



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 12:45 pm BST

PDB ID : 1FUU
Title : YEAST INITIATION FACTOR 4A
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Deposited on : 2000-09-15
Resolution : 2.50 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

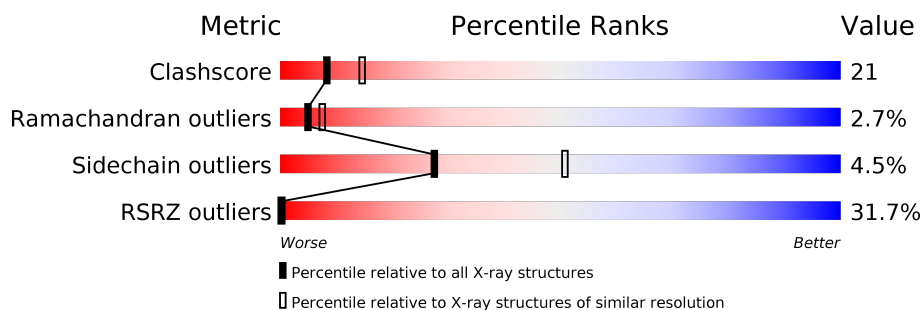
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 $\leq 5\%$. 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	394	
1	B	394	

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 4800 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 YEAST INITIATION FACTOR 4A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	215	1660	1060	277	313	1	9	0	0	0
1	B	380	2994	1898	500	582	3	11	64	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MSE	MET	modified residue	UNP P10081
A	53	MSE	MET	modified residue	UNP P10081
A	94	MSE	MET	modified residue	UNP P10081
A	110	MSE	MET	modified residue	UNP P10081
A	116	MSE	MET	modified residue	UNP P10081
A	165	MSE	MET	modified residue	UNP P10081
A	174	MSE	MET	modified residue	UNP P10081
A	203	MSE	MET	modified residue	UNP P10081
A	215	MSE	MET	modified residue	UNP P10081
A	302	MSE	MET	modified residue	UNP P10081
A	371	MSE	MET	modified residue	UNP P10081
B	26	MSE	MET	modified residue	UNP P10081
B	53	MSE	MET	modified residue	UNP P10081
B	94	MSE	MET	modified residue	UNP P10081
B	110	MSE	MET	modified residue	UNP P10081
B	116	MSE	MET	modified residue	UNP P10081
B	165	MSE	MET	modified residue	UNP P10081
B	174	MSE	MET	modified residue	UNP P10081
B	203	MSE	MET	modified residue	UNP P10081
B	215	MSE	MET	modified residue	UNP P10081
B	302	MSE	MET	modified residue	UNP P10081
B	371	MSE	MET	modified residue	UNP P10081

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	76	Total 76	O 76	0	0
2	B	70	Total 70	O 70	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	38.80Å 71.20Å 73.20Å 94.00° 89.60° 101.00°	Depositor
Resolution (Å)	40.00 – 2.50 27.09 – 2.51	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.50) 84.9 (27.09-2.51)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.97 (at 2.50Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.243 , 0.273 0.251 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	27.7	Xtrriage
Anisotropy	0.147	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 62.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	4800	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.81% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.41	0/1678	0.66	1/2258 (0.0%)
1	B	0.35	0/3027	0.57	0/4074
All	All	0.37	0/4705	0.61	1/6332 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	18	LYS	N-CA-C	-5.51	96.12	111.00

There are no chirality outliers.

There are no planarity outliers.

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	1660	0	1669	64	0
1	B	2994	0	3000	134	0
2	A	76	0	0	2	0
2	B	70	0	0	2	0
All	All	4800	0	4669	193	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 21.

All (193) 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:211:THR:HA	1:B:215:MSE:HE3	1.46	0.98
1:A:42:GLU:HG3	1:B:127:THR:H	1.36	0.91
1:B:272:VAL:HG13	1:B:314:ILE:HG22	1.58	0.83
1:B:261:GLN:HG2	1:B:311:ARG:HA	1.63	0.80
1:B:118:ILE:HD12	1:B:118:ILE:O	1.85	0.77
1:B:94:MSE:HE3	1:B:143:VAL:HB	1.66	0.77
1:B:52:ILE:HG22	1:B:53:MSE:HE2	1.68	0.75
1:B:11:GLN:HG3	1:B:12:ILE:H	1.51	0.75
1:B:45:SER:O	1:B:49:GLN:HG3	1.86	0.75
1:B:259:VAL:HG22	1:B:311:ARG:NH2	2.03	0.74
1:B:260:THR:HG23	1:B:329:SER:HB3	1.68	0.73
1:B:228:LEU:HG	1:B:344:ILE:HG21	1.71	0.73
1:B:26:MSE:SE	1:B:53:MSE:HE3	2.39	0.72
1:B:344:ILE:HD12	1:B:345:HIS:N	2.04	0.72
1:B:337:PRO:HG3	1:B:346:ARG:NH1	2.06	0.69
1:B:105:ILE:O	1:B:109:VAL:HG12	1.94	0.67
1:B:228:LEU:HD23	1:B:229:THR:N	2.10	0.67
1:B:319:LEU:O	1:B:323:ILE:HG13	1.96	0.66
1:A:58:GLY:HA2	1:A:82:ARG:HH21	1.61	0.66
1:B:344:ILE:HD12	1:B:345:HIS:H	1.61	0.66
1:B:61:VAL:HG13	1:B:219:VAL:CG2	2.26	0.65
1:B:52:ILE:HG22	1:B:53:MSE:CE	2.27	0.65
1:B:292:ASP:OD2	1:B:293:LEU:HD12	1.98	0.64
1:B:340:LYS:HE2	1:B:373:GLU:HB3	1.80	0.63
1:A:44:PRO:HB2	1:A:49:GLN:HG2	1.79	0.63
1:B:128:SER:OG	1:B:130:VAL:HG22	1.99	0.63
1:A:45:SER:O	1:A:49:GLN:HG3	1.97	0.62
1:B:44:PRO:HB2	1:B:49:GLN:HG2	1.80	0.62
1:B:118:ILE:HA	1:B:140:GLN:OE1	2.01	0.61
1:B:146:PRO:HB2	1:B:179:PHE:CD2	2.36	0.61
1:B:337:PRO:HG3	1:B:346:ARG:CZ	2.31	0.61
1:B:279:LEU:O	1:B:284:PHE:HB2	1.99	0.61
1:B:62:LEU:HD11	1:B:203:MSE:SE	2.51	0.61
1:A:203:MSE:HE3	1:A:208:LEU:HD12	1.82	0.60
1:B:167:ILE:HD13	1:B:197:VAL:HB	1.84	0.60
1:B:56:ILE:HD11	1:B:78:ALA:HA	1.83	0.60
1:B:230:LEU:HD21	1:B:344:ILE:HG22	1.83	0.60
1:B:369:GLY:O	1:B:373:GLU:HG2	2.02	0.60
1:B:347:ILE:O	1:B:347:ILE:HG13	2.02	0.59
1:A:42:GLU:HG3	1:B:127:THR:N	2.14	0.59
1:A:82:ARG:NH2	1:A:195:GLN:HE22	2.01	0.59
1:B:16:TYR:CE2	1:B:18:LYS:HB3	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:241:GLU:HA	1:B:365:ASN:ND2	2.18	0.58
1:B:228:LEU:CG	1:B:344:ILE:HG21	2.34	0.58
1:B:186:ILE:O	1:B:190:LEU:HD13	2.05	0.57
1:A:175:LEU:HD23	1:A:206:ASP:HB3	1.85	0.57
1:B:94:MSE:CE	1:B:143:VAL:HB	2.34	0.57
1:A:82:ARG:NH2	1:A:195:GLN:NE2	2.52	0.57
1:A:58:GLY:HA2	1:A:82:ARG:NH2	2.18	0.57
1:B:330:LEU:HD22	1:B:393:LEU:HD21	1.86	0.56
1:B:239:ASN:HD21	1:B:241:GLU:HG2	1.71	0.56
1:B:264:ILE:HG12	1:B:332:ILE:HB	1.87	0.56
1:B:339:ASN:ND2	1:B:341:GLU:HB3	2.21	0.55
1:B:205:ASN:HD22	1:B:208:LEU:HD12	1.72	0.55
1:A:26:MSE:HB2	1:A:28:LEU:CD2	2.37	0.55
1:B:235:GLN:HB3	1:B:382:ILE:HG12	1.87	0.55
1:A:121:HIS:CD2	1:A:135:GLY:HA3	2.42	0.54
1:B:240:VAL:HG21	1:B:246:LYS:HG2	1.89	0.54
1:B:240:VAL:HG21	1:B:246:LYS:CG	2.37	0.54
1:B:61:VAL:HG13	1:B:219:VAL:HG22	1.88	0.54
1:A:62:LEU:HD11	1:A:203:MSE:HE1	1.88	0.53
1:B:208:LEU:O	1:B:212:THR:HG22	2.08	0.53
1:A:17:ASP:HB2	2:A:446:HOH:O	2.07	0.53
1:B:259:VAL:HG12	1:B:260:THR:N	2.25	0.52
1:B:273:GLU:HG2	1:B:290:TYR:OH	2.10	0.52
1:B:84:ASP:OD1	1:B:86:SER:HB3	2.10	0.52
1:B:272:VAL:HG13	1:B:314:ILE:CG2	2.35	0.51
1:B:348:GLY:O	1:B:349:ARG:HB3	2.10	0.51
1:A:181:GLU:CD	1:A:181:GLU:H	2.14	0.51
1:A:82:ARG:HH22	1:A:195:GLN:NE2	2.08	0.51
1:B:253:LEU:HD12	1:B:389:ILE:HD13	1.93	0.51
1:B:368:VAL:C	1:B:370:ALA:H	2.14	0.51
1:B:253:LEU:CD1	1:B:389:ILE:HD13	2.40	0.51
1:B:182:GLN:O	1:B:186:ILE:HG13	2.11	0.51
1:B:384:GLU:O	1:B:386:PRO:HD3	2.11	0.51
1:A:104:GLN:HE21	1:A:104:GLN:HA	1.75	0.51
1:A:42:GLU:HB3	1:A:43:GLU:OE2	2.10	0.50
1:B:64:GLN:HA	1:B:200:SER:O	2.10	0.50
1:A:216:ARG:O	1:A:217:ASN:C	2.50	0.50
1:B:87:VAL:HB	1:B:91:GLN:NE2	2.27	0.50
1:A:71:LYS:O	1:A:74:THR:HB	2.11	0.50
1:B:343:TYR:CZ	1:B:347:ILE:HD11	2.46	0.50
1:B:56:ILE:CD1	1:B:81:GLN:HB3	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ARG:HD3	2:A:400:HOH:O	2.12	0.50
1:B:257:ILE:HG13	1:B:258:SER:N	2.27	0.50
1:A:106:GLN:O	1:A:110:MSE:HG2	2.12	0.50
1:B:233:ILE:HA	1:B:357:GLY:O	2.12	0.49
1:B:234:LYS:HB3	1:B:236:PHE:HE1	1.78	0.49
1:A:26:MSE:HB2	1:A:28:LEU:HD21	1.95	0.49
1:A:79:ALA:O	1:A:83:ILE:HG12	2.13	0.49
1:A:186:ILE:O	1:A:190:LEU:HD13	2.13	0.48
1:B:305:PHE:CD2	1:B:313:LEU:HD22	2.48	0.48
1:A:34:ARG:HH12	1:B:99:ARG:HD2	1.78	0.48
1:B:106:GLN:O	1:B:110:MSE:HG2	2.13	0.48
1:A:61:VAL:HG13	1:A:219:VAL:HG22	1.95	0.48
1:B:11:GLN:HG3	1:B:12:ILE:N	2.26	0.48
1:A:104:GLN:HA	1:A:104:GLN:NE2	2.29	0.48
1:B:181:GLU:O	1:B:185:GLN:HG3	2.13	0.48
1:B:228:LEU:O	1:B:229:THR:HB	2.14	0.48
1:B:343:TYR:CE2	1:B:347:ILE:HD11	2.49	0.48
1:B:228:LEU:CD2	1:B:229:THR:N	2.77	0.48
1:B:240:VAL:HG12	1:B:249:CYS:SG	2.53	0.48
1:B:324:ASP:O	1:B:326:GLN:N	2.47	0.48
1:B:366:GLU:C	1:B:368:VAL:H	2.17	0.48
1:B:248:GLU:OE2	1:B:248:GLU:HA	2.14	0.48
1:B:253:LEU:O	1:B:257:ILE:HG23	2.13	0.48
1:B:363:VAL:HB	1:B:367:ASP:HB2	1.96	0.48
1:A:16:TYR:CE2	1:A:18:LYS:HB3	2.48	0.48
1:A:199:LEU:HD22	1:A:199:LEU:N	2.28	0.48
1:A:59:HIS:O	1:A:61:VAL:HG23	2.14	0.48
1:B:225:LYS:O	1:B:226:ASP:HB3	2.14	0.48
1:A:167:ILE:CD1	1:A:197:VAL:HB	2.44	0.47
1:B:106:GLN:O	1:B:110:MSE:CG	2.62	0.47
1:A:224:LYS:O	1:A:225:LYS:CB	2.62	0.47
1:B:325:VAL:O	1:B:325:VAL:HG23	2.13	0.47
1:B:259:VAL:HA	1:B:311:ARG:CZ	2.44	0.47
1:B:282:ASP:O	1:B:283:LYS:HB2	2.14	0.47
1:B:237:TYR:CD2	1:B:371:MSE:HE1	2.50	0.47
1:A:175:LEU:HD23	1:A:206:ASP:CB	2.45	0.47
1:A:82:ARG:HH11	1:A:82:ARG:HB3	1.80	0.47
1:B:349:ARG:HH11	1:B:349:ARG:HG3	1.78	0.47
1:B:239:ASN:ND2	1:B:241:GLU:HG2	2.30	0.46
1:A:61:VAL:C	1:A:215:MSE:HE1	2.35	0.46
1:B:216:ARG:O	1:B:217:ASN:C	2.53	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:TYR:O	1:A:17:ASP:C	2.52	0.46
1:A:50:ARG:HE	1:A:50:ARG:HB2	1.27	0.46
1:A:109:VAL:HG22	1:A:120:VAL:HG21	1.96	0.46
1:B:121:HIS:CD2	1:B:135:GLY:HA3	2.50	0.46
1:B:306:ARG:HG2	1:B:306:ARG:O	2.16	0.46
1:B:344:ILE:HG23	1:B:378:TYR:CE2	2.51	0.46
1:A:21:TYR:O	1:A:44:PRO:HD2	2.16	0.46
1:A:61:VAL:O	1:A:215:MSE:HE1	2.15	0.46
1:B:228:LEU:HD21	1:B:230:LEU:HG	1.98	0.46
1:A:128:SER:C	1:A:130:VAL:H	2.19	0.46
1:B:199:LEU:N	1:B:199:LEU:HD22	2.31	0.46
1:A:97:PRO:HD2	1:A:101:LEU:HD13	1.96	0.46
1:A:34:ARG:HH12	1:B:99:ARG:CD	2.28	0.46
1:A:61:VAL:HG13	1:A:219:VAL:CG2	2.46	0.45
1:B:236:PHE:O	1:B:360:ILE:HA	2.17	0.45
1:A:97:PRO:HD2	1:A:101:LEU:CD1	2.47	0.45
1:A:198:LEU:HD23	1:A:198:LEU:C	2.37	0.45
1:A:203:MSE:HE3	1:A:208:LEU:CD1	2.46	0.45
1:B:276:THR:HG23	1:B:286:VAL:HG13	1.99	0.45
1:B:50:ARG:HE	1:B:50:ARG:HB2	1.27	0.45
1:B:259:VAL:O	1:B:260:THR:HB	2.17	0.45
1:B:242:GLU:HB2	1:B:245:TYR:HD1	1.82	0.44
1:B:241:GLU:O	1:B:364:THR:HB	2.16	0.44
1:A:37:PHE:CE1	1:B:126:GLY:HA3	2.52	0.44
1:B:259:VAL:HG12	1:B:260:THR:H	1.83	0.44
1:A:128:SER:C	1:A:130:VAL:N	2.71	0.44
1:B:172:ASP:N	1:B:172:ASP:OD1	2.51	0.44
1:B:51:ALA:O	1:B:55:ILE:HG13	2.17	0.43
1:A:128:SER:O	1:A:130:VAL:N	2.51	0.43
1:A:135:GLY:O	1:A:139:ALA:HB2	2.17	0.43
1:A:51:ALA:O	1:A:55:ILE:HG13	2.18	0.43
1:B:234:LYS:HB3	1:B:236:PHE:CE1	2.53	0.43
1:B:242:GLU:HB2	1:B:245:TYR:CD1	2.53	0.43
1:A:121:HIS:HE1	1:A:132:ASP:OD2	2.01	0.43
1:A:94:MSE:CE	1:A:143:VAL:HB	2.47	0.43
1:B:198:LEU:C	1:B:198:LEU:HD23	2.38	0.43
1:A:83:ILE:HG21	1:A:118:ILE:HD12	2.00	0.43
1:B:71:LYS:O	1:B:74:THR:HB	2.19	0.43
1:B:205:ASN:HA	1:B:208:LEU:HD12	2.01	0.43
1:B:71:LYS:HE2	2:B:418:HOH:O	2.19	0.43
1:B:14:THR:HA	1:B:220:ARG:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:VAL:HG21	1:B:53:MSE:HG3	2.00	0.42
1:B:393:LEU:HD12	1:B:393:LEU:N	2.34	0.42
1:B:59:HIS:HD2	2:B:423:HOH:O	2.01	0.42
1:B:56:ILE:HD12	1:B:81:GLN:CG	2.49	0.42
1:B:51:ALA:O	1:B:54:PRO:HG2	2.19	0.42
1:A:156:ARG:HG2	1:A:156:ARG:HH11	1.84	0.42
1:B:198:LEU:HD13	1:B:215:MSE:HE1	2.00	0.42
1:A:28:LEU:HA	1:A:81:GLN:OE1	2.20	0.42
1:B:303:LYS:O	1:B:307:SER:HB3	2.18	0.42
1:B:349:ARG:NH1	1:B:349:ARG:HG3	2.34	0.42
1:B:241:GLU:HG2	1:B:365:ASN:HD21	1.84	0.42
1:B:211:THR:CA	1:B:215:MSE:HE3	2.34	0.42
1:A:62:LEU:HD21	1:A:203:MSE:HE2	2.00	0.42
1:A:165:MSE:SE	1:A:167:ILE:HD11	2.70	0.42
1:B:158:PHE:CD1	1:B:158:PHE:C	2.92	0.41
1:B:240:VAL:O	1:B:241:GLU:HB2	2.20	0.41
1:B:11:GLN:OE1	1:B:11:GLN:HA	2.19	0.41
1:A:127:THR:HG23	1:A:127:THR:O	2.20	0.41
1:B:135:GLY:O	1:B:139:ALA:HB2	2.20	0.41
1:B:290:TYR:H	1:B:293:LEU:HD13	1.86	0.41
1:A:62:LEU:HD21	1:A:203:MSE:CE	2.51	0.41
1:B:130:VAL:HG23	1:B:131:GLU:N	2.36	0.41
1:B:149:VAL:O	1:B:153:ILE:HG13	2.20	0.41
1:A:167:ILE:HD12	1:A:197:VAL:HB	2.03	0.41
1:B:26:MSE:CB	1:B:28:LEU:HD13	2.51	0.41
1:B:94:MSE:HE2	1:B:141:ILE:CG2	2.51	0.41
1:B:293:LEU:H	1:B:293:LEU:HD12	1.86	0.40
1:A:58:GLY:CA	1:A:82:ARG:HH21	2.32	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	213/394 (54%)	203 (95%)	6 (3%)	4 (2%)	8	13
1	B	376/394 (95%)	328 (87%)	36 (10%)	12 (3%)	4	5
All	All	589/788 (75%)	531 (90%)	42 (7%)	16 (3%)	5	7

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	LYS
1	B	228	LEU
1	B	325	VAL
1	B	326	GLN
1	A	17	ASP
1	B	226	ASP
1	B	307	SER
1	B	308	GLY
1	B	310	SER
1	A	126	GLY
1	B	17	ASP
1	B	259	VAL
1	B	261	GLN
1	A	129	PHE
1	B	292	ASP
1	B	309	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	179/336 (53%)	163 (91%)	16 (9%)	9	19
1	B	330/336 (98%)	323 (98%)	7 (2%)	53	78
All	All	509/672 (76%)	486 (96%)	23 (4%)	27	51

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	17	ASP
1	A	18	LYS
1	A	24	ASP
1	A	34	ARG
1	A	50	ARG
1	A	66	GLN
1	A	69	THR
1	A	82	ARG
1	A	109	VAL
1	A	112	LEU
1	A	129	PHE
1	A	158	PHE
1	A	175	LEU
1	A	181	GLU
1	A	188	THR
1	B	17	ASP
1	B	50	ARG
1	B	109	VAL
1	B	112	LEU
1	B	158	PHE
1	B	175	LEU
1	B	270	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	104	GLN
1	A	121	HIS
1	A	152	ASN
1	A	195	GLN
1	A	217	ASN
1	B	59	HIS
1	B	121	HIS
1	B	152	ASN
1	B	195	GLN
1	B	205	ASN
1	B	217	ASN
1	B	239	ASN
1	B	261	GLN
1	B	267	ASN
1	B	281	ASN

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Mol	Chain	Res	Type
1	B	296	GLN
1	B	326	GLN
1	B	339	ASN
1	B	365	ASN

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 [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, 95th 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	206/394 (52%)	0.80	21 (10%) 6 6	8, 26, 48, 77	0
1	B	369/394 (93%)	2.18	161 (43%) 0 0	9, 38, 110, 114	18 (4%)
All	All	575/788 (72%)	1.69	182 (31%) 0 0	8, 30, 108, 114	18 (3%)

All (182) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	325	VAL	17.5
1	B	257	ILE	12.6
1	B	318	LEU	9.5
1	B	285	THR	8.8
1	B	381	GLN	8.6
1	B	327	GLN	8.5
1	B	259	VAL	8.1
1	B	357	GLY	7.9
1	B	309	SER	7.9
1	B	332	ILE	7.7
1	B	391	THR	7.6
1	B	319	LEU	7.2
1	B	277	THR	7.1
1	B	330	LEU	7.1
1	B	256	SER	7.0
1	B	264	ILE	7.0
1	B	362	PHE	7.0
1	B	339	ASN	6.9
1	B	307	SER	6.8
1	B	284	PHE	6.8
1	B	258	SER	6.5
1	B	320	ALA	6.5
1	B	321	ARG	6.5
1	B	229	THR	6.4

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Mol	Chain	Res	Type	RSRZ
1	B	311	ARG	6.4
1	B	389	ILE	6.2
1	B	282	ASP	6.0
1	B	333	ASN	6.0
1	B	363	VAL	5.9
1	B	237	TYR	5.8
1	B	300	THR	5.7
1	B	380	THR	5.7
1	B	317	ASP	5.7
1	B	238	VAL	5.6
1	A	129	PHE	5.4
1	B	338	ALA	5.4
1	B	308	GLY	5.3
1	B	365	ASN	5.3
1	B	263	VAL	5.3
1	B	268	THR	5.3
1	B	372	ARG	5.2
1	B	313	LEU	5.2
1	B	366	GLU	5.2
1	B	298	ARG	5.2
1	B	265	PHE	5.2
1	B	260	THR	5.1
1	B	294	PRO	5.1
1	B	130	VAL	5.1
1	B	301	ILE	5.0
1	B	360	ILE	5.0
1	B	255	ASP	4.9
1	B	326	GLN	4.9
1	A	86	SER	4.9
1	B	383	GLU	4.8
1	B	351	GLY	4.8
1	B	228	LEU	4.7
1	B	291	SER	4.7
1	B	286	VAL	4.7
1	A	127	THR	4.5
1	B	296	GLN	4.5
1	B	305	PHE	4.5
1	B	340	LYS	4.5
1	B	361	ASN	4.4
1	B	297	GLU	4.4
1	B	374	LEU	4.4
1	B	306	ARG	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	281	ASN	4.4
1	B	314	ILE	4.3
1	B	387	SER	4.3
1	B	382	ILE	4.3
1	B	373	GLU	4.2
1	B	283	LYS	4.2
1	B	310	SER	4.2
1	B	379	SER	4.2
1	B	388	ASP	4.1
1	A	223	VAL	4.1
1	B	295	GLN	4.1
1	A	128	SER	4.1
1	B	390	ALA	4.1
1	B	394	ASN	4.1
1	B	290	TYR	4.0
1	B	368	VAL	4.0
1	B	359	ALA	4.0
1	B	279	LEU	3.9
1	B	358	VAL	3.9
1	B	253	LEU	3.9
1	B	347	ILE	3.8
1	B	369	GLY	3.8
1	B	226	ASP	3.7
1	B	293	LEU	3.7
1	B	376	LYS	3.7
1	B	331	VAL	3.6
1	B	128	SER	3.5
1	B	191	PRO	3.5
1	B	315	SER	3.5
1	B	280	ARG	3.5
1	B	254	TYR	3.5
1	B	232	GLY	3.5
1	B	367	ASP	3.4
1	B	364	THR	3.3
1	B	378	TYR	3.3
1	B	269	ARG	3.3
1	B	356	LYS	3.3
1	A	167	ILE	3.2
1	B	289	ILE	3.2
1	B	292	ASP	3.2
1	B	225	LYS	3.2
1	B	349	ARG	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	377	PHE	3.1
1	B	346	ARG	3.1
1	B	385	LEU	3.1
1	B	392	LEU	3.1
1	B	86	SER	3.1
1	B	231	GLU	3.1
1	B	336	LEU	3.1
1	B	168	LEU	3.0
1	B	262	ALA	3.0
1	B	224	LYS	3.0
1	B	236	PHE	3.0
1	A	192	PRO	3.0
1	B	276	THR	2.9
1	B	345	HIS	2.9
1	B	287	SER	2.9
1	B	132	ASP	2.9
1	B	393	LEU	2.9
1	B	304	GLU	2.9
1	B	334	TYR	2.9
1	B	384	GLU	2.9
1	B	234	LYS	2.9
1	B	131	GLU	2.8
1	B	239	ASN	2.8
1	B	129	PHE	2.8
1	B	251	THR	2.8
1	B	127	THR	2.8
1	B	324	ASP	2.8
1	B	348	GLY	2.7
1	B	156	ARG	2.7
1	B	249	CYS	2.7
1	B	244	GLU	2.7
1	B	252	ASP	2.7
1	B	350	GLY	2.6
1	B	299	ASP	2.6
1	A	79	ALA	2.6
1	A	125	GLY	2.6
1	A	225	LYS	2.6
1	B	17	ASP	2.6
1	B	386	PRO	2.6
1	B	278	LYS	2.6
1	A	185	GLN	2.5
1	B	323	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	17	ASP	2.5
1	B	167	ILE	2.5
1	B	248	GLU	2.5
1	B	245	TYR	2.5
1	A	197	VAL	2.5
1	B	197	VAL	2.5
1	B	250	LEU	2.4
1	B	312	ILE	2.4
1	B	375	GLU	2.4
1	B	242	GLU	2.4
1	B	266	CYS	2.4
1	B	78	ALA	2.4
1	B	316	THR	2.4
1	B	227	GLU	2.4
1	B	342	ASN	2.4
1	B	343	TYR	2.4
1	A	78	ALA	2.4
1	B	223	VAL	2.4
1	B	13	GLN	2.3
1	A	181	GLU	2.3
1	A	224	LYS	2.3
1	A	168	LEU	2.3
1	B	199	LEU	2.3
1	A	100	GLU	2.3
1	B	337	PRO	2.2
1	A	196	VAL	2.2
1	B	240	VAL	2.2
1	B	126	GLY	2.1
1	A	61	VAL	2.0
1	B	113	ALA	2.0
1	A	130	VAL	2.0
1	B	370	ALA	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 carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.