



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 03:35 am GMT

PDB ID : 4TUY
Title : Tubulin-Rhizoxin complex
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Deposited on : 2014-06-25
Resolution : 2.10 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

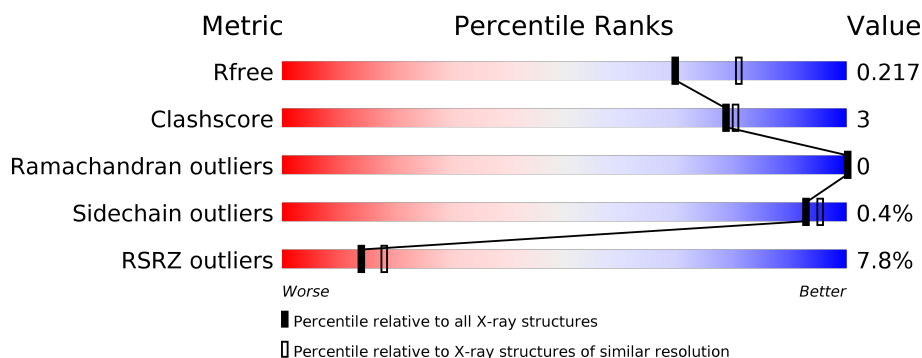
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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. 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	451	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>•</div> </div> </div>
1	C	451	<div> <div></div> <div> <div>90%</div> <div>7%</div> <div>•</div> </div> </div>
2	B	445	<div> <div>%</div> <div> <div></div> <div>88%</div> <div>8%</div> <div>5%</div> </div> </div>
2	D	445	<div> <div>7%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div>5%</div> </div> </div>
3	E	143	<div> <div>6%</div> <div> <div></div> <div>80%</div> <div>•</div> <div>16%</div> </div> </div>
4	F	384	<div> <div>30%</div> <div> <div></div> <div>80%</div> <div>7%</div> <div>13%</div> </div> </div>

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 18801 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 Tubulin alpha-1B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	12	0
			3475	2210	583	657	25			
1	C	440	Total	C	N	O	S	0	10	0
			3475	2203	585	663	24			

- Molecule 2 is a protein called Tubulin beta-2B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	424	Total	C	N	O	S	0	8	0
			3372	2121	571	652	28			
2	D	422	Total	C	N	O	S	0	3	0
			3325	2090	563	644	28			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	120	Total	C	N	O	S	0	2	0
			1002	619	182	196	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	-	expression tag	UNP P63043
E	4	ALA	-	expression tag	UNP P63043

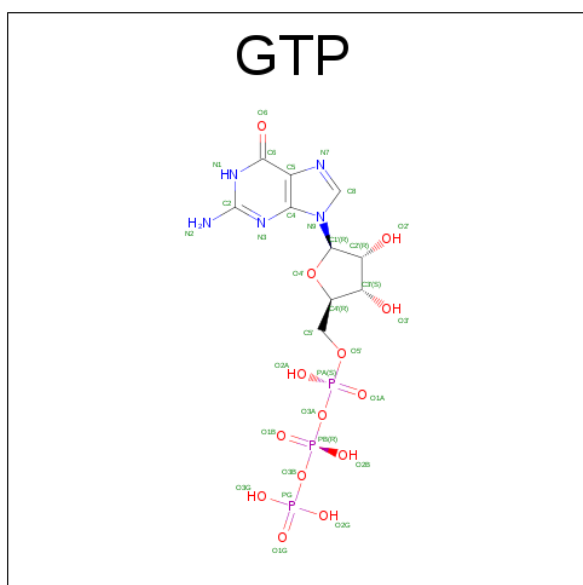
- Molecule 4 is a protein called Tubulin-Tyrosine Ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	335	Total	C	N	O	S	0	0	0
			2749	1768	467	500	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	379	HIS	-	expression tag	UNP E1BQ43
F	380	HIS	-	expression tag	UNP E1BQ43
F	381	HIS	-	expression tag	UNP E1BQ43
F	382	HIS	-	expression tag	UNP E1BQ43
F	383	HIS	-	expression tag	UNP E1BQ43
F	384	HIS	-	expression tag	UNP E1BQ43

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Mg	0	0
			1	1		
6	A	1	Total	Mg	0	0
			1	1		
6	D	1	Total	Mg	0	0
			1	1		
6	C	1	Total	Mg	0	0
			1	1		

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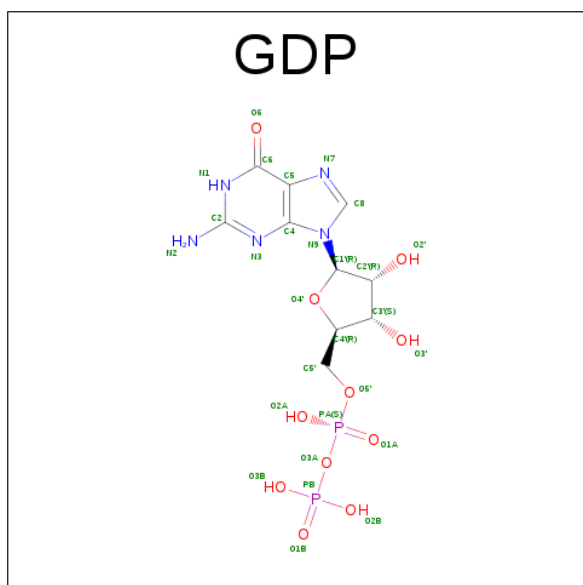
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

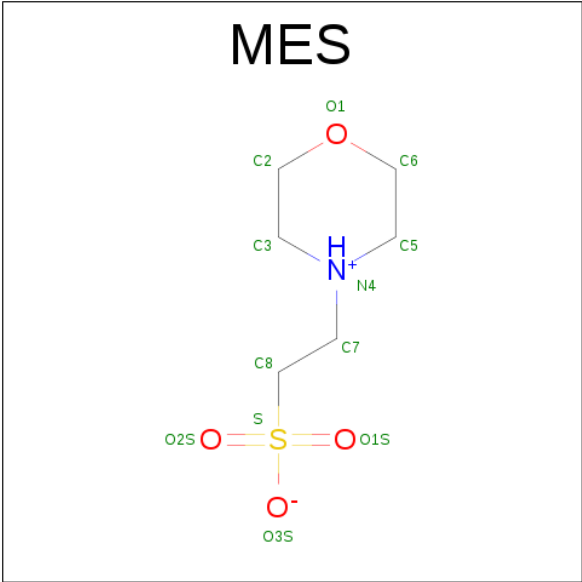
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	C	1	Total	Ca	0	0
			1	1		

- Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



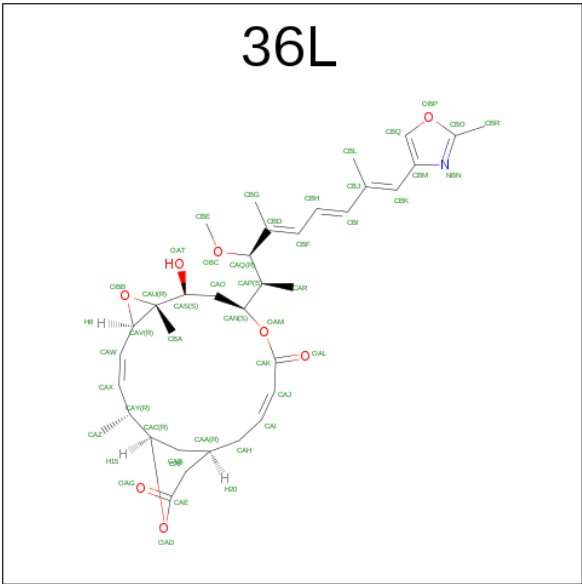
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
8	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 9 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).

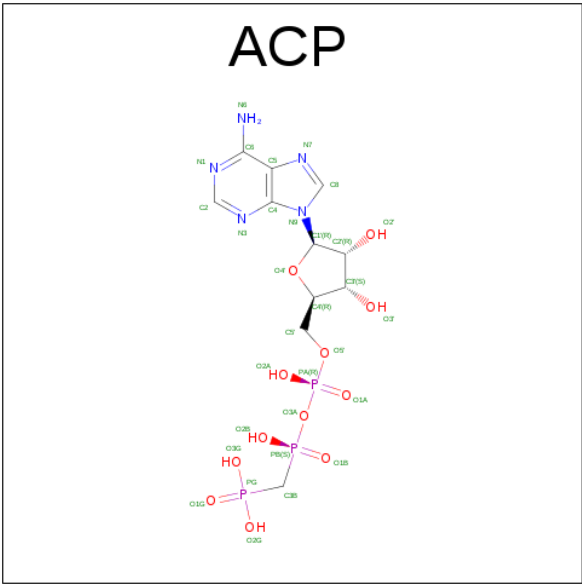


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 10 is (1R,2R,3E,5R,7R,8S,10S,13E,16R)-8-hydroxy-10-[(2S,3R,4E,6E,8E)-3-methoxy-4,8-dimethyl-9-(2-methyl-1,3-oxazol-4-yl)nona-4,6,8-trien-2-yl]-2,7-dimethyl-6,11,19-trioxatricyclo[14.3.1.0 5,7]icosa-3,13-diene-12,18-dione (three-letter code: 36L) (formula: C₃₅H₄₇NO₈).



- Molecule 11 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	F	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

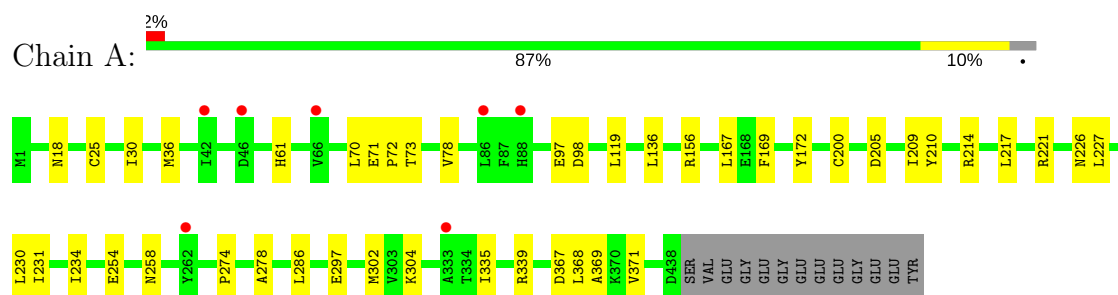
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	244	Total	O	0	0
			244	244		
12	B	226	Total	O	0	0
			226	226		
12	C	378	Total	O	0	0
			378	378		
12	D	172	Total	O	0	0
			172	172		
12	E	74	Total	O	0	0
			74	74		
12	F	95	Total	O	0	0
			95	95		

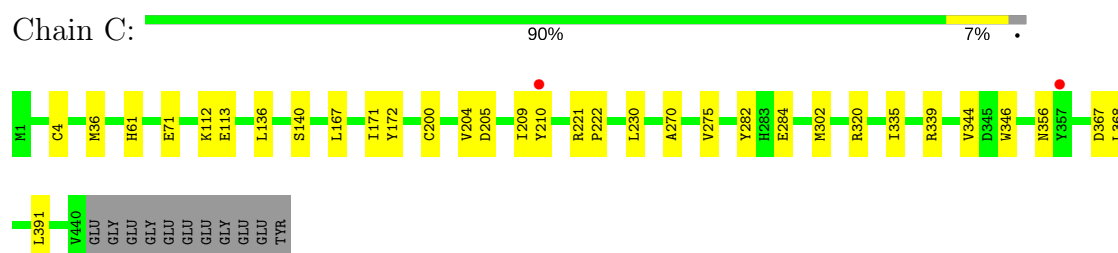
3 Residue-property plots [i](#)

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.

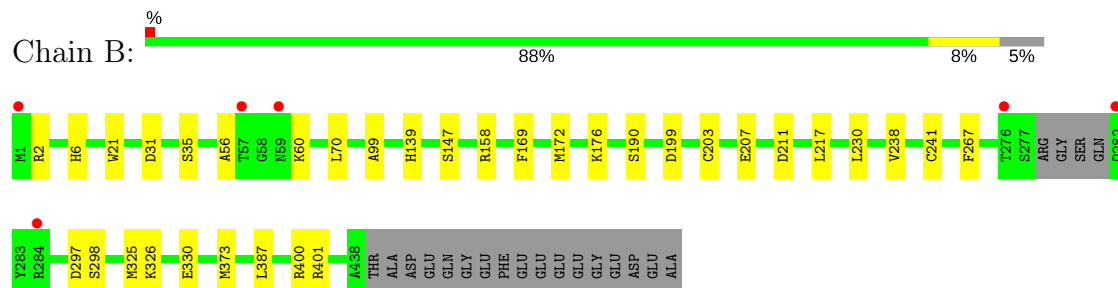
• Molecule 1: Tubulin alpha-1B chain



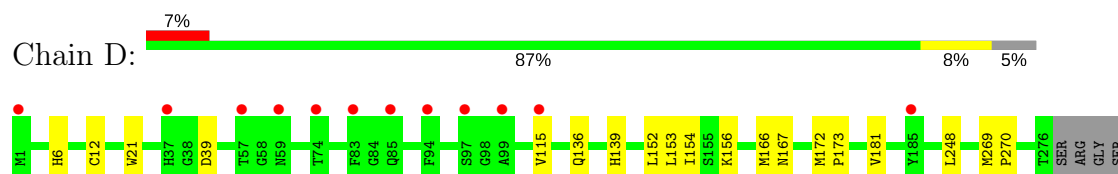
• Molecule 1: Tubulin alpha-1B chain

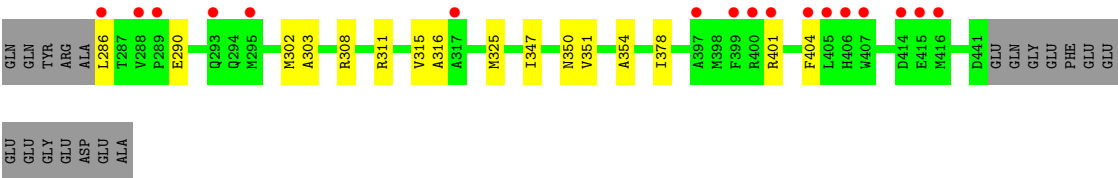


• Molecule 2: Tubulin beta-2B chain

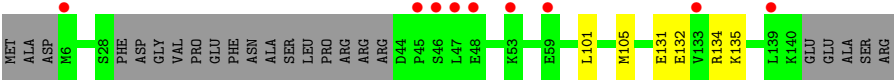
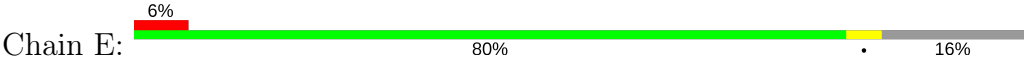


• Molecule 2: Tubulin beta-2B chain

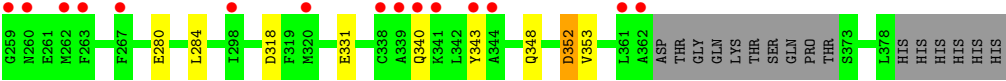
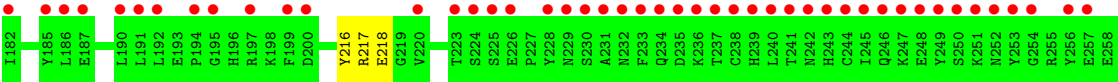
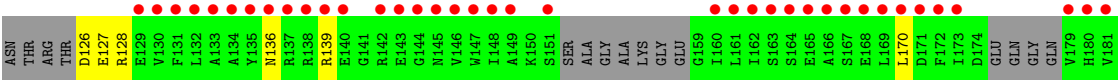
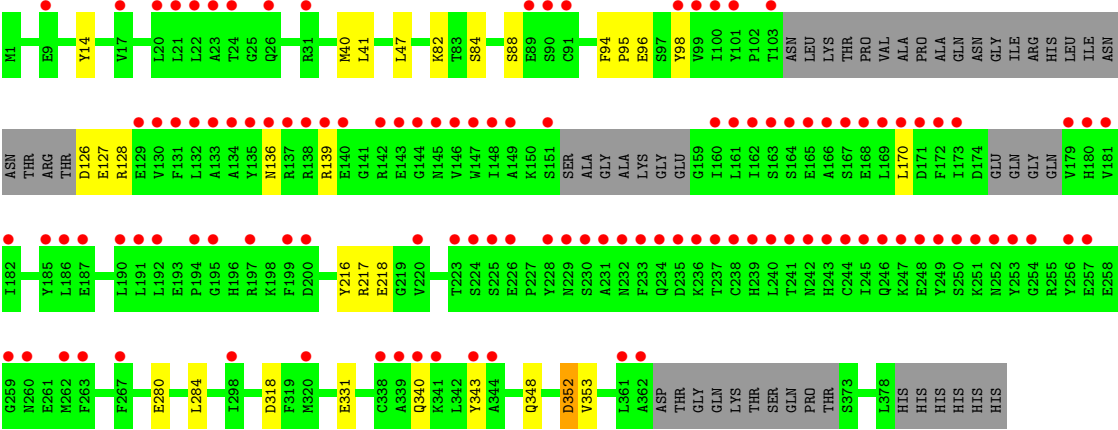
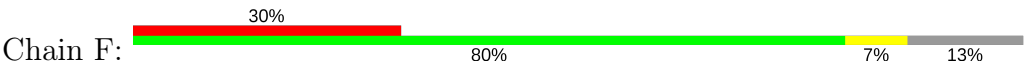




● Molecule 3: Stathmin-4



● Molecule 4: Tubulin-Tyrosine Ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.31Å 156.92Å 181.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	62.70 – 2.10 68.38 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (62.70-2.10) 100.0 (68.38-2.10)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.10Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.9_1692)	Depositor
R, R_{free}	0.184 , 0.217 0.184 , 0.217	Depositor DCC
R_{free} test set	8658 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.282	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18801	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, MG, CA, 36L, GTP, ACP, MES

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	0.22	0/3590	0.39	0/4875
1	C	0.23	0/3583	0.39	0/4867
2	B	0.22	0/3467	0.38	0/4695
2	D	0.21	0/3407	0.37	0/4615
3	E	0.21	0/1016	0.32	0/1348
4	F	0.21	0/2810	0.37	0/3794
All	All	0.22	0/17873	0.38	0/24194

There are no bond length outliers.

There are no bond angle outliers.

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	3475	0	3429	30	0
1	C	3475	0	3410	18	0
2	B	3372	0	3265	21	0
2	D	3325	0	3211	24	0
3	E	1002	0	1026	3	0
4	F	2749	0	2728	16	0
5	A	32	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	32	0	12	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	F	1	0	0	0	0
7	A	1	0	0	0	0
7	C	1	0	0	0	0
8	B	28	0	12	0	0
8	D	28	0	12	1	0
9	B	12	0	13	3	0
10	D	44	0	47	10	0
11	F	31	0	14	2	0
12	A	244	0	0	2	0
12	B	226	0	0	2	0
12	C	378	0	0	1	0
12	D	172	0	0	3	0
12	E	74	0	0	0	0
12	F	95	0	0	0	0
All	All	18801	0	17191	113	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 3.

All (113) 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)
10:D:503:36L:H40	10:D:503:36L:H47	1.20	1.13
10:D:503:36L:H40	10:D:503:36L:CBQ	1.91	0.96
2:D:404:PHE:HE1	10:D:503:36L:H41	1.36	0.90
2:D:404:PHE:CE1	10:D:503:36L:H41	2.14	0.82
1:A:71:GLU:OE2	1:A:73:THR:OG1	1.97	0.82
2:B:147[A]:SER:HG	2:B:190:SER:HG	1.32	0.74
2:B:211:ASP:OD2	12:B:753:HOH:O	2.06	0.73
2:D:270:PRO:HG2	2:D:302:MET:HB2	1.69	0.73
1:C:367:ASP:OD2	12:C:902:HOH:O	2.09	0.70
3:E:131:GLU:OE2	3:E:134:ARG:NH2	2.24	0.68
2:D:269:MET:HG3	2:D:303:ALA:HB3	1.76	0.68
2:B:199:ASP:OD2	9:B:503:MES:H52	1.95	0.66
4:F:318:ASP:OD2	11:F:401:ACP:O3G	2.12	0.66
2:D:401:ARG:HD2	10:D:503:36L:H44	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:326:LYS:NZ	2:B:330:GLU:OE2	2.27	0.65
4:F:82:LYS:NZ	4:F:127:GLU:OE1	2.29	0.64
4:F:348:GLN:NE2	4:F:352:ASP:OD1	2.31	0.64
4:F:280:GLU:HA	4:F:284:LEU:HB2	1.81	0.62
10:D:503:36L:H35	10:D:503:36L:OAL	2.00	0.61
1:A:209[A]:ILE:HG23	1:A:230:LEU:HD23	1.82	0.61
2:D:181:VAL:HG21	10:D:503:36L:CBK	2.34	0.57
1:C:270:ALA:HB3	1:C:302:MET:HE2	1.85	0.57
1:C:209:ILE:HG23	1:C:230:LEU:HD23	1.89	0.55
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.25	0.54
2:B:56:ALA:HB3	2:B:60:LYS:HB2	1.90	0.54
2:B:158:ARG:CZ	9:B:503:MES:H21	2.38	0.53
2:B:400:ARG:HG3	2:B:401:ARG:HG2	1.90	0.53
2:B:6:HIS:CD2	2:B:21:TRP:HE1	2.27	0.52
1:C:112:LYS:NZ	1:C:113:GLU:OE2	2.41	0.52
2:D:286:LEU:N	2:D:290:GLU:OE1	2.42	0.52
2:B:176:LYS:HD2	2:B:207:GLU:HG3	1.91	0.52
2:D:308:ARG:NH1	12:D:601:HOH:O	2.39	0.52
4:F:128:ARG:NH1	4:F:170:LEU:HD13	2.25	0.51
1:A:209[B]:ILE:HD13	1:A:231:ILE:HD11	1.92	0.51
1:A:221:ARG:NH2	2:B:325:MET:SD	2.84	0.51
1:A:209[B]:ILE:HD12	1:A:227:LEU:HB3	1.92	0.51
1:A:221:ARG:HG2	2:B:325:MET:HB3	1.93	0.51
1:A:71:GLU:O	12:A:665:HOH:O	2.19	0.51
1:C:4[A]:CYS:SG	1:C:136:LEU:HG	2.51	0.50
1:A:210:TYR:CE2	1:A:214:ARG:HD2	2.46	0.50
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.94	0.50
1:C:167:LEU:HG	1:C:200:CYS:HB3	1.94	0.50
2:B:31:ASP:OD2	2:B:35:SER:HB2	2.12	0.49
1:A:274:PRO:HB3	1:A:286:LEU:HD12	1.95	0.49
1:C:172:TYR:HB3	1:C:205:ASP:HA	1.95	0.49
1:A:71:GLU:HG2	1:A:72:PRO:HD2	1.95	0.49
2:D:115:VAL:HG23	2:D:153:LEU:HD23	1.95	0.48
4:F:340:GLN:HA	4:F:343:TYR:HD2	1.79	0.48
1:A:226:ASN:ND2	1:A:367:ASP:OD2	2.44	0.48
2:D:316:ALA:HB3	2:D:378:ILE:HB	1.96	0.47
2:D:12:CYS:HB2	8:D:501:GDP:C8	2.49	0.47
3:E:132:GLU:HA	3:E:135:LYS:HG2	1.96	0.47
1:A:304:LYS:NZ	12:A:768:HOH:O	2.47	0.47
4:F:40:MET:HE1	4:F:47:LEU:HG	1.98	0.46
1:C:140:SER:HA	1:C:171:ILE:HB	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:128:ARG:HH12	4:F:170:LEU:HD13	1.81	0.46
4:F:84:SER:O	4:F:88:SER:N	2.42	0.46
1:C:335:ILE:HG23	1:C:339:ARG:HG3	1.96	0.46
1:A:254:GLU:HG2	1:A:258:ASN:ND2	2.31	0.46
2:B:241[B]:CYS:SG	12:B:665:HOH:O	2.61	0.46
1:C:204:VAL:HG22	1:C:302:MET:HE3	1.96	0.45
2:D:347:ILE:HG22	2:D:350:ASN:HB3	1.98	0.45
4:F:136:ASN:HA	4:F:139:ARG:HB3	1.99	0.45
4:F:14:TYR:HB3	4:F:41:LEU:HD13	1.97	0.45
1:C:36:MET:HB3	1:C:61:HIS:CE1	2.50	0.45
2:D:311:ARG:NH1	12:D:632:HOH:O	2.49	0.45
2:D:401:ARG:CD	10:D:503:36L:H44	2.44	0.45
1:A:335:ILE:HG23	1:A:339:ARG:HD2	1.99	0.45
2:D:39:ASP:N	2:D:39:ASP:OD1	2.49	0.44
1:A:136[B]:LEU:HD23	1:A:169:PHE:HE1	1.83	0.44
1:C:172:TYR:CE2	1:C:391:LEU:HD22	2.52	0.44
4:F:126:ASP:OD1	4:F:128:ARG:HG3	2.17	0.44
2:B:172:MET:HG3	2:B:387:LEU:HD11	2.00	0.44
1:A:278:ALA:HA	1:A:369:ALA:HB2	1.99	0.44
2:D:248:LEU:HD23	2:D:354:ALA:HB2	1.99	0.44
4:F:331:GLU:OE2	11:F:401:ACP:O2B	2.35	0.44
1:A:209[A]:ILE:HD11	1:A:302[A]:MET:SD	2.57	0.44
2:B:203:CYS:SG	2:B:267:PHE:HB3	2.58	0.44
2:D:152:LEU:O	2:D:156:LYS:HG2	2.18	0.43
2:B:217:LEU:HD11	2:B:230:LEU:HD21	2.00	0.43
1:A:167:LEU:HG	1:A:200:CYS:HB3	2.01	0.43
1:C:221:ARG:HG3	2:D:325:MET:HG2	2.00	0.43
2:B:70:LEU:HD12	2:B:99:ALA:HB2	2.01	0.42
4:F:96:GLU:OE2	4:F:98:TYR:OH	2.24	0.42
2:B:199:ASP:OD1	9:B:503:MES:H32	2.19	0.42
10:D:503:36L:H1	10:D:503:36L:H7	1.86	0.42
1:A:25:CYS:HB3	1:A:30:ILE:O	2.20	0.42
1:A:217:LEU:HD21	1:A:368:LEU:HD23	2.01	0.42
2:D:167:ASN:ND2	12:D:648:HOH:O	2.51	0.42
3:E:101:LEU:O	3:E:105:MET:HG2	2.20	0.42
4:F:94:PHE:HA	4:F:95:PRO:HD3	1.90	0.42
1:A:119:LEU:HD11	1:A:156:ARG:HB3	2.01	0.42
1:A:274:PRO:HG2	1:A:371:VAL:HG11	2.02	0.41
1:C:210:TYR:CZ	1:C:222:PRO:HD2	2.55	0.41
2:D:136:GLN:HA	2:D:167:ASN:O	2.20	0.41
2:D:315:VAL:HB	2:D:351:VAL:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:320:ARG:HA	1:C:356:ASN:O	2.20	0.41
2:D:172:MET:HA	2:D:173:PRO:HD3	1.82	0.41
1:A:297:GLU:OE2	1:A:339:ARG:NH2	2.34	0.41
1:A:18:ASN:HD21	1:A:78:VAL:HG22	1.85	0.41
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.55	0.41
1:A:70:LEU:HB2	1:A:98:ASP:HA	2.02	0.41
2:D:154:ILE:HG23	2:D:166:MET:HG2	2.03	0.41
1:C:282:TYR:O	1:C:284:GLU:HG2	2.21	0.41
1:C:275:VAL:HG13	1:C:368:LEU:HD21	2.03	0.41
1:A:230:LEU:O	1:A:234:ILE:HD12	2.21	0.41
4:F:216:TYR:CZ	4:F:218:GLU:HB2	2.56	0.41
1:A:71:GLU:HB2	1:A:98:ASP:HB3	2.03	0.41
1:A:97:GLU:OE2	2:B:2:ARG:NH2	2.54	0.41
10:D:503:36L:CBQ	10:D:503:36L:CBL	2.76	0.41
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.57	0.40
2:B:169:PHE:HE2	2:B:238[A]:VAL:HG21	1.87	0.40
2:B:297:ASP:OD1	2:B:298:SER:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	448/451 (99%)	437 (98%)	11 (2%)	0	100	100
1	C	448/451 (99%)	441 (98%)	7 (2%)	0	100	100
2	B	428/445 (96%)	420 (98%)	8 (2%)	0	100	100
2	D	421/445 (95%)	414 (98%)	7 (2%)	0	100	100
3	E	118/143 (82%)	117 (99%)	1 (1%)	0	100	100
4	F	325/384 (85%)	315 (97%)	10 (3%)	0	100	100
All	All	2188/2319 (94%)	2144 (98%)	44 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	381/379 (100%)	381 (100%)	0	100	100
1	C	381/379 (100%)	380 (100%)	1 (0%)	94	96
2	B	375/383 (98%)	373 (100%)	2 (0%)	91	94
2	D	368/383 (96%)	367 (100%)	1 (0%)	94	96
3	E	110/127 (87%)	110 (100%)	0	100	100
4	F	302/342 (88%)	299 (99%)	3 (1%)	80	85
All	All	1917/1993 (96%)	1910 (100%)	7 (0%)	93	95

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	139	HIS
2	B	373	MET
1	C	71	GLU
2	D	139	HIS
4	F	217	ARG
4	F	352	ASP
4	F	353	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

Of 14 ligands modelled in this entry, 7 are monoatomic - leaving 7 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	GTP	A	501	6	27,34,34	1.15	2 (7%)	27,54,54	2.03	6 (22%)
8	GDP	B	501	6	25,30,30	1.16	2 (8%)	26,47,47	2.06	6 (23%)
9	MES	B	503	-	12,12,12	2.13	1 (8%)	14,16,16	1.50	3 (21%)
5	GTP	C	501	6	27,34,34	1.15	2 (7%)	27,54,54	1.98	6 (22%)
8	GDP	D	501	6	25,30,30	1.14	2 (8%)	26,47,47	2.07	6 (23%)
10	36L	D	503	-	39,47,47	1.17	3 (7%)	41,67,67	1.37	7 (17%)
11	ACP	F	401	6	27,33,33	1.38	5 (18%)	30,52,52	1.59	3 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GTP	A	501	6	-	0/18/38/38	0/3/3/3
8	GDP	B	501	6	-	0/12/32/32	0/3/3/3
9	MES	B	503	-	-	0/6/14/14	0/1/1/1
5	GTP	C	501	6	-	0/18/38/38	0/3/3/3
8	GDP	D	501	6	-	0/12/32/32	0/3/3/3
10	36L	D	503	-	-	1/51/73/73	0/0/4/4
11	ACP	F	401	6	-	0/15/38/38	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	503	MES	C8-S	-7.12	1.66	1.77
10	D	503	36L	OBB-CAU	-4.25	1.40	1.45
10	D	503	36L	OBB-CAV	-4.24	1.40	1.45
10	D	503	36L	OAD-CAC	-2.37	1.43	1.46
11	F	401	ACP	PB-O2B	2.01	1.61	1.56
11	F	401	ACP	PB-O3A	2.74	1.61	1.58
11	F	401	ACP	PG-O3G	2.75	1.61	1.54
11	F	401	ACP	PG-O2G	2.79	1.61	1.54
8	B	501	GDP	C5-C4	2.95	1.47	1.40
5	A	501	GTP	C5-C4	2.99	1.47	1.40
5	C	501	GTP	C5-C4	3.00	1.47	1.40
8	D	501	GDP	C5-C4	3.02	1.47	1.40
11	F	401	ACP	C5-C4	3.14	1.47	1.40
8	D	501	GDP	C6-C5	3.77	1.48	1.41
5	C	501	GTP	C6-C5	3.79	1.48	1.41
8	B	501	GDP	C6-C5	3.81	1.48	1.41
5	A	501	GTP	C6-C5	3.86	1.48	1.41

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	401	ACP	N3-C2-N1	-5.87	123.74	128.86
8	B	501	GDP	C6-C5-C4	-4.08	116.78	120.84
5	A	501	GTP	C6-C5-C4	-4.02	116.85	120.84
8	D	501	GDP	C6-C5-C4	-3.91	116.95	120.84
5	C	501	GTP	C5-C6-N1	-3.88	117.96	123.48
8	D	501	GDP	C5-C6-N1	-3.84	118.01	123.48
5	A	501	GTP	C5-C6-N1	-3.83	118.03	123.48
5	C	501	GTP	C6-C5-C4	-3.75	117.11	120.84
8	B	501	GDP	C5-C6-N1	-3.70	118.22	123.48
11	F	401	ACP	PA-O3A-PB	-3.53	121.02	132.39
8	B	501	GDP	N3-C2-N1	-3.37	122.54	127.46
5	A	501	GTP	N3-C2-N1	-3.30	122.64	127.46
8	D	501	GDP	N3-C2-N1	-3.29	122.66	127.46
5	C	501	GTP	N3-C2-N1	-3.22	122.75	127.46
10	D	503	36L	CAB-CAC-CAY	-3.08	110.19	114.31
8	D	501	GDP	C4-C5-N7	-2.88	106.62	109.41
11	F	401	ACP	C4-C5-N7	-2.80	106.70	109.41
5	C	501	GTP	C4-C5-N7	-2.74	106.76	109.41
5	A	501	GTP	C4-C5-N7	-2.74	106.76	109.41
8	B	501	GDP	C4-C5-N7	-2.66	106.84	109.41
10	D	503	36L	OAM-CAK-OAL	-2.53	118.88	123.32
10	D	503	36L	CBE-OBC-CAQ	-2.29	110.39	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	D	503	36L	CBL-CBJ-CBK	-2.14	120.62	124.85
10	D	503	36L	OAD-CAC-CAY	2.20	110.32	105.69
10	D	503	36L	OAM-CAK-CAJ	2.28	116.66	111.41
9	B	503	MES	O1S-S-C8	2.41	108.86	106.79
10	D	503	36L	OBB-CAU-CBA	2.60	117.80	114.12
9	B	503	MES	O2S-S-C8	2.83	109.23	106.79
9	B	503	MES	O3S-S-C8	3.28	110.10	106.06
8	B	501	GDP	C6-N1-C2	4.41	122.40	116.06
5	C	501	GTP	C6-N1-C2	4.42	122.41	116.06
8	D	501	GDP	C6-N1-C2	4.47	122.49	116.06
5	A	501	GTP	C6-N1-C2	4.49	122.51	116.06
5	C	501	GTP	C2-N3-C4	4.84	120.82	115.16
8	D	501	GDP	C2-N3-C4	4.93	120.91	115.16
5	A	501	GTP	C2-N3-C4	4.93	120.91	115.16
8	B	501	GDP	C2-N3-C4	5.05	121.06	115.16

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	D	503	36L	CBJ-CBK-CBM-NBN

There are no ring outliers.

4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	503	MES	3	0
8	D	501	GDP	1	0
10	D	503	36L	10	0
11	F	401	ACP	2	0

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	438/451 (97%)	0.26	7 (1%) 72 76	28, 43, 76, 92	0
1	C	440/451 (97%)	0.23	2 (0%) 90 92	22, 34, 57, 106	0
2	B	424/445 (95%)	0.34	6 (1%) 75 79	24, 41, 73, 113	1 (0%)
2	D	422/445 (94%)	0.56	29 (6%) 18 22	31, 52, 83, 108	4 (0%)
3	E	120/143 (83%)	0.71	9 (7%) 15 19	35, 57, 90, 101	0
4	F	335/384 (87%)	1.65	116 (34%) 0 0	35, 68, 128, 158	0
All	All	2179/2319 (93%)	0.57	169 (7%) 14 18	22, 46, 89, 158	5 (0%)

All (169) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	249	TYR	9.7
4	F	161	LEU	9.7
4	F	173	ILE	9.1
4	F	172	PHE	8.2
4	F	251	LYS	7.2
4	F	169	LEU	6.8
4	F	162	ILE	6.7
4	F	233	PHE	6.7
1	A	262	TYR	6.4
4	F	245	ILE	6.4
4	F	234	GLN	6.3
4	F	182	ILE	5.8
4	F	179	VAL	5.8
4	F	235	ASP	5.2
4	F	244	CYS	5.1
4	F	147	TRP	5.1
4	F	149	ALA	5.0
4	F	134	ALA	5.0
4	F	148	ILE	5.0

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Mol	Chain	Res	Type	RSRZ
4	F	253	TYR	5.0
4	F	240	LEU	4.9
4	F	181	VAL	4.9
4	F	232	ASN	4.9
4	F	250	SER	4.9
4	F	192	LEU	4.8
4	F	130	VAL	4.7
4	F	224	SER	4.6
4	F	248	GLU	4.6
4	F	160	ILE	4.6
4	F	132	LEU	4.6
4	F	100	ILE	4.5
4	F	236	LYS	4.4
4	F	21	LEU	4.4
4	F	259	GLY	4.4
2	D	405	LEU	4.3
3	E	133	VAL	4.3
2	D	57	THR	4.2
4	F	252	ASN	4.2
4	F	225	SER	4.2
3	E	45	PRO	4.2
4	F	133	ALA	4.2
4	F	101	TYR	4.2
4	F	256	TYR	4.1
4	F	166	ALA	4.0
4	F	142	ARG	4.0
4	F	17	VAL	3.9
2	D	404	PHE	3.9
4	F	135	TYR	3.8
4	F	139	ARG	3.8
4	F	89	GLU	3.8
2	B	1	MET	3.8
4	F	163	SER	3.8
4	F	165	GLU	3.8
2	D	94	PHE	3.8
4	F	131	PHE	3.8
4	F	186	LEU	3.7
4	F	140	GLU	3.7
1	C	357	TYR	3.7
4	F	170	LEU	3.7
4	F	129	GLU	3.6
4	F	103	THR	3.6

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Mol	Chain	Res	Type	RSRZ
4	F	246	GLN	3.6
4	F	239	HIS	3.5
2	D	99	ALA	3.5
4	F	199	PHE	3.5
2	B	284	ARG	3.5
4	F	339	ALA	3.4
4	F	241	THR	3.4
4	F	20	LEU	3.4
4	F	180	HIS	3.3
4	F	194	PRO	3.3
2	D	37	HIS	3.2
4	F	231	ALA	3.2
4	F	138	ARG	3.2
4	F	263	PHE	3.1
4	F	344	ALA	3.0
2	B	57	THR	3.0
4	F	223	THR	3.0
2	D	286	LEU	3.0
4	F	145	ASN	3.0
4	F	164	SER	3.0
4	F	238	CYS	3.0
2	D	400	ARG	3.0
4	F	99	VAL	3.0
4	F	228	TYR	2.9
3	E	48	GLU	2.9
2	D	74	THR	2.9
2	D	97	SER	2.9
4	F	137	ARG	2.9
4	F	9	GLU	2.9
4	F	243	HIS	2.8
2	D	115	VAL	2.8
4	F	136	ASN	2.8
2	D	83	PHE	2.8
2	B	282	GLN	2.8
4	F	320	MET	2.8
4	F	146	VAL	2.8
4	F	31	ARG	2.8
4	F	237	THR	2.8
4	F	168	GLU	2.8
4	F	167	SER	2.8
4	F	230	SER	2.8
2	D	401	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
4	F	197	ARG	2.8
3	E	47	LEU	2.8
4	F	143	GLU	2.7
1	A	333	ALA	2.7
4	F	195	GLY	2.7
4	F	242	ASN	2.7
4	F	171	ASP	2.7
4	F	229	ASN	2.7
4	F	185	TYR	2.6
4	F	341	LYS	2.6
1	A	88	HIS	2.6
4	F	26	GLN	2.6
1	A	42	ILE	2.6
4	F	260	ASN	2.6
3	E	139	LEU	2.6
4	F	200	ASP	2.5
1	A	86	LEU	2.5
4	F	362	ALA	2.5
3	E	59	GLU	2.5
4	F	257	GLU	2.5
1	A	66[A]	VAL	2.5
4	F	24	THR	2.5
2	D	289	PRO	2.5
4	F	226	GLU	2.5
4	F	220	VAL	2.5
4	F	144	GLY	2.5
4	F	23	ALA	2.5
4	F	91	CYS	2.4
4	F	90	SER	2.4
4	F	22	LEU	2.4
4	F	254	GLY	2.4
2	D	293	GLN	2.4
2	D	317	ALA	2.4
3	E	46	SER	2.4
3	E	53	LYS	2.4
2	D	414	ASP	2.4
4	F	187	GLU	2.3
4	F	191	LEU	2.3
2	D	295	MET	2.3
4	F	343	TYR	2.3
2	D	415	GLU	2.3
2	D	288	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
4	F	247	LYS	2.3
2	D	59	ASN	2.3
2	D	416	MET	2.3
2	D	1	MET	2.2
4	F	340	GLN	2.2
4	F	361	LEU	2.2
3	E	6	MET	2.2
2	D	397	ALA	2.2
4	F	298	ILE	2.2
2	D	407	TRP	2.1
2	D	399	PHE	2.1
2	B	276	THR	2.1
2	D	406	HIS	2.1
1	A	46	ASP	2.1
1	C	210	TYR	2.1
2	D	185	TYR	2.1
4	F	151	SER	2.1
4	F	267	PHE	2.1
4	F	98	TYR	2.1
4	F	190	LEU	2.1
2	D	85	GLN	2.1
2	B	59	ASN	2.0
4	F	262	MET	2.0
4	F	338	CYS	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 [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
10	36L	D	503	44/44	0.84	0.30	1.60	51,64,73,74	0
5	GTP	C	501	32/32	0.99	0.15	0.44	18,26,29,34	0
5	GTP	A	501	32/32	0.98	0.14	0.39	22,29,34,37	0
8	GDP	B	501	28/28	0.98	0.15	0.30	23,29,34,34	0
8	GDP	D	501	28/28	0.95	0.14	-0.20	37,46,60,60	0
9	MES	B	503	12/12	0.95	0.15	-0.81	43,52,62,64	0
11	ACP	F	401	31/31	0.91	0.16	-1.60	61,71,119,144	0
7	CA	C	503	1/1	0.98	0.04	-2.74	43,43,43,43	0
7	CA	A	503	1/1	0.92	0.06	-3.38	59,59,59,59	0
6	MG	B	502	1/1	1.00	0.15	-	20,20,20,20	0
6	MG	C	502	1/1	0.98	0.14	-	25,25,25,25	0
6	MG	A	502	1/1	0.99	0.11	-	29,29,29,29	0
6	MG	F	402	1/1	0.87	0.06	-	61,61,61,61	0
6	MG	D	502	1/1	0.92	0.08	-	45,45,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.