56
1:A:86:ASP:OD2	1:A:86:ASP:C	2.44	0.56
1:A:26:PHE:HB2	1:B:78:ALA:HB3	1.87	0.56
1:A:42:THR:HG23	2:A:231:HOH:O	2.06	0.56
1:A:139:LYS:CE	2:A:244:HOH:O	2.45	0.55
1:A:24:THR:O	1:A:25:GLU:HB3	2.06	0.55
1:A:128:GLU:HG2	2:A:292:HOH:O	2.04	0.55
1:A:42:THR:HG22	2:A:171:HOH:O	2.05	0.55
1:B:57:LEU:HA	1:B:70:VAL:HA	1.88	0.55
1:B:139:LYS:HD2	1:B:154:GLU:OE1	2.07	0.55
1:A:134:VAL:HG13	1:A:139:LYS:CE	2.33	0.55
1:B:144:ASP:OD2	1:B:148:VAL:HB	2.06	0.55
1:A:102:GLY:H	1:B:102:GLY:H	1.54	0.55
1:B:29:MSE:HA	1:B:83:VAL:CG2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:MSE:HE2	1:A:31:LEU:HD11	1.89	0.55
1:B:99:GLU:HB3	2:B:200:HOH:O	2.06	0.55
1:B:22:VAL:HG13	2:B:246:HOH:O	2.06	0.55
1:A:35:GLN:HG3	2:A:271:HOH:O	2.07	0.55
1:A:69:HIS:O	1:A:89:SER:HB2	2.07	0.55
1:B:71:LEU:HD23	2:B:281:HOH:O	2.06	0.55
1:A:35:GLN:HG3	2:A:272:HOH:O	2.06	0.55
1:A:30:LEU:C	1:A:30:LEU:HD23	2.27	0.55
1:A:31:LEU:HA	1:A:85:CYS:HG	1.72	0.55
1:A:106:LEU:HD21	1:A:153:ALA:CB	2.34	0.55
1:A:87:VAL:HG11	1:A:96:ALA:HB2	1.88	0.54
1:B:80:SER:O	1:B:81:SER:HB3	2.07	0.54
1:A:45:LYS:NZ	1:A:52:GLU:OE1	2.32	0.54
1:A:101:SER:HB2	1:B:102:GLY:HA3	1.89	0.54
1:A:87:VAL:HG13	1:A:88:SER:N	2.22	0.54
1:A:139:LYS:CE	2:A:245:HOH:O	2.46	0.54
1:A:128:GLU:HG2	2:A:293:HOH:O	2.06	0.54
1:A:34:ALA:HB2	1:A:88:SER:HB3	1.88	0.54
1:A:27:LYS:HB2	1:B:106:LEU:HB3	1.89	0.54
1:A:97:LYS:HE3	1:B:100:GLY:HA3	1.89	0.54
1:A:109:THR:O	1:A:154:GLU:HA	2.08	0.54
1:A:144:ASP:HB2	1:A:145:PRO:CD	2.38	0.54
1:B:119:ALA:HB1	1:B:142:VAL:HG21	1.89	0.54
1:B:34:ALA:HB2	1:B:88:SER:HB3	1.90	0.54
1:B:109:THR:O	1:B:154:GLU:HA	2.08	0.54
1:A:26:PHE:HA	1:B:106:LEU:O	2.08	0.54
1:B:106:LEU:HD11	1:B:153:ALA:HB2	1.90	0.53
1:B:40:ALA:HA	1:B:146:PHE:CE2	2.43	0.53
1:B:144:ASP:HB2	1:B:145:PRO:CD	2.39	0.53
1:A:25:GLU:HB2	2:A:281:HOH:O	2.07	0.53
1:A:144:ASP:HB2	1:A:145:PRO:CD	2.39	0.53
1:A:144:ASP:HB2	1:A:145:PRO:CD	2.39	0.53
1:A:76:ASN:OD1	1:A:81:SER:HB3	2.09	0.53
1:B:37:VAL:HG23	1:B:86:ASP:HB2	1.90	0.52
1:B:101:SER:O	1:B:101:SER:OG	2.27	0.52
1:B:56:SER:O	1:B:70:VAL:HG13	2.10	0.52
1:B:57:LEU:HD13	2:B:235:HOH:O	2.09	0.52
1:A:128:GLU:HG2	2:A:291:HOH:O	2.08	0.52
1:A:52:GLU:O	1:A:53:SER:HB2	2.10	0.52
1:B:120:VAL:HG21	1:B:126:LYS:HB2	1.92	0.52
1:A:26:PHE:HB2	1:B:78:ALA:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:GLN:O	1:B:83:VAL:HG22	2.10	0.52
1:A:129:VAL:HG23	1:A:129:VAL:O	2.10	0.52
1:A:144:ASP:HB2	1:A:145:PRO:CD	2.40	0.52
1:A:144:ASP:HB2	1:A:145:PRO:CD	2.40	0.52
1:A:91:PRO:HG2	1:B:133:GLU:HG2	1.92	0.51
1:A:139:LYS:HD2	1:A:154:GLU:OE2	2.10	0.51
1:A:35:GLN:HE21	1:A:35:GLN:HA	1.76	0.51
1:B:141:LYS:NZ	2:B:275:HOH:O	2.43	0.51
1:A:144:ASP:HB2	1:A:145:PRO:CD	2.41	0.51
1:A:128:GLU:HG2	2:A:292:HOH:O	2.09	0.51
1:A:134:VAL:CG1	1:A:139:LYS:HE2	2.39	0.51
1:A:70:VAL:HG23	1:A:70:VAL:O	2.11	0.51
1:A:141:LYS:HE3	1:B:93:PHE:CZ	2.45	0.51
1:A:27:LYS:NZ	2:A:248:HOH:O	2.41	0.51
1:A:34:ALA:HA	1:A:86:ASP:OD1	2.09	0.51
1:A:99:GLU:HG3	2:A:210:HOH:O	2.11	0.51
1:A:95:THR:HA	2:A:256:HOH:O	2.09	0.51
1:B:37:VAL:HG22	1:B:84:VAL:HG12	1.92	0.51
1:A:131:GLU:O	1:A:135:GLU:HG3	2.10	0.51
1:B:109:THR:HG23	1:B:111:ASP:H	1.75	0.51
1:A:76:ASN:HA	1:A:80:SER:O	2.11	0.51
1:B:55:HIS:HA	1:B:73:SER:HA	1.92	0.51
1:B:23:PHE:N	2:B:233:HOH:O	2.44	0.51
1:A:25:GLU:HA	2:B:199:HOH:O	2.11	0.51
1:B:116:VAL:CG2	1:B:140:GLY:HA3	2.40	0.51
1:B:112:ALA:H	1:B:154:GLU:CD	2.14	0.51
1:A:70:VAL:HB	1:A:89:SER:HG	1.74	0.50
1:B:29:MSE:HA	1:B:83:VAL:CG2	2.38	0.50
1:B:85:CYS:O	1:B:85:CYS:SG	2.70	0.50
1:A:131:GLU:O	1:A:135:GLU:HG3	2.11	0.50
1:A:21:LEU:HD21	1:B:115:ALA:HA	1.92	0.50
1:B:132:ALA:HB2	2:B:220:HOH:O	2.11	0.50
1:B:131:GLU:O	1:B:135:GLU:HG3	2.12	0.50
1:A:154:GLU:O	1:A:154:GLU:HG2	2.12	0.50
1:A:106:LEU:C	1:A:106:LEU:HD23	2.32	0.50
1:A:35:GLN:OE1	2:A:289:HOH:O	2.20	0.50
1:B:134:VAL:HG13	1:B:139:LYS:HG2	1.92	0.50
1:A:139:LYS:CE	2:A:243:HOH:O	2.47	0.50
1:A:71:LEU:HD23	2:A:169:HOH:O	2.12	0.49
1:B:33:GLU:HG2	2:B:179:HOH:O	2.12	0.49
1:B:142:VAL:HG23	1:B:142:VAL:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:251:HOH:O	1:B:100:GLY:HA3	2.11	0.49
1:A:149:THR:CG2	1:A:151:ILE:HD11	2.41	0.49
1:A:34:ALA:HA	1:A:86:ASP:OD1	2.12	0.49
1:A:23:PHE:CE1	1:B:109:THR:HB	2.47	0.49
1:A:24:THR:O	1:A:25:GLU:HB3	2.11	0.49
1:A:25:GLU:HB2	2:A:285:HOH:O	2.10	0.49
1:B:129:VAL:HG22	2:B:234:HOH:O	2.11	0.49
1:B:150:TRP:C	1:B:151:ILE:HD12	2.33	0.49
1:B:120:VAL:HA	1:B:124:ALA:O	2.13	0.49
1:B:144:ASP:HB2	1:B:145:PRO:CD	2.43	0.49
1:A:70:VAL:HG12	1:A:89:SER:C	2.33	0.49
1:A:139:LYS:HD2	1:A:154:GLU:HB3	1.93	0.49
1:A:106:LEU:C	1:A:106:LEU:HD23	2.33	0.49
1:A:102:GLY:CA	1:B:103:VAL:HG23	2.38	0.48
1:A:98:SER:O	1:A:99:GLU:O	2.31	0.48
1:A:126:LYS:HE2	1:A:128:GLU:OE2	2.13	0.48
1:B:36:LYS:HE2	2:B:236:HOH:O	2.12	0.48
1:B:126:LYS:HA	1:B:142:VAL:HG12	1.95	0.48
1:A:22:VAL:HG22	1:A:23:PHE:N	2.29	0.48
1:B:83:VAL:HG23	1:B:85:CYS:SG	2.54	0.48
1:A:106:LEU:C	1:A:106:LEU:HD23	2.34	0.48
1:B:31:LEU:HD13	1:B:93:PHE:HB3	1.94	0.48
1:B:41:VAL:CG1	1:B:45:LYS:HE3	2.42	0.48
1:B:144:ASP:OD2	1:B:148:VAL:HB	2.13	0.48
1:A:70:VAL:HG13	1:B:136:LEU:HD23	1.95	0.48
1:B:151:ILE:N	1:B:151:ILE:CD1	2.76	0.48
1:B:32:VAL:O	1:B:87:VAL:HG12	2.13	0.48
1:A:35:GLN:O	2:A:266:HOH:O	2.19	0.48
1:A:45:LYS:HD3	2:A:228:HOH:O	2.13	0.48
1:B:46:SER:O	1:B:118:LYS:HE2	2.13	0.48
1:B:109:THR:O	1:B:109:THR:HG23	2.11	0.47
1:B:47:ALA:O	1:B:118:LYS:HE2	2.14	0.47
1:B:25:GLU:HB2	1:B:27:LYS:HZ1	1.79	0.47
1:A:33:GLU:OE2	1:A:96:ALA:HB3	2.13	0.47
1:B:128:GLU:HA	2:B:232:HOH:O	2.15	0.47
1:A:26:PHE:HB2	1:B:78:ALA:HB3	1.94	0.47
1:B:40:ALA:HA	1:B:146:PHE:CE2	2.48	0.47
1:B:56:SER:OG	1:B:71:LEU:HB3	2.13	0.47
1:B:99:GLU:CB	2:B:200:HOH:O	2.63	0.47
1:B:80:SER:OG	1:B:81:SER:N	2.45	0.47
1:A:129:VAL:HG22	2:A:188:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:80:SER:O	1:B:81:SER:HB3	2.15	0.47
1:A:71:LEU:HD12	1:A:72:SER:N	2.30	0.47
1:A:102:GLY:HA3	1:B:103:VAL:CG2	2.37	0.47
1:A:46:SER:O	1:A:118:LYS:HE2	2.14	0.47
1:B:41:VAL:HG12	1:B:45:LYS:HE3	1.97	0.47
1:B:128:GLU:HG2	2:B:284:HOH:O	2.14	0.47
1:B:132:ALA:O	1:B:135:GLU:HB2	2.15	0.47
1:A:51:ILE:O	1:A:76:ASN:ND2	2.47	0.47
1:B:57:LEU:HD12	1:B:57:LEU:N	2.30	0.47
1:B:128:GLU:HA	2:B:236:HOH:O	2.14	0.47
1:B:130:THR:O	1:B:134:VAL:HG23	2.14	0.47
1:A:28:GLN:HA	1:B:105:PHE:HD1	1.80	0.47
1:B:53:SER:HB3	1:B:76:ASN:ND2	2.30	0.47
1:A:106:LEU:C	1:A:106:LEU:HD23	2.36	0.47
1:B:112:ALA:HB1	1:B:140:GLY:HA3	1.95	0.47
1:A:86:ASP:OD2	1:A:88:SER:N	2.44	0.46
1:A:141:LYS:HG3	1:A:151:ILE:HD13	1.98	0.46
1:A:144:ASP:OD2	1:A:146:PHE:HD2	1.98	0.46
1:B:33:GLU:CG	2:B:176:HOH:O	2.50	0.46
1:A:33:GLU:OE2	1:A:96:ALA:HB3	2.14	0.46
1:A:144:ASP:OD2	1:A:145:PRO:HD2	2.16	0.46
1:A:53:SER:O	1:A:74:GLU:OE1	2.33	0.46
1:B:131:GLU:O	1:B:135:GLU:HG3	2.16	0.46
1:A:93:PHE:HZ	1:B:151:ILE:HD11	1.81	0.46
1:B:57:LEU:HG	1:B:70:VAL:HA	1.96	0.46
1:A:96:ALA:O	1:A:97:LYS:C	2.52	0.46
1:B:128:GLU:HA	2:B:234:HOH:O	2.14	0.46
1:B:141:LYS:HE3	1:B:149:THR:HG23	1.97	0.46
1:A:141:LYS:NZ	2:A:230:HOH:O	2.48	0.46
1:A:70:VAL:HG13	1:A:90:LEU:HD21	1.98	0.46
1:B:55:HIS:NE2	1:B:57:LEU:HD11	2.30	0.46
1:B:75:LEU:O	1:B:81:SER:HB2	2.16	0.46
1:A:24:THR:HG21	2:A:252:HOH:O	2.15	0.46
1:A:99:GLU:CG	2:A:210:HOH:O	2.62	0.46
1:A:99:GLU:HB2	2:A:209:HOH:O	2.16	0.45
1:A:70:VAL:O	1:A:71:LEU:C	2.54	0.45
1:B:130:THR:O	1:B:134:VAL:HG23	2.15	0.45
1:A:94:SER:O	1:A:95:THR:HG23	2.16	0.45
1:A:52:GLU:HG2	1:A:53:SER:N	2.31	0.45
1:A:70:VAL:HG13	1:B:136:LEU:CD2	2.47	0.45
1:A:141:LYS:NZ	2:A:231:HOH:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:138:PHE:HA	1:B:152:PHE:O	2.16	0.45
1:A:101:SER:N	2:A:198:HOH:O	2.49	0.45
1:A:41:VAL:HG13	1:A:75:LEU:HD21	1.98	0.45
1:A:40:ALA:HA	1:A:146:PHE:CE2	2.51	0.45
1:A:26:PHE:HD2	1:B:80:SER:HB3	1.81	0.45
1:A:110:LYS:N	2:A:240:HOH:O	2.47	0.45
1:A:141:LYS:CG	1:A:151:ILE:HD12	2.43	0.45
1:B:129:VAL:HG23	1:B:129:VAL:O	2.17	0.45
1:B:131:GLU:HG3	1:B:135:GLU:OE2	2.16	0.45
1:B:119:ALA:CB	1:B:142:VAL:HG21	2.46	0.45
1:B:40:ALA:HA	1:B:146:PHE:CE2	2.51	0.45
1:B:46:SER:O	1:B:118:LYS:HE2	2.17	0.45
1:B:41:VAL:CG1	1:B:45:LYS:HE3	2.47	0.44
1:A:25:GLU:HB2	2:A:281:HOH:O	2.17	0.44
1:A:106:LEU:HD11	1:A:138:PHE:CE1	2.52	0.44
1:B:40:ALA:HA	1:B:146:PHE:CE2	2.52	0.44
1:A:138:PHE:HB3	1:A:151:ILE:CG2	2.47	0.44
1:A:33:GLU:HB2	1:A:36:LYS:HD2	1.97	0.44
1:B:109:THR:O	1:B:154:GLU:HA	2.17	0.44
1:A:150:TRP:O	1:A:151:ILE:HD13	2.18	0.44
1:A:39:ASP:O	1:A:42:THR:HB	2.17	0.44
1:A:70:VAL:CG1	1:A:89:SER:O	2.65	0.44
1:A:141:LYS:NZ	2:A:233:HOH:O	2.50	0.44
1:A:91:PRO:HB2	1:B:132:ALA:HB1	1.99	0.44
1:B:130:THR:HG23	1:B:133:GLU:OE2	2.18	0.44
1:B:40:ALA:HA	1:B:146:PHE:CZ	2.52	0.44
1:A:76:ASN:OD1	1:A:81:SER:HB3	2.17	0.44
1:A:141:LYS:NZ	2:A:230:HOH:O	2.51	0.44
1:B:86:ASP:OD1	1:B:88:SER:OG	2.32	0.44
1:A:92:GLY:HA3	2:B:275:HOH:O	2.17	0.44
1:A:141:LYS:HG3	1:A:151:ILE:HD13	1.99	0.44
1:A:106:LEU:HD23	1:A:107:LEU:N	2.33	0.44
1:A:70:VAL:HG13	1:A:90:LEU:CD2	2.47	0.44
1:A:91:PRO:HG3	1:B:136:LEU:HD12	1.99	0.44
1:B:35:GLN:C	1:B:36:LYS:HD3	2.38	0.43
1:B:34:ALA:HB2	1:B:88:SER:HB3	2.00	0.43
1:B:37:VAL:HB	1:B:70:VAL:HB	2.00	0.43
1:A:144:ASP:HB2	1:A:145:PRO:CD	2.48	0.43
1:B:34:ALA:HB2	1:B:88:SER:HB3	2.00	0.43
1:A:92:GLY:HA3	1:B:133:GLU:OE1	2.18	0.43
1:B:33:GLU:HB3	1:B:36:LYS:HG2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:VAL:O	1:A:41:VAL:HG23	2.17	0.43
1:A:37:VAL:HG13	1:A:84:VAL:HG12	2.00	0.43
2:A:255:HOH:O	1:B:99:GLU:HB2	2.18	0.43
1:A:138:PHE:CE1	1:A:153:ALA:HB2	2.53	0.43
1:A:135:GLU:HG2	2:A:296:HOH:O	2.17	0.43
1:A:144:ASP:CG	1:A:146:PHE:H	2.21	0.43
1:A:141:LYS:HE3	1:B:93:PHE:CZ	2.54	0.43
1:A:52:GLU:O	1:A:53:SER:HB2	2.18	0.43
1:A:71:LEU:HD12	1:A:72:SER:H	1.84	0.43
1:A:149:THR:HG22	1:A:151:ILE:CD1	2.47	0.43
1:B:131:GLU:HA	1:B:134:VAL:CG2	2.49	0.43
1:A:93:PHE:CZ	1:B:151:ILE:HD11	2.54	0.43
1:B:29:MSE:HG2	1:B:83:VAL:HG21	2.01	0.43
1:A:76:ASN:HA	1:A:81:SER:HB3	2.01	0.43
1:A:22:VAL:HG22	1:A:23:PHE:N	2.33	0.43
1:B:141:LYS:HA	1:B:150:TRP:O	2.18	0.43
1:B:36:LYS:HE2	2:B:238:HOH:O	2.19	0.43
1:B:128:GLU:HA	2:B:232:HOH:O	2.19	0.43
1:A:90:LEU:O	1:A:91:PRO:C	2.56	0.43
1:A:97:LYS:O	1:A:101:SER:HB3	2.19	0.43
1:A:76:ASN:HA	1:A:80:SER:O	2.19	0.43
1:B:35:GLN:C	1:B:36:LYS:HD3	2.39	0.43
1:A:106:LEU:HD23	1:A:106:LEU:C	2.40	0.43
1:B:57:LEU:HD12	1:B:57:LEU:N	2.34	0.43
1:A:108:GLY:HA3	1:B:25:GLU:HG2	2.01	0.43
1:B:109:THR:C	1:B:111:ASP:N	2.70	0.42
1:A:42:THR:HA	1:A:45:LYS:HG3	2.01	0.42
1:A:45:LYS:HE2	2:A:269:HOH:O	2.17	0.42
1:A:71:LEU:HB3	1:A:86:ASP:HB3	2.00	0.42
1:A:39:ASP:CG	2:A:253:HOH:O	2.42	0.42
1:A:31:LEU:HD23	1:A:87:VAL:CG2	2.40	0.42
1:A:104:THR:HA	1:A:149:THR:O	2.20	0.42
1:B:126:LYS:HE2	1:B:128:GLU:OE2	2.19	0.42
1:A:106:LEU:HD23	1:A:107:LEU:N	2.34	0.42
1:A:120:VAL:O	1:A:121:ASP:C	2.57	0.42
1:B:33:GLU:HB3	1:B:36:LYS:CG	2.50	0.42
1:B:74:GLU:HA	1:B:83:VAL:HG12	2.02	0.42
1:A:85:CYS:O	1:A:85:CYS:SG	2.75	0.42
1:B:40:ALA:HA	1:B:146:PHE:CE2	2.54	0.42
1:A:106:LEU:C	1:A:106:LEU:HD23	2.40	0.42
1:B:57:LEU:HD12	1:B:57:LEU:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:LYS:NZ	2:A:252:HOH:O	2.44	0.42
1:A:29:MSE:SE	1:B:151:ILE:HD12	2.70	0.42
1:B:138:PHE:HB3	1:B:151:ILE:CG2	2.50	0.41
1:A:141:LYS:NZ	2:A:286:HOH:O	2.44	0.41
1:A:97:LYS:HD3	2:A:213:HOH:O	2.20	0.41
1:A:90:LEU:O	1:A:93:PHE:HB2	2.19	0.41
1:A:41:VAL:CG1	1:A:45:LYS:HE3	2.51	0.41
1:A:24:THR:HG21	2:A:250:HOH:O	2.19	0.41
1:B:34:ALA:HA	1:B:86:ASP:OD1	2.20	0.41
1:A:106:LEU:C	1:A:106:LEU:HD23	2.41	0.41
1:A:22:VAL:HG22	1:A:23:PHE:N	2.36	0.41
1:A:40:ALA:HA	1:A:146:PHE:CZ	2.55	0.41
1:A:137:GLY:HA2	2:A:243:HOH:O	2.21	0.41
1:A:80:SER:HB3	2:A:187:HOH:O	2.20	0.41
1:B:90:LEU:HB3	1:B:93:PHE:HD2	1.85	0.41
1:B:141:LYS:HG3	1:B:150:TRP:O	2.20	0.41
1:B:40:ALA:HA	1:B:146:PHE:CE2	2.55	0.41
1:B:90:LEU:HB3	1:B:93:PHE:CD2	2.55	0.41
1:B:33:GLU:OE1	1:B:36:LYS:HE3	2.20	0.41
1:A:26:PHE:CD2	1:B:80:SER:HB3	2.55	0.41
1:B:34:ALA:HA	1:B:86:ASP:OD1	2.20	0.41
1:A:95:THR:CB	2:A:256:HOH:O	2.66	0.41
1:B:101:SER:C	1:B:103:VAL:H	2.24	0.41
1:A:138:PHE:CG	1:A:151:ILE:HG21	2.54	0.41
1:A:30:LEU:HD11	1:A:148:VAL:CG2	2.50	0.41
1:A:26:PHE:HB2	1:B:78:ALA:HB3	2.03	0.41
1:A:24:THR:OG1	1:B:108:GLY:HA3	2.20	0.41
1:B:56:SER:OG	1:B:71:LEU:HB3	2.21	0.41
1:B:57:LEU:HD12	1:B:57:LEU:N	2.36	0.41
1:A:41:VAL:HG13	1:A:45:LYS:HE3	2.03	0.41
1:B:57:LEU:HD12	1:B:57:LEU:N	2.36	0.41
1:A:35:GLN:CG	2:A:271:HOH:O	2.66	0.41
1:A:35:GLN:HA	1:A:35:GLN:NE2	2.35	0.41
1:A:94:SER:O	1:A:95:THR:CG2	2.69	0.41
1:B:116:VAL:CG2	1:B:140:GLY:HA3	2.51	0.41
1:B:41:VAL:CG1	1:B:45:LYS:HE3	2.51	0.41
1:A:70:VAL:HG23	1:B:136:LEU:HD13	2.02	0.41
1:B:57:LEU:HD12	1:B:57:LEU:N	2.36	0.41
1:B:39:ASP:CG	2:B:195:HOH:O	2.59	0.41
1:B:108:GLY:HA2	1:B:153:ALA:O	2.21	0.41
1:A:70:VAL:HG12	1:A:89:SER:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:CYS:SG	1:A:85:CYS:O	2.80	0.40
1:B:41:VAL:CG1	1:B:45:LYS:HE3	2.51	0.40
1:B:141:LYS:HE3	1:B:149:THR:CG2	2.51	0.40
1:A:27:LYS:HE2	2:A:218:HOH:O	2.22	0.40
1:A:141:LYS:NZ	2:A:230:HOH:O	2.55	0.40
1:A:91:PRO:CD	1:B:136:LEU:HD12	2.52	0.40
1:A:144:ASP:HB2	1:A:145:PRO:HD2	2.04	0.40
1:A:150:TRP:C	1:A:151:ILE:HD13	2.41	0.40
1:A:118:LYS:HE3	2:A:291:HOH:O	2.21	0.40
1:B:120:VAL:HA	1:B:124:ALA:O	2.20	0.40
1:A:42:THR:HG21	2:A:207:HOH:O	2.21	0.40
1:B:129:VAL:HG21	1:B:139:LYS:O	2.22	0.40
1:B:72:SER:HA	1:B:84:VAL:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	1-A	116/166 (70%)	110 (95%)	6 (5%)	0	100 100
1	1-B	118/166 (71%)	112 (95%)	6 (5%)	0	100 100
1	2-A	116/166 (70%)	113 (97%)	3 (3%)	0	100 100
1	2-B	118/166 (71%)	111 (94%)	6 (5%)	1 (1%)	19 7
1	3-A	116/166 (70%)	107 (92%)	6 (5%)	3 (3%)	5 1
1	3-B	118/166 (71%)	112 (95%)	6 (5%)	0	100 100
1	4-A	116/166 (70%)	111 (96%)	5 (4%)	0	100 100
1	4-B	118/166 (71%)	112 (95%)	4 (3%)	2 (2%)	9 2
1	5-A	116/166 (70%)	113 (97%)	3 (3%)	0	100 100
1	5-B	118/166 (71%)	114 (97%)	4 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	6-A	116/166 (70%)	110 (95%)	4 (3%)	2 (2%)	9 2
1	6-B	118/166 (71%)	110 (93%)	8 (7%)	0	100 100
1	7-A	116/166 (70%)	110 (95%)	6 (5%)	0	100 100
1	7-B	118/166 (71%)	114 (97%)	4 (3%)	0	100 100
1	8-A	116/166 (70%)	108 (93%)	6 (5%)	2 (2%)	9 2
1	8-B	118/166 (71%)	114 (97%)	4 (3%)	0	100 100
All	All	1872/2656 (70%)	1781 (95%)	81 (4%)	10 (0%)	29 15

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	2-B	98	SER
1	4-B	93	PHE
1	4-B	110	LYS
1	8-A	99	GLU
1	6-A	122	ALA
1	3-A	24	THR
1	8-A	111	ASP
1	3-A	25	GLU
1	6-A	123	GLY
1	3-A	100	GLY

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	1-A	94/131 (72%)	94 (100%)	0	100 100
1	1-B	95/131 (72%)	94 (99%)	1 (1%)	73 68
1	2-A	94/131 (72%)	93 (99%)	1 (1%)	73 68
1	2-B	95/131 (72%)	93 (98%)	2 (2%)	53 42
1	3-A	94/131 (72%)	91 (97%)	3 (3%)	39 25
1	3-B	95/131 (72%)	94 (99%)	1 (1%)	73 68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	4-A	94/131 (72%)	94 (100%)	0	100	100
1	4-B	95/131 (72%)	94 (99%)	1 (1%)	73	68
1	5-A	94/131 (72%)	93 (99%)	1 (1%)	73	68
1	5-B	95/131 (72%)	94 (99%)	1 (1%)	73	68
1	6-A	94/131 (72%)	92 (98%)	2 (2%)	53	42
1	6-B	95/131 (72%)	94 (99%)	1 (1%)	73	68
1	7-A	94/131 (72%)	93 (99%)	1 (1%)	73	68
1	7-B	95/131 (72%)	93 (98%)	2 (2%)	53	42
1	8-A	94/131 (72%)	92 (98%)	2 (2%)	53	42
1	8-B	95/131 (72%)	94 (99%)	1 (1%)	73	68
All	All	1512/2096 (72%)	1492 (99%)	20 (1%)	69	62

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1-B	55	HIS
1	2-A	131	GLU
1	2-B	55	HIS
1	2-B	80	SER
1	3-A	39	ASP
1	3-A	109	THR
1	3-A	144	ASP
1	3-B	55	HIS
1	4-B	55	HIS
1	5-A	131	GLU
1	5-B	55	HIS
1	6-A	42	THR
1	6-A	109	THR
1	6-B	55	HIS
1	7-A	82	PHE
1	7-B	55	HIS
1	7-B	83	VAL
1	8-A	28	GLN
1	8-A	131	GLU
1	8-B	55	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	2-A	28	GLN
1	2-A	35	GLN
1	2-A	76	ASN
1	2-B	55	HIS
1	3-B	55	HIS
1	4-B	55	HIS

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 monosaccharides 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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	1-A	119/166 (71%)	-0.10	3 (2%) 57 52	13, 19, 38, 57	119 (100%)
1	1-B	121/166 (72%)	0.13	10 (8%) 11 8	10, 21, 40, 48	121 (100%)
1	2-A	119/166 (71%)	-0.10	3 (2%) 57 52	13, 19, 38, 57	119 (100%)
1	2-B	121/166 (72%)	0.13	10 (8%) 11 8	10, 21, 40, 48	121 (100%)
1	3-A	119/166 (71%)	-0.10	3 (2%) 57 52	13, 19, 38, 57	119 (100%)
1	3-B	121/166 (72%)	0.13	10 (8%) 11 8	10, 21, 40, 48	121 (100%)
1	4-A	119/166 (71%)	-0.10	3 (2%) 57 52	13, 19, 38, 57	119 (100%)
1	4-B	121/166 (72%)	0.13	10 (8%) 11 8	10, 21, 40, 48	121 (100%)
1	5-A	119/166 (71%)	-0.10	3 (2%) 57 52	13, 19, 38, 57	119 (100%)
1	5-B	121/166 (72%)	0.13	10 (8%) 11 8	10, 21, 40, 48	121 (100%)
1	6-A	119/166 (71%)	-0.10	3 (2%) 57 52	13, 19, 38, 57	119 (100%)
1	6-B	121/166 (72%)	0.13	10 (8%) 11 8	10, 21, 40, 48	121 (100%)
1	7-A	119/166 (71%)	-0.10	3 (2%) 57 52	13, 19, 38, 57	119 (100%)
1	7-B	121/166 (72%)	0.13	10 (8%) 11 8	10, 21, 40, 48	121 (100%)
1	8-A	119/166 (71%)	-0.10	3 (2%) 57 52	13, 19, 38, 57	119 (100%)
1	8-B	121/166 (72%)	0.13	10 (8%) 11 8	10, 21, 40, 48	121 (100%)
All	All	1920/2656 (72%)	0.02	104 (5%) 32 20	10, 20, 40, 57	1920 (100%)

All (104) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-B	69	HIS	3.8
1	2-B	69	HIS	3.8
1	3-B	69	HIS	3.8
1	4-B	69	HIS	3.8
1	5-B	69	HIS	3.8

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Mol	Chain	Res	Type	RSRZ
1	6-B	69	HIS	3.8
1	7-B	69	HIS	3.8
1	8-B	69	HIS	3.8
1	1-B	134	VAL	2.8
1	2-B	134	VAL	2.8
1	3-B	134	VAL	2.8
1	4-B	134	VAL	2.8
1	5-B	134	VAL	2.8
1	6-B	134	VAL	2.8
1	7-B	134	VAL	2.8
1	8-B	134	VAL	2.8
1	1-B	57	LEU	2.6
1	2-B	57	LEU	2.6
1	3-B	57	LEU	2.6
1	4-B	57	LEU	2.6
1	5-B	57	LEU	2.6
1	6-B	57	LEU	2.6
1	7-B	57	LEU	2.6
1	8-B	57	LEU	2.6
1	1-A	69	HIS	2.5
1	2-A	69	HIS	2.5
1	3-A	69	HIS	2.5
1	4-A	69	HIS	2.5
1	5-A	69	HIS	2.5
1	6-A	69	HIS	2.5
1	7-A	69	HIS	2.5
1	8-A	69	HIS	2.5
1	1-B	135	GLU	2.3
1	2-B	135	GLU	2.3
1	3-B	135	GLU	2.3
1	4-B	135	GLU	2.3
1	5-B	135	GLU	2.3
1	6-B	135	GLU	2.3
1	7-B	135	GLU	2.3
1	8-B	135	GLU	2.3
1	1-B	56	SER	2.3
1	2-B	56	SER	2.3
1	3-B	56	SER	2.3
1	4-B	56	SER	2.3
1	5-B	56	SER	2.3
1	6-B	56	SER	2.3
1	7-B	56	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	8-B	56	SER	2.3
1	1-A	99	GLU	2.3
1	2-A	99	GLU	2.3
1	3-A	99	GLU	2.3
1	4-A	99	GLU	2.3
1	5-A	99	GLU	2.3
1	6-A	99	GLU	2.3
1	7-A	99	GLU	2.3
1	8-A	99	GLU	2.3
1	1-B	111	ASP	2.3
1	2-B	111	ASP	2.3
1	3-B	111	ASP	2.3
1	4-B	111	ASP	2.3
1	5-B	111	ASP	2.3
1	6-B	111	ASP	2.3
1	7-B	111	ASP	2.3
1	8-B	111	ASP	2.3
1	1-B	31	LEU	2.3
1	2-B	31	LEU	2.3
1	3-B	31	LEU	2.3
1	4-B	31	LEU	2.3
1	5-B	31	LEU	2.3
1	6-B	31	LEU	2.3
1	7-B	31	LEU	2.3
1	8-B	31	LEU	2.3
1	1-B	154	GLU	2.2
1	2-B	154	GLU	2.2
1	3-B	154	GLU	2.2
1	4-B	154	GLU	2.2
1	5-B	154	GLU	2.2
1	6-B	154	GLU	2.2
1	7-B	154	GLU	2.2
1	8-B	154	GLU	2.2
1	1-A	24	THR	2.2
1	2-A	24	THR	2.2
1	3-A	24	THR	2.2
1	4-A	24	THR	2.2
1	5-A	24	THR	2.2
1	6-A	24	THR	2.2
1	7-A	24	THR	2.2
1	8-A	24	THR	2.2
1	1-B	55	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	2-B	55	HIS	2.1
1	3-B	55	HIS	2.1
1	4-B	55	HIS	2.1
1	5-B	55	HIS	2.1
1	6-B	55	HIS	2.1
1	7-B	55	HIS	2.1
1	8-B	55	HIS	2.1
1	1-B	131	GLU	2.1
1	2-B	131	GLU	2.1
1	3-B	131	GLU	2.1
1	4-B	131	GLU	2.1
1	5-B	131	GLU	2.1
1	6-B	131	GLU	2.1
1	7-B	131	GLU	2.1
1	8-B	131	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.