Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 02:07 am BST

PDB ID	:	4KM3
Title	:	Discovery of a novel structural motif in methionine aminopeptidase from Streptococci with possible post-translational modification
Authors	:	Arya, T.; Addlagatta, A.
Deposited on	:	2013-05-08
Resolution	:	3.20 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 following versions of software and data (see references ⓘ) were used in the production of this report:

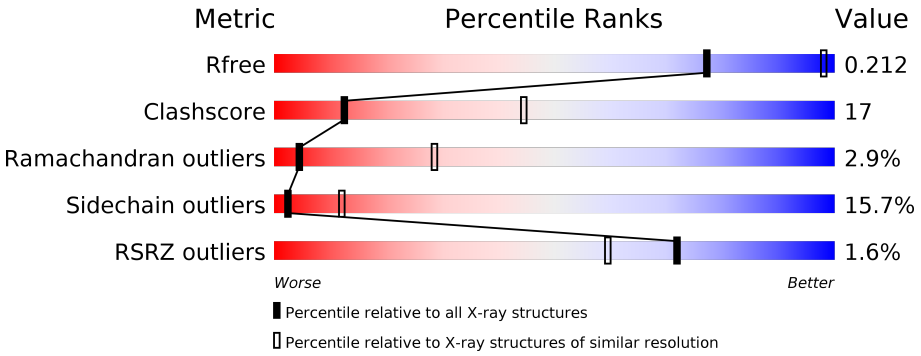
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 on 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	A	286	2% 63% 30% 6%
1	B	286	% 58% 30% 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4378 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 Methionine aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	0	0
			2215	1393	374	429	19			
1	B	277	Total	C	N	O	S	0	0	0
			2143	1350	358	417	18			

- Molecule 2 is water.

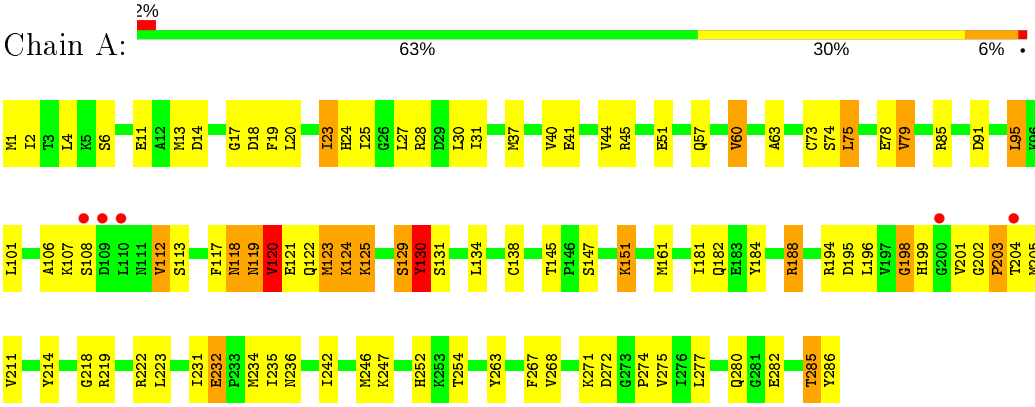
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	12	Total	O	0	0
			12	12		
2	B	8	Total	O	0	0
			8	8		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

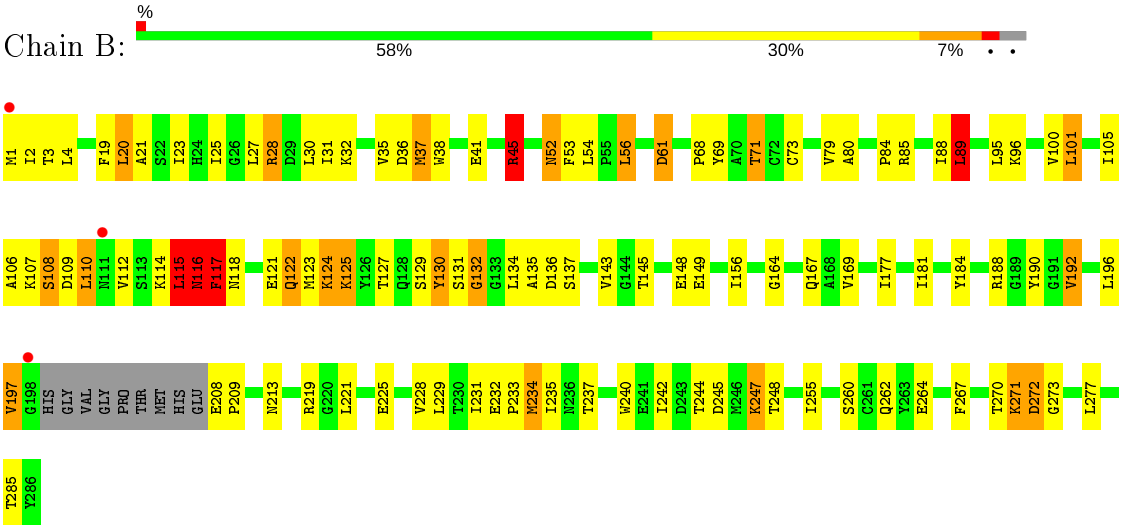
- Molecule 1: Methionine aminopeptidase

Chain A:



- Molecule 1: Methionine aminopeptidase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	109.69Å 109.69Å 164.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	23.75 – 3.20 23.75 – 3.20	Depositor EDS
% Data completeness (in resolution range)	91.6 (23.75-3.20) 91.8 (23.75-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	3.55 (at 3.23Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.210 , 0.285 0.172 , 0.212	Depositor DCC
R_{free} test set	875 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å^2)	49.7	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 15.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	0.279 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.733 for H,K,L 0.267 for K,H,-L	Depositor
Outliers	0 of 16986 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	4378	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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	A	0.57	0/2258	0.80	0/3051
1	B	0.53	0/2182	0.79	2/2947 (0.1%)
All	All	0.55	0/4440	0.79	2/5998 (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	A	0	4
1	B	0	4
All	All	0	8

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	45	ARG	NE-CZ-NH1	6.15	123.37	120.30
1	B	115	LEU	CA-CB-CG	5.10	127.03	115.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	ASN	Peptide
1	A	125	LYS	Peptide
1	A	198	GLY	Peptide
1	A	218	GLY	Peptide
1	B	116	ASN	Peptide
1	B	117	PHE	Peptide
1	B	122	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	B	125	LYS	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	A	2215	0	2173	70	0
1	B	2143	0	2103	78	0
2	A	12	0	0	0	0
2	B	8	0	0	1	0
All	All	4378	0	4276	145	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 (145) 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:B:123:MET:N	1:B:123:MET:SD	2.35	0.99
1:B:79:VAL:HG21	1:B:242:ILE:HD12	1.64	0.79
1:B:232:GLU:HG2	1:B:262:GLN:HE21	1.49	0.78
1:A:124:LYS:O	1:A:124:LYS:CG	2.32	0.77
1:A:106:ALA:HB3	1:A:112:VAL:HG21	1.70	0.74
1:A:41:GLU:OE2	1:A:45:ARG:NH1	2.24	0.71
1:B:115:LEU:HD13	1:B:115:LEU:O	1.90	0.70
1:B:52:ASN:ND2	1:B:115:LEU:HD12	2.09	0.68
1:A:99:MET:HE2	1:A:101:LEU:HD11	1.77	0.66
1:A:236:ASN:ND2	1:A:254:THR:HG22	2.11	0.66
1:A:124:LYS:O	1:A:124:LYS:HG2	1.96	0.65
1:A:99:MET:CE	1:A:101:LEU:HD11	2.27	0.65
1:A:204:THR:O	1:A:204:THR:HG22	1.96	0.65
1:B:21:ALA:O	1:B:25:ILE:HG13	1.97	0.64
1:B:277:LEU:O	2:B:301:HOH:O	2.14	0.63
1:A:24:HIS:HA	1:A:27:LEU:HD12	1.81	0.62
1:A:268:VAL:HG23	1:A:277:LEU:HD21	1.81	0.61
1:B:41:GLU:OE1	1:B:71:THR:HB	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:GLN:HG2	1:A:123:MET:H	1.65	0.60
1:B:32:LYS:O	1:B:35:VAL:HG12	2.00	0.60
1:B:79:VAL:HG21	1:B:242:ILE:CD1	2.31	0.60
1:A:282:GLU:O	1:A:285:THR:HG22	2.03	0.58
1:B:52:ASN:HD22	1:B:115:LEU:HD12	1.68	0.58
1:B:232:GLU:CG	1:B:262:GLN:HE21	2.16	0.58
1:B:231:ILE:HG22	1:B:233:PRO:HD3	1.86	0.57
1:B:229:LEU:HB2	1:B:267:PHE:CZ	2.39	0.57
1:B:231:ILE:O	1:B:264:GLU:HA	2.04	0.57
1:A:268:VAL:CG2	1:A:277:LEU:HD21	2.34	0.56
1:B:122:GLN:NE2	1:B:122:GLN:O	2.38	0.56
1:A:45:ARG:CZ	1:A:120:VAL:HG12	2.34	0.56
1:B:56:LEU:HA	1:B:127:THR:HG23	1.88	0.56
1:B:36:ASP:O	1:B:37:MET:C	2.45	0.54
1:B:115:LEU:HD13	1:B:115:LEU:C	2.28	0.54
1:A:219:ARG:HD3	1:A:219:ARG:N	2.23	0.54
1:B:124:LYS:HD3	1:B:124:LYS:O	2.08	0.54
1:B:208:GLU:HG3	1:B:209:PRO:HD2	1.89	0.54
1:A:57:GLN:HG2	1:A:204:THR:HG23	1.89	0.53
1:B:130:TYR:CD2	1:B:130:TYR:O	2.61	0.53
1:A:40:VAL:O	1:A:44:VAL:HG23	2.08	0.53
1:B:270:THR:HG22	1:B:271:LYS:O	2.09	0.52
1:B:271:LYS:O	1:B:272:ASP:HB2	2.09	0.52
1:A:181:ILE:HD11	1:A:231:ILE:HD11	1.93	0.51
1:A:202:GLY:N	1:A:203:PRO:HD2	2.26	0.51
1:A:184:TYR:O	1:A:188:ARG:NE	2.41	0.51
1:A:280:GLN:HG2	1:A:286:TYR:CE2	2.46	0.51
1:B:233:PRO:O	1:B:262:GLN:HA	2.09	0.51
1:A:25:ILE:O	1:A:28:ARG:HG3	2.11	0.50
1:A:20:LEU:HD13	1:A:99:MET:HE2	1.94	0.50
1:B:68:PRO:HG2	1:B:69:TYR:CD2	2.47	0.50
1:A:205:MET:CE	1:A:208:GLU:HB2	2.41	0.50
1:A:201:VAL:O	1:A:205:MET:HB2	2.13	0.49
1:A:204:THR:O	1:A:204:THR:CG2	2.61	0.49
1:A:45:ARG:NH2	1:A:120:VAL:HG12	2.28	0.49
1:B:196:LEU:O	1:B:197:VAL:C	2.50	0.49
1:B:245:ASP:OD1	1:B:248:THR:N	2.41	0.49
1:A:57:GLN:O	1:A:60:VAL:HG12	2.12	0.49
1:A:201:VAL:O	1:A:205:MET:CB	2.61	0.48
1:A:242:ILE:HD11	1:A:252:HIS:HB3	1.95	0.48
1:A:45:ARG:CZ	1:A:120:VAL:CG1	2.91	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:LEU:HD12	1:A:97:VAL:HG23	1.95	0.48
1:B:130:TYR:CE1	1:B:132:GLY:HA2	2.48	0.48
1:A:267:PHE:HA	1:A:277:LEU:HG	1.94	0.48
1:A:13:MET:O	1:A:17:GLY:N	2.47	0.48
1:B:56:LEU:HD12	1:B:100:VAL:HG12	1.96	0.48
1:A:124:LYS:HG3	1:A:124:LYS:O	2.10	0.48
1:B:54:LEU:HD12	1:B:131:SER:HB2	1.96	0.47
1:B:244:THR:O	1:B:245:ASP:C	2.50	0.47
1:A:75:LEU:H	1:A:78:GLU:HB2	1.80	0.47
1:A:194:ARG:HG2	1:A:214:TYR:CE1	2.50	0.47
1:B:232:GLU:N	1:B:233:PRO:HD3	2.30	0.47
1:A:201:VAL:HG12	1:A:203:PRO:O	2.15	0.47
1:A:79:VAL:HG23	1:A:234:MET:HG2	1.97	0.46
1:B:124:LYS:CD	1:B:124:LYS:O	2.64	0.46
1:B:271:LYS:O	1:B:272:ASP:CB	2.63	0.46
1:A:117:PHE:CZ	1:A:119:ASN:HB2	2.51	0.46
1:B:148:GLU:O	1:B:149:GLU:C	2.55	0.46
1:A:198:GLY:HA2	1:B:219:ARG:O	2.16	0.46
1:A:98:ASP:HA	1:A:138:CYS:HA	1.97	0.45
1:B:116:ASN:O	1:B:118:ASN:N	2.49	0.45
1:B:270:THR:O	1:B:273:GLY:N	2.49	0.45
1:A:41:GLU:HG3	1:A:45:ARG:HD2	1.99	0.45
1:A:242:ILE:CD1	1:A:252:HIS:HB3	2.47	0.45
1:B:156:ILE:HG23	1:B:184:TYR:HE1	1.81	0.45
1:B:167:GLN:O	1:B:169:VAL:HG22	2.17	0.45
1:B:31:ILE:CG2	1:B:143:VAL:HG22	2.47	0.45
1:A:129:SER:O	1:A:131:SER:N	2.49	0.45
1:B:164:GLY:CA	1:B:177:ILE:HG23	2.47	0.44
1:B:88:ILE:HG22	1:B:89:LEU:O	2.16	0.44
1:A:151:LYS:HA	1:A:151:LYS:CE	2.48	0.44
1:A:122:GLN:CG	1:A:123:MET:H	2.31	0.44
1:B:61:ASP:N	1:B:61:ASP:OD2	2.51	0.44
1:A:204:THR:O	1:A:205:MET:HG2	2.18	0.44
1:A:205:MET:HE2	1:A:208:GLU:HB2	1.99	0.44
1:B:37:MET:SD	1:B:73:CYS:HB3	2.58	0.44
1:B:267:PHE:N	1:B:267:PHE:CD2	2.85	0.43
1:B:192:VAL:O	1:B:240:TRP:HB2	2.18	0.43
1:B:156:ILE:N	1:B:156:ILE:HD13	2.33	0.43
1:B:190:TYR:HB3	1:B:235:ILE:HG23	1.99	0.43
1:A:2:ILE:HG23	1:B:1:MET:HA	2.01	0.43
1:B:156:ILE:HG23	1:B:184:TYR:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:TYR:CD2	1:B:84:PRO:HD2	2.54	0.43
1:B:80:ALA:HB2	1:B:234:MET:HE3	2.00	0.43
1:B:131:SER:O	1:B:131:SER:OG	2.25	0.43
1:B:25:ILE:HA	1:B:28:ARG:CD	2.48	0.43
1:A:45:ARG:HG2	1:A:120:VAL:HG11	2.01	0.43
1:B:114:LYS:O	1:B:116:ASN:OD1	2.37	0.43
1:B:181:ILE:HG21	1:B:213:ASN:HB3	2.01	0.43
1:A:234:MET:C	1:A:235:ILE:HD12	2.40	0.42
1:B:109:ASP:CG	1:B:110:LEU:H	2.22	0.42
1:A:31:ILE:O	1:A:31:ILE:HG22	2.18	0.42
1:B:108:SER:N	1:B:112:VAL:O	2.49	0.42
1:B:96:LYS:N	1:B:96:LYS:HD3	2.35	0.42
1:A:57:GLN:CG	1:A:204:THR:HG23	2.49	0.42
1:B:95:LEU:HD13	1:B:95:LEU:C	2.40	0.42
1:A:37:MET:SD	1:A:73:CYS:HB3	2.60	0.42
1:A:118:ASN:HD22	1:A:118:ASN:N	2.17	0.42
1:A:205:MET:HE1	1:A:208:GLU:H	1.85	0.42
1:B:100:VAL:HG22	1:B:136:ASP:HA	2.02	0.42
1:B:114:LYS:HG3	1:B:116:ASN:OD1	2.20	0.41
1:B:23:ILE:O	1:B:27:LEU:HG	2.20	0.41
1:A:14:ASP:O	1:A:18:ASP:N	2.48	0.41
1:B:100:VAL:HA	1:B:135:ALA:O	2.20	0.41
1:A:119:ASN:O	1:A:124:LYS:NZ	2.53	0.41
1:A:219:ARG:CD	1:A:219:ARG:N	2.83	0.41
1:B:20:LEU:HD11	1:B:137:SER:HB3	2.03	0.41
1:B:25:ILE:HA	1:B:28:ARG:NE	2.34	0.41
1:B:41:GLU:OE1	1:B:84:PRO:HG3	2.20	0.41
1:A:51:GLU:N	1:A:51:GLU:OE2	2.53	0.41
1:A:2:ILE:HG22	1:B:2:ILE:HG12	2.02	0.41
1:A:232:GLU:HA	1:A:263:TYR:O	2.20	0.41
1:A:91:ASP:OD2	1:A:91:ASP:C	2.59	0.41
1:A:182:GLN:HB2	1:A:214:TYR:HA	2.03	0.41
1:B:20:LEU:HD22	1:B:101:LEU:HD22	2.03	0.41
1:B:19:PHE:CE1	1:B:53:PHE:CD2	3.09	0.41
1:B:235:ILE:O	1:B:260:SER:HA	2.21	0.41
1:A:201:VAL:O	1:A:201:VAL:HG12	2.20	0.40
1:A:19:PHE:CZ	1:A:23:ILE:HD11	2.56	0.40
1:B:247:LYS:HD3	1:B:247:LYS:N	2.36	0.40
1:B:45:ARG:HH11	1:B:45:ARG:HG2	1.86	0.40
1:A:275:VAL:O	1:A:275:VAL:HG13	2.20	0.40
1:B:36:ASP:O	1:B:38:TRP:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:GLN:O	1:A:60:VAL:CG1	2.69	0.40
1:A:130:TYR:CG	1:A:130:TYR:O	2.75	0.40
1:B:4:LEU:HD13	1:B:225:GLU:O	2.20	0.40
1:B:30:LEU:HD12	1:B:30:LEU: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	A	284/286 (99%)	242 (85%)	32 (11%)	10 (4%)	3 24
1	B	273/286 (96%)	227 (83%)	40 (15%)	6 (2%)	6 35
All	All	557/572 (97%)	469 (84%)	72 (13%)	16 (3%)	4 28

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	108	SER
1	A	112	VAL
1	A	119	ASN
1	B	89	LEU
1	B	117	PHE
1	B	197	VAL
1	A	130	TYR
1	A	199	HIS
1	B	108	SER
1	A	147	SER
1	B	132	GLY
1	A	63	ALA
1	A	195	ASP
1	B	106	ALA

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Mol	Chain	Res	Type
1	A	274	PRO
1	A	120	VAL

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	A	236/236 (100%)	199 (84%)	37 (16%)	2 12
1	B	228/236 (97%)	192 (84%)	36 (16%)	2 12
All	All	464/472 (98%)	391 (84%)	73 (16%)	2 12

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	4	LEU
1	A	6	SER
1	A	11	GLU
1	A	23	ILE
1	A	30	LEU
1	A	60	VAL
1	A	74	SER
1	A	75	LEU
1	A	79	VAL
1	A	85	ARG
1	A	95	LEU
1	A	107	LYS
1	A	113	SER
1	A	120	VAL
1	A	121	GLU
1	A	123	MET
1	A	124	LYS
1	A	125	LYS
1	A	129	SER
1	A	130	TYR

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Mol	Chain	Res	Type
1	A	134	LEU
1	A	145	THR
1	A	151	LYS
1	A	161	MET
1	A	188	ARG
1	A	196	LEU
1	A	203	PRO
1	A	211	VAL
1	A	222	ARG
1	A	223	LEU
1	A	232	GLU
1	A	246	MET
1	A	247	LYS
1	A	271	LYS
1	A	272	ASP
1	A	285	THR
1	B	3	THR
1	B	20	LEU
1	B	28	ARG
1	B	37	MET
1	B	45	ARG
1	B	52	ASN
1	B	56	LEU
1	B	61	ASP
1	B	71	THR
1	B	85	ARG
1	B	89	LEU
1	B	101	LEU
1	B	105	ILE
1	B	107	LYS
1	B	110	LEU
1	B	115	LEU
1	B	116	ASN
1	B	117	PHE
1	B	121	GLU
1	B	124	LYS
1	B	125	LYS
1	B	129	SER
1	B	130	TYR
1	B	134	LEU
1	B	145	THR
1	B	188	ARG

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Mol	Chain	Res	Type
1	B	192	VAL
1	B	221	LEU
1	B	228	VAL
1	B	234	MET
1	B	237	THR
1	B	247	LYS
1	B	255	ILE
1	B	271	LYS
1	B	272	ASP
1	B	285	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	57	GLN
1	A	116	ASN
1	A	118	ASN
1	A	172	ASN
1	A	280	GLN
1	B	52	ASN
1	B	122	GLN
1	B	128	GLN
1	B	152	ASN
1	B	262	GLN
1	B	280	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 carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 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	A	286/286 (100%)	0.13	6 (2%)	63	49	23, 42, 87, 118	0
1	B	277/286 (96%)	0.08	3 (1%)	80	69	22, 44, 77, 123	0
All	All	563/572 (98%)	0.11	9 (1%)	72	59	22, 43, 83, 123	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	198	GLY	3.5
1	B	111	ASN	3.5
1	A	204	THR	3.1
1	A	200	GLY	2.8
1	A	110	LEU	2.6
1	A	206	HIS	2.6
1	B	1	MET	2.6
1	A	109	ASP	2.3
1	A	108	SER	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.