Full wwPDB X-ray Structure Validation Report ⓘ

Sep 21, 2021 – 10:12 AM JST

PDB ID	:	7EUM
Title	:	Crystal structure of apo Nmar_1308 protein at cryogenic temperature
Authors	:	DeMirci, H.; Destan, E.; Yuksel, B.; Ayan, E.
Deposited on	:	2021-05-18
Resolution	:	2.15 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:

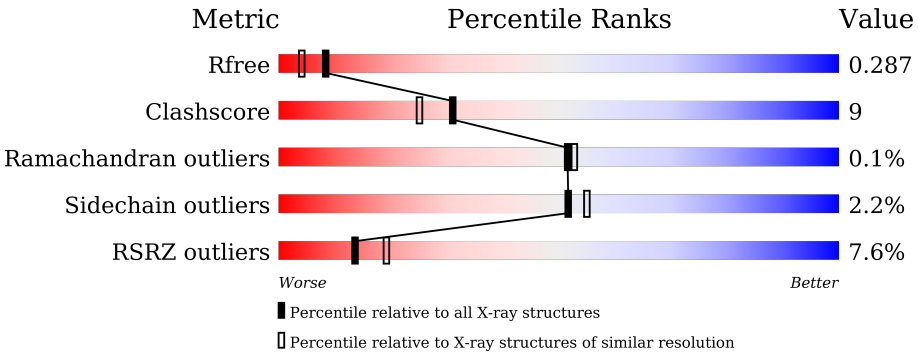
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.1

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 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	A	254	6% 76% 15% • 9%
1	B	254	10% 74% 17% • 7%
1	C	254	4% 71% 21% • 7%
1	D	254	12% 66% 22% • 9%
1	E	254	7% 70% 19% • 9%
1	F	254	3% 76% 14% 10%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10771 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 Enoyl-CoA hydratase/isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	237	Total	C	N	O	S	0	1	0
			1789	1119	310	345	15			
1	D	230	Total	C	N	O	S	0	0	0
			1719	1076	298	332	13			
1	F	229	Total	C	N	O	S	0	0	0
			1711	1071	297	331	12			
1	A	232	Total	C	N	O	S	0	0	0
			1736	1085	301	337	13			
1	E	230	Total	C	N	O	S	0	0	0
			1719	1075	299	333	12			
1	B	236	Total	C	N	O	S	0	0	0
			1761	1099	305	345	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP A9A2G5
D	0	HIS	-	expression tag	UNP A9A2G5
F	0	HIS	-	expression tag	UNP A9A2G5
A	0	HIS	-	expression tag	UNP A9A2G5
E	0	HIS	-	expression tag	UNP A9A2G5
B	0	HIS	-	expression tag	UNP A9A2G5

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	73	Total	O	0	0
			73	73		
2	D	54	Total	O	0	0
			54	54		
2	F	75	Total	O	0	1
			76	76		

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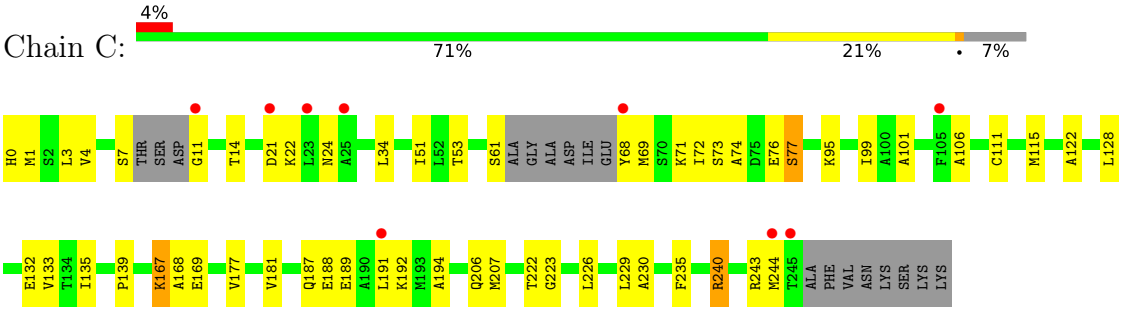
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	56	Total O 56 56	0	0
2	E	39	Total O 39 39	0	0
2	B	38	Total O 38 38	0	0

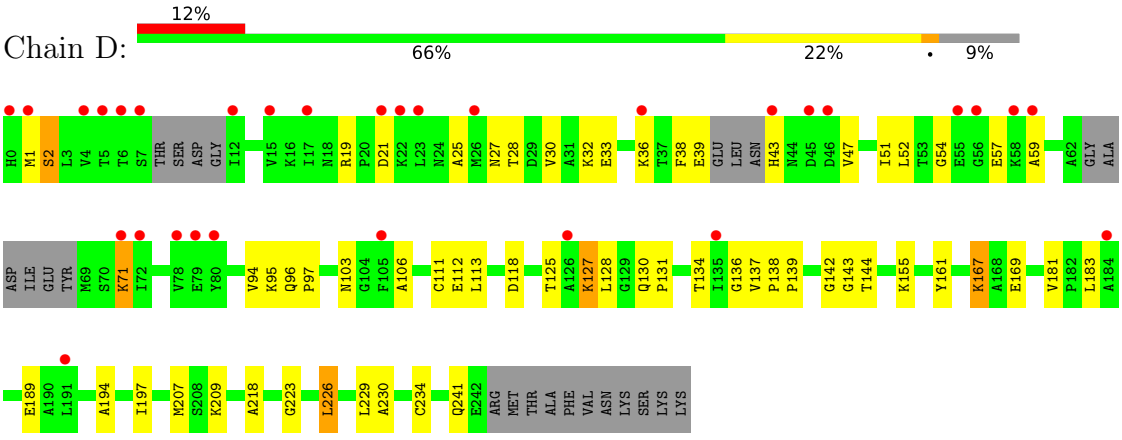
3 Residue-property plots (i)

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.

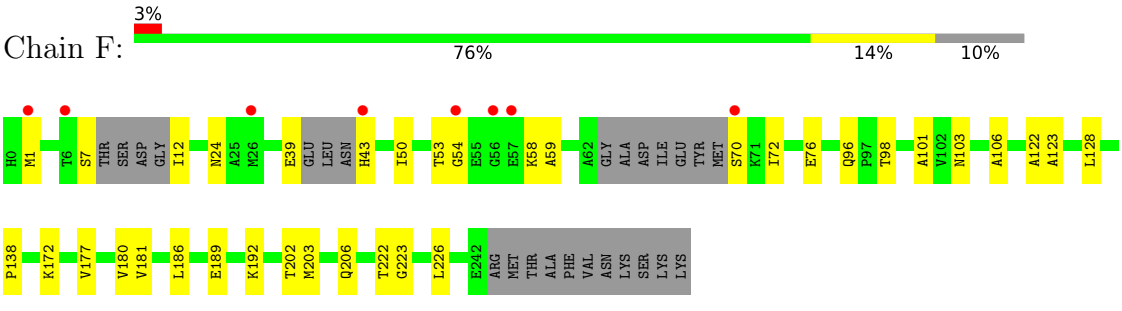
• Molecule 1: Enoyl-CoA hydratase/isomerase



• Molecule 1: Enoyl-CoA hydratase/isomerase

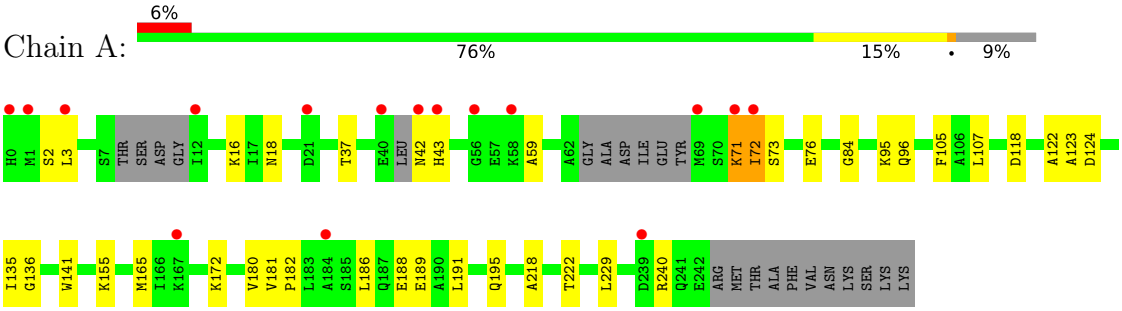


• Molecule 1: Enoyl-CoA hydratase/isomerase



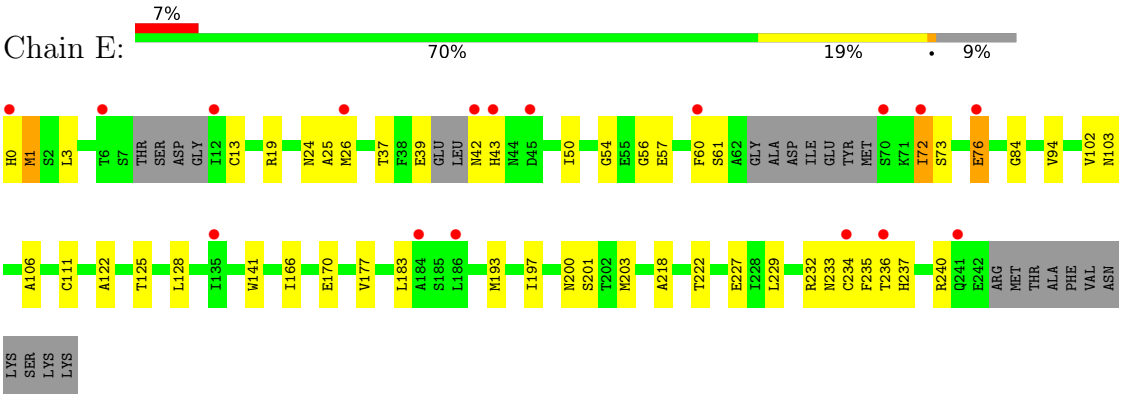
• Molecule 1: Enoyl-CoA hydratase/isomerase

Chain A:



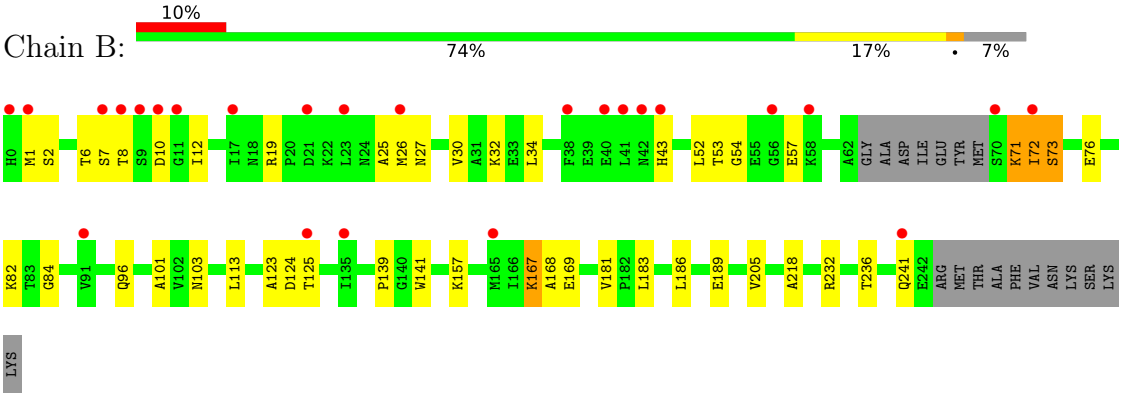
- Molecule 1: Enoyl-CoA hydratase/isomerase

Chain E:



- Molecule 1: Enoyl-CoA hydratase/isomerase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	75.87Å 75.87Å 207.97Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.69 – 2.15 37.93 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.69-2.15) 97.2 (37.93-2.00)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.44 (at 2.00Å)	Xtriage
Refinement program	PHENIX dev_3318	Depositor
R, R_{free}	0.245 , 0.284 0.245 , 0.287	Depositor DCC
R_{free} test set	2001 reflections (2.28%)	wwPDB-VP
Wilson B-factor (Å^2)	41.4	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 51.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.069 for -h,-k,l 0.089 for h,-h-k,-l 0.315 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	10771	wwPDB-VP
Average B, all atoms (Å^2)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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	0.24	0/1753	0.44	0/2362
1	B	0.27	0/1780	0.48	0/2403
1	C	0.24	0/1808	0.43	0/2436
1	D	0.24	0/1736	0.46	1/2339 (0.0%)
1	E	0.24	0/1736	0.43	0/2340
1	F	0.24	0/1728	0.43	0/2329
All	All	0.25	0/10541	0.45	1/14209 (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	1
1	B	0	2
1	E	0	1
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	226	LEU	CA-CB-CG	5.04	126.88	115.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	72	ILE	Peptide
1	B	71	LYS	Peptide
1	B	72	ILE	Peptide

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Mol	Chain	Res	Type	Group
1	E	72	ILE	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	1736	0	1783	27	0
1	B	1761	0	1806	39	0
1	C	1789	0	1839	36	0
1	D	1719	0	1771	49	0
1	E	1719	0	1768	42	0
1	F	1711	0	1762	21	0
2	A	56	0	0	0	0
2	B	38	0	0	3	0
2	C	73	0	0	1	0
2	D	54	0	0	2	0
2	E	39	0	0	1	0
2	F	76	0	0	1	0
All	All	10771	0	10729	192	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 9.

All (192) 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:C:7:SER:HG	1:C:11:GLY:N	1.71	0.87
1:F:72:ILE:HB	1:F:76:GLU:HG3	1.57	0.87
1:B:125:THR:HG21	1:B:183:LEU:HD12	1.58	0.83
1:D:19:ARG:HH21	1:D:25:ALA:HB3	1.42	0.82
1:A:2:SER:HB2	1:A:16:LYS:HB2	1.63	0.81
1:C:244:MET:HG2	1:A:135:ILE:HB	1.65	0.77
1:D:38:PHE:HD2	1:D:94:VAL:HG11	1.52	0.73
1:C:71:LYS:HA	1:B:241:GLN:HE22	1.53	0.73
1:C:167:LYS:HD3	1:C:169:GLU:H	1.55	0.71
1:A:188:GLU:HA	1:A:191:LEU:HD12	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:52:LEU:HD21	1:B:113:LEU:HD21	1.74	0.68
1:B:6:THR:HA	1:B:10:ASP:HB2	1.75	0.67
1:B:139:PRO:O	2:B:301:HOH:O	2.12	0.65
1:B:7:SER:OG	1:B:8:THR:N	2.28	0.65
1:B:123:ALA:HB2	1:B:186:LEU:HD22	1.78	0.65
1:F:43:HIS:HB3	1:F:96:GLN:HE22	1.63	0.64
1:B:19:ARG:NH1	1:B:25:ALA:O	2.32	0.63
1:B:32:LYS:NZ	2:B:302:HOH:O	2.31	0.63
1:B:7:SER:HB2	1:B:12:ILE:HB	1.81	0.63
1:D:112:GLU:HG3	1:D:130:GLN:HE22	1.63	0.62
1:D:52:LEU:HD21	1:D:113:LEU:HD21	1.82	0.62
1:D:167:LYS:HE3	1:D:169:GLU:HB3	1.81	0.61
1:E:233:ASN:O	1:E:236:THR:OG1	2.15	0.61
1:B:26:MET:CE	1:B:113:LEU:HD12	2.31	0.61
1:C:1:MET:HE1	1:C:34:LEU:HG	1.81	0.61
1:E:54:GLY:O	1:E:103:ASN:ND2	2.33	0.60
1:D:167:LYS:HD2	1:D:169:GLU:H	1.66	0.60
1:F:54:GLY:O	1:F:103:ASN:ND2	2.35	0.59
1:C:72:ILE:HB	1:C:76:GLU:HG3	1.82	0.59
1:D:43:HIS:HB3	1:D:96:GLN:HE22	1.67	0.59
1:B:26:MET:HE1	1:B:113:LEU:HD12	1.86	0.58
1:C:240:ARG:HA	1:A:136:GLY:HA3	1.85	0.58
1:D:181:VAL:HG11	1:D:189:GLU:HG3	1.85	0.58
1:B:7:SER:HB2	1:B:12:ILE:HD12	1.85	0.58
1:E:166:ILE:HB	1:E:170:GLU:HG3	1.86	0.58
1:B:54:GLY:O	1:B:103:ASN:ND2	2.30	0.58
1:E:57:GLU:HA	1:E:103:ASN:HD22	1.69	0.57
1:C:133:VAL:HG21	1:B:205:VAL:HG23	1.84	0.57
1:C:207:MET:HB3	1:C:230:ALA:HB1	1.86	0.57
1:C:240:ARG:HH12	1:A:72:ILE:N	2.02	0.57
1:E:0:HIS:N	2:E:306:HOH:O	2.37	0.57
1:A:123:ALA:HB2	1:A:186:LEU:HD22	1.86	0.56
1:D:241:GLN:HA	1:F:70:SER:HB2	1.87	0.56
1:F:24:ASN:ND2	1:F:59:ALA:O	2.38	0.56
1:B:73:SER:O	1:B:76:GLU:N	2.37	0.56
1:D:106:ALA:O	1:D:128:LEU:HA	2.05	0.56
1:A:59:ALA:HA	1:A:105:PHE:H	1.70	0.55
1:B:124:ASP:O	1:B:167:LYS:NZ	2.39	0.55
1:B:181:VAL:HG11	1:B:189:GLU:HG3	1.88	0.55
1:A:188:GLU:O	1:A:191:LEU:HB2	2.06	0.55
1:D:127:LYS:HE3	1:D:167:LYS:HA	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:243:ARG:HB2	1:A:135:ILE:O	2.07	0.54
1:D:94:VAL:HG23	1:D:96:GLN:O	2.08	0.54
1:A:43:HIS:HB3	1:A:96:GLN:HE22	1.73	0.54
1:A:181:VAL:HG11	1:A:189:GLU:HG2	1.89	0.54
1:C:51:ILE:HD11	1:C:194:ALA:HB2	1.90	0.53
1:C:4:VAL:HG23	1:C:14:THR:HB	1.89	0.53
1:E:84:GLY:HA3	1:E:141:TRP:CD1	2.43	0.53
1:D:125:THR:OG1	1:D:183:LEU:HD12	2.08	0.53
1:C:188:GLU:HG2	1:C:192:LYS:HE3	1.90	0.53
1:D:234:CYS:SG	1:F:138:PRO:HD3	2.49	0.53
1:F:172:LYS:HD2	1:F:180:VAL:HG23	1.91	0.53
1:E:19:ARG:NH1	1:E:25:ALA:O	2.42	0.53
1:F:7:SER:HG	1:F:12:ILE:N	2.06	0.52
1:E:42:ASN:O	1:E:43:HIS:ND1	2.42	0.52
1:E:235:PHE:HA	1:E:240:ARG:HD2	1.90	0.52
1:D:27:ASN:OD1	1:D:30:VAL:N	2.28	0.52
1:F:7:SER:OG	1:F:12:ILE:N	2.43	0.51
1:D:28:THR:O	1:D:32:LYS:HG2	2.11	0.51
1:C:73:SER:OG	1:C:74:ALA:N	2.43	0.51
1:D:97:PRO:HG2	1:D:197:ILE:HG21	1.92	0.51
1:E:26:MET:HE2	1:E:141:TRP:HZ3	1.76	0.51
1:D:39:GLU:OE2	1:D:43:HIS:ND1	2.44	0.51
1:F:106:ALA:HB3	1:F:128:LEU:HG	1.93	0.51
1:D:161:TYR:O	1:E:200:ASN:ND2	2.44	0.50
1:E:125:THR:HG21	1:E:183:LEU:HD22	1.93	0.50
1:D:43:HIS:HD2	1:D:47:VAL:HB	1.77	0.50
1:D:223:GLY:HA2	1:D:226:LEU:HD23	1.94	0.50
1:E:13:CYS:HB3	1:E:50:ILE:HD13	1.93	0.50
1:A:73:SER:HB3	1:A:76:GLU:HG2	1.94	0.49
1:C:223:GLY:HA2	1:C:226:LEU:HD12	1.95	0.49
1:A:135:ILE:HG13	1:A:136:GLY:H	1.78	0.49
1:B:73:SER:HB3	1:B:76:GLU:HB3	1.95	0.49
1:B:241:GLN:OE1	1:B:241:GLN:HA	2.13	0.49
1:C:53:THR:HB	1:C:101:ALA:HB3	1.94	0.48
1:D:118:ASP:OD2	1:D:209:LYS:NZ	2.31	0.48
1:A:84:GLY:HA3	1:A:141:TRP:CD1	2.47	0.48
1:C:222:THR:HG21	1:D:218:ALA:HB2	1.94	0.48
1:F:123:ALA:HB2	1:F:186:LEU:HD22	1.94	0.48
1:B:43:HIS:HB3	1:B:96:GLN:HE22	1.79	0.48
1:E:73:SER:O	1:E:76:GLU:N	2.46	0.48
1:F:50:ILE:HB	1:F:98:THR:HG22	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:181:VAL:HG11	1:C:189:GLU:HG2	1.94	0.47
1:A:3:LEU:HD21	1:A:37:THR:CG2	2.44	0.47
1:C:187:GLN:NE2	2:C:307:HOH:O	2.47	0.47
1:C:24:ASN:HB2	1:C:61:SER:HA	1.97	0.47
1:D:144:THR:OG1	1:E:227:GLU:OE1	2.25	0.47
1:B:167:LYS:HG2	1:B:168:ALA:H	1.80	0.47
1:D:95:LYS:HE3	1:D:96:GLN:NE2	2.30	0.47
1:F:53:THR:HB	1:F:101:ALA:HB3	1.97	0.47
1:B:53:THR:HB	1:B:101:ALA:HB3	1.96	0.47
1:B:1:MET:HE1	1:B:34:LEU:HG	1.97	0.46
1:B:72:ILE:HG13	1:B:73:SER:HB3	1.96	0.46
1:A:191:LEU:O	1:A:195:GLN:HG3	2.15	0.46
1:A:124:ASP:OD1	1:A:182:PRO:HA	2.16	0.46
1:B:6:THR:HA	1:B:10:ASP:CB	2.46	0.46
1:B:84:GLY:HA3	1:B:141:TRP:CD1	2.50	0.46
1:C:106:ALA:O	1:C:128:LEU:HA	2.16	0.46
1:E:56:GLY:O	1:E:57:GLU:HG3	2.16	0.46
1:E:106:ALA:O	1:E:111:CYS:HB2	2.17	0.46
1:A:42:ASN:HD21	1:A:95:LYS:HD3	1.81	0.45
1:F:39:GLU:OE2	1:F:43:HIS:ND1	2.49	0.45
1:A:107:LEU:HD21	1:A:165:MET:HE3	1.97	0.45
1:E:232:ARG:O	1:E:236:THR:HG23	2.16	0.45
1:D:207:MET:HB3	1:D:230:ALA:HB1	1.97	0.45
1:C:229:LEU:HB3	1:D:229:LEU:HB3	1.99	0.45
1:A:72:ILE:HG13	1:A:73:SER:HB3	1.97	0.45
1:C:51:ILE:HD13	1:C:99:ILE:HB	1.99	0.45
1:E:39:GLU:HB2	1:E:42:ASN:O	2.16	0.45
1:E:122:ALA:HB2	1:E:177:VAL:HG11	1.98	0.45
1:F:189:GLU:OE1	2:F:301:HOH:O	2.21	0.45
1:A:155:LYS:HA	1:A:155:LYS:HD2	1.79	0.45
1:A:71:LYS:HB2	1:A:71:LYS:HE2	1.62	0.45
1:A:118:ASP:HB3	1:B:157:LYS:HD3	2.00	0.45
1:C:21:ASP:OD1	1:C:22:LYS:HG2	2.17	0.44
1:D:139:PRO:O	2:D:301:HOH:O	2.21	0.44
1:D:143:GLY:N	2:D:301:HOH:O	2.50	0.44
1:E:43:HIS:CE1	1:E:94:VAL:HG21	2.51	0.44
1:D:51:ILE:HD11	1:D:194:ALA:HB2	1.99	0.44
1:B:167:LYS:HE3	1:B:169:GLU:HB2	1.99	0.44
1:D:43:HIS:CD2	1:D:47:VAL:HB	2.53	0.44
1:B:7:SER:N	1:B:10:ASP:HA	2.32	0.44
1:D:33:GLU:OE2	1:D:36:LYS:NZ	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:26:MET:HG3	1:E:61:SER:OG	2.17	0.44
1:E:103:ASN:OD1	1:E:103:ASN:N	2.45	0.44
1:E:26:MET:HE2	1:E:141:TRP:CZ3	2.53	0.44
1:F:203:MET:HB2	1:F:203:MET:HE2	1.86	0.43
1:E:43:HIS:HE1	1:E:94:VAL:HG21	1.82	0.43
1:C:187:GLN:O	1:C:191:LEU:HG	2.18	0.43
1:D:57:GLU:O	1:D:183:LEU:HD11	2.18	0.43
1:A:229:LEU:HB3	1:E:229:LEU:HB3	2.01	0.43
1:C:74:ALA:HA	1:C:77:SER:HB3	2.00	0.43
1:C:240:ARG:O	1:C:244:MET:HG3	2.19	0.43
1:F:222:THR:HG21	1:B:218:ALA:HB2	1.99	0.43
1:D:155:LYS:HD3	1:D:155:LYS:HA	1.84	0.43
1:B:183:LEU:HD23	1:B:183:LEU:O	2.18	0.42
1:E:193:MET:O	1:E:197:ILE:HG13	2.19	0.42
1:B:27:ASN:OD1	1:B:30:VAL:HG23	2.19	0.42
1:D:167:LYS:HE3	1:D:169:GLU:CB	2.49	0.42
1:D:71:LYS:HA	1:E:240:ARG:CZ	2.49	0.42
1:D:112:GLU:HG3	1:D:130:GLN:NE2	2.33	0.42
1:A:122:ALA:HB3	1:A:180:VAL:HG12	2.02	0.42
1:C:106:ALA:O	1:C:111:CYS:HB2	2.19	0.42
1:D:1:MET:HE3	1:D:2:SER:N	2.35	0.42
1:D:32:LYS:O	1:D:36:LYS:HG3	2.20	0.42
1:A:222:THR:HG21	1:E:218:ALA:HB2	2.01	0.42
1:B:57:GLU:HG2	1:B:183:LEU:HD21	2.02	0.42
1:B:82:LYS:HA	1:B:82:LYS:HD2	1.86	0.42
1:D:54:GLY:O	1:D:103:ASN:ND2	2.45	0.42
1:F:223:GLY:HA2	1:F:226:LEU:HD12	2.02	0.42
1:E:1:MET:HE1	1:E:37:THR:OG1	2.20	0.42
1:C:132:GLU:HG2	1:C:139:PRO:HA	2.02	0.42
1:C:167:LYS:HE2	1:C:168:ALA:HB3	2.02	0.42
1:D:138:PRO:HD3	1:E:234:CYS:SG	2.60	0.41
1:F:202:THR:O	1:F:206:GLN:HG2	2.20	0.41
1:E:19:ARG:HB2	1:E:24:ASN:HA	2.02	0.41
1:D:131:PRO:O	1:D:134:THR:OG1	2.35	0.41
1:F:123:ALA:HA	1:F:181:VAL:O	2.20	0.41
1:E:60:PHE:HB2	1:E:102:VAL:HA	2.02	0.41
1:E:106:ALA:O	1:E:128:LEU:HA	2.21	0.41
1:D:137:VAL:HG11	1:E:235:PHE:CE1	2.56	0.41
1:F:122:ALA:HB2	1:F:177:VAL:HG11	2.01	0.41
1:C:76:GLU:H	1:C:76:GLU:HG2	1.64	0.41
1:E:72:ILE:HG22	1:E:73:SER:CB	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:LYS:O	1:C:206:GLN:HG2	2.21	0.41
1:D:27:ASN:OD1	1:D:30:VAL:HG12	2.20	0.41
1:D:106:ALA:O	1:D:111:CYS:HB2	2.20	0.41
1:D:167:LYS:CE	1:D:169:GLU:CB	2.99	0.41
1:D:136:GLY:HA2	1:E:201:SER:CB	2.51	0.41
1:B:7:SER:H	1:B:10:ASP:HB3	1.85	0.41
1:B:232:ARG:O	1:B:236:THR:HG23	2.21	0.41
1:C:111:CYS:O	1:C:115:MET:HG3	2.21	0.41
1:D:59:ALA:N	1:D:103:ASN:O	2.54	0.41
1:E:237:HIS:O	1:E:240:ARG:HG2	2.22	0.41
1:B:167:LYS:HG2	1:B:168:ALA:N	2.34	0.41
1:D:142:GLY:N	1:E:227:GLU:OE2	2.51	0.40
1:B:1:MET:N	2:B:306:HOH:O	2.53	0.40
1:A:218:ALA:HB2	1:E:222:THR:HG21	2.03	0.40
1:C:122:ALA:HB2	1:C:177:VAL:HG11	2.04	0.40
1:C:68:TYR:CE1	1:C:135:ILE:HD12	2.57	0.40
1:E:170:GLU:H	1:E:170:GLU:HG2	1.56	0.40
1:E:203:MET:HG3	1:E:234:CYS:SG	2.62	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	224/254 (88%)	214 (96%)	10 (4%)	0	100	100
1	B	232/254 (91%)	217 (94%)	14 (6%)	1 (0%)	34	29
1	C	232/254 (91%)	227 (98%)	5 (2%)	0	100	100
1	D	222/254 (87%)	214 (96%)	8 (4%)	0	100	100
1	E	222/254 (87%)	210 (95%)	12 (5%)	0	100	100
1	F	221/254 (87%)	216 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1353/1524 (89%)	1298 (96%)	54 (4%)	1 (0%)	51 53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	73	SER

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	187/205 (91%)	183 (98%)	4 (2%)	53 57
1	B	190/205 (93%)	187 (98%)	3 (2%)	62 67
1	C	193/205 (94%)	186 (96%)	7 (4%)	35 33
1	D	185/205 (90%)	180 (97%)	5 (3%)	44 46
1	E	185/205 (90%)	182 (98%)	3 (2%)	62 67
1	F	184/205 (90%)	181 (98%)	3 (2%)	62 67
All	All	1124/1230 (91%)	1099 (98%)	25 (2%)	52 55

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	0	HIS
1	C	3	LEU
1	C	69	MET
1	C	77	SER
1	C	167	LYS
1	C	235	PHE
1	C	240	ARG
1	D	2	SER
1	D	21	ASP
1	D	71	LYS
1	D	127	LYS

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Mol	Chain	Res	Type
1	D	167	LYS
1	F	1	MET
1	F	58	LYS
1	F	192	LYS
1	A	18	ASN
1	A	71	LYS
1	A	172	LYS
1	A	240	ARG
1	E	1	MET
1	E	3	LEU
1	E	76	GLU
1	B	2	SER
1	B	71	LYS
1	B	167	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	130	GLN
1	A	18	ASN
1	B	206	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 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	A	232/254 (91%)	0.54	16 (6%) 16 23	35, 65, 100, 126	0
1	B	236/254 (92%)	0.69	25 (10%) 6 9	32, 66, 116, 164	0
1	C	237/254 (93%)	0.21	9 (3%) 40 49	32, 52, 85, 100	0
1	D	230/254 (90%)	0.67	31 (13%) 3 3	31, 69, 107, 138	0
1	E	230/254 (90%)	0.46	17 (7%) 14 20	36, 64, 100, 117	0
1	F	229/254 (90%)	0.15	8 (3%) 44 52	31, 52, 84, 102	0
All	All	1394/1524 (91%)	0.46	106 (7%) 13 19	31, 61, 101, 164	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	8	THR	15.9
1	B	56	GLY	12.3
1	B	9	SER	11.4
1	B	7	SER	7.7
1	C	68	TYR	6.3
1	D	43	HIS	6.3
1	E	42	ASN	6.1
1	F	43	HIS	5.9
1	E	72	ILE	5.6
1	B	42	ASN	5.4
1	D	80	TYR	5.3
1	B	1	MET	5.2
1	A	69	MET	5.2
1	A	43	HIS	5.0
1	C	11	GLY	4.7
1	D	58	LYS	4.5
1	B	41	LEU	4.4
1	A	42	ASN	4.4
1	F	1	MET	4.4

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Mol	Chain	Res	Type	RSRZ
1	D	45	ASP	4.4
1	B	40	GLU	4.4
1	D	135	ILE	4.3
1	D	22	LYS	4.3
1	A	72	ILE	4.1
1	E	241	GLN	4.1
1	C	23	LEU	4.0
1	F	6	THR	3.9
1	D	23	LEU	3.9
1	D	0	HIS	3.8
1	A	0	HIS	3.8
1	B	10	ASP	3.7
1	A	3	LEU	3.7
1	A	40	GLU	3.7
1	B	58	LYS	3.6
1	E	45	ASP	3.6
1	B	0	HIS	3.6
1	D	56	GLY	3.6
1	A	56	GLY	3.5
1	B	43	HIS	3.5
1	D	4	VAL	3.5
1	D	191	LEU	3.5
1	D	71	LYS	3.4
1	B	11	GLY	3.4
1	D	17	ILE	3.4
1	D	7	SER	3.4
1	D	184	ALA	3.4
1	D	21	ASP	3.4
1	B	23	LEU	3.3
1	A	58	LYS	3.2
1	D	36	LYS	3.2
1	A	21	ASP	3.1
1	A	1	MET	3.1
1	E	186	LEU	3.1
1	E	43	HIS	3.0
1	B	26	MET	3.0
1	D	6	THR	3.0
1	E	6	THR	3.0
1	E	60	PHE	2.9
1	D	1	MET	2.8
1	E	236	THR	2.7
1	D	26	MET	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	135	ILE	2.7
1	E	234	CYS	2.7
1	F	70	SER	2.7
1	D	55	GLU	2.6
1	E	12	ILE	2.6
1	A	71	LYS	2.6
1	B	72	ILE	2.6
1	C	191	LEU	2.6
1	D	126	ALA	2.5
1	E	184	ALA	2.5
1	D	5	THR	2.5
1	D	78	VAL	2.5
1	B	17	ILE	2.4
1	D	12	ILE	2.4
1	E	0	HIS	2.4
1	A	184	ALA	2.4
1	A	167	LYS	2.3
1	C	105	PHE	2.3
1	C	25	ALA	2.2
1	C	244	MET	2.2
1	F	56	GLY	2.2
1	E	70	SER	2.2
1	D	72	ILE	2.2
1	D	105	PHE	2.2
1	B	91	VAL	2.2
1	F	57	GLU	2.2
1	E	26	MET	2.2
1	D	15	VAL	2.1
1	B	125	THR	2.1
1	E	135	ILE	2.1
1	B	241	GLN	2.1
1	F	26	MET	2.1
1	B	70	SER	2.1
1	A	239	ASP	2.1
1	B	38	PHE	2.1
1	B	165	MET	2.1
1	C	21	ASP	2.1
1	D	46	ASP	2.1
1	D	59	ALA	2.1
1	B	21	ASP	2.0
1	F	54	GLY	2.0
1	A	12	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	245	THR	2.0
1	D	79	GLU	2.0
1	E	76	GLU	2.0

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.