



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:38 AM UTC

PDB ID : 3FP4 / pdb_00003fp4
Title : Crystal structure of Tom71 complexed with Ssa1 C-terminal fragment
Authors : Li, J.; Qian, X.; Hu, J.; Sha, B.
Deposited on : 2009-01-03
Resolution : 2.14 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

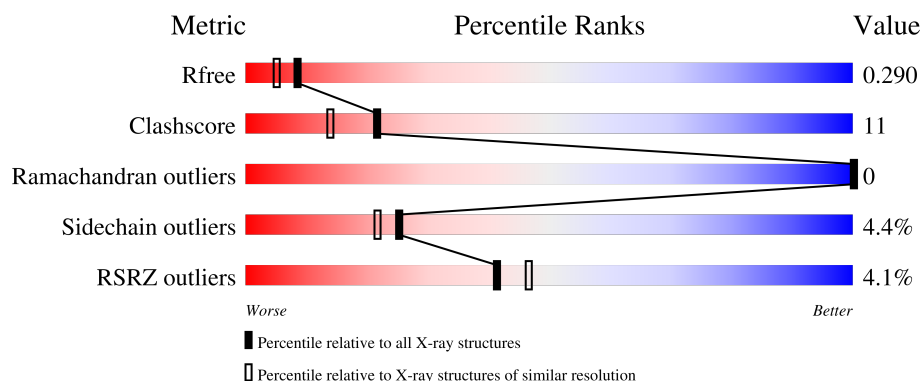
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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}	180053	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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 $\leq 5\%$. 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	537	 4% 67% 22% 10%
2	Q	12	 8% 25% 25% 8% 42%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	A	1	-	-	X	-
3	CL	A	642	-	-	X	-
3	CL	A	648	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4391 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 TPR repeat-containing protein YHR117W.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	483	Total	C	N	O	S	0	28	0
			4043	2604	650	777	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	GLY	-	expression tag	UNP P38825
A	104	SER	-	expression tag	UNP P38825
A	105	HIS	-	expression tag	UNP P38825
A	106	MET	-	expression tag	UNP P38825

- Molecule 2 is a protein called Ssa1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	Q	7	Total	C	N	O	0	0	0
			55	33	7	15			

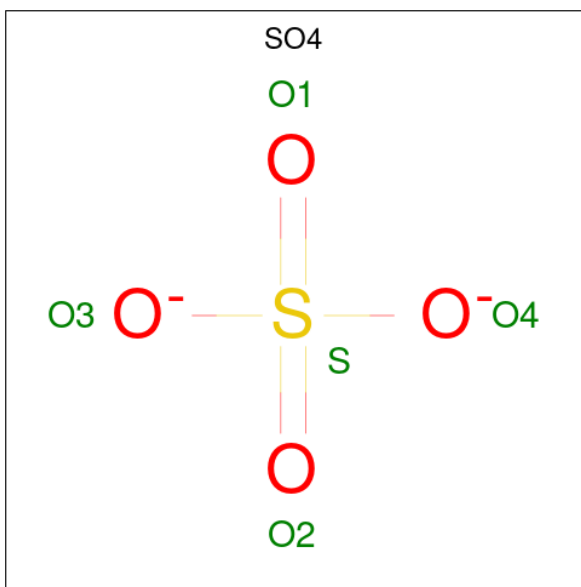
- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	11	Total	Cl	0	0
			11	11		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Na	0	0
			3	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

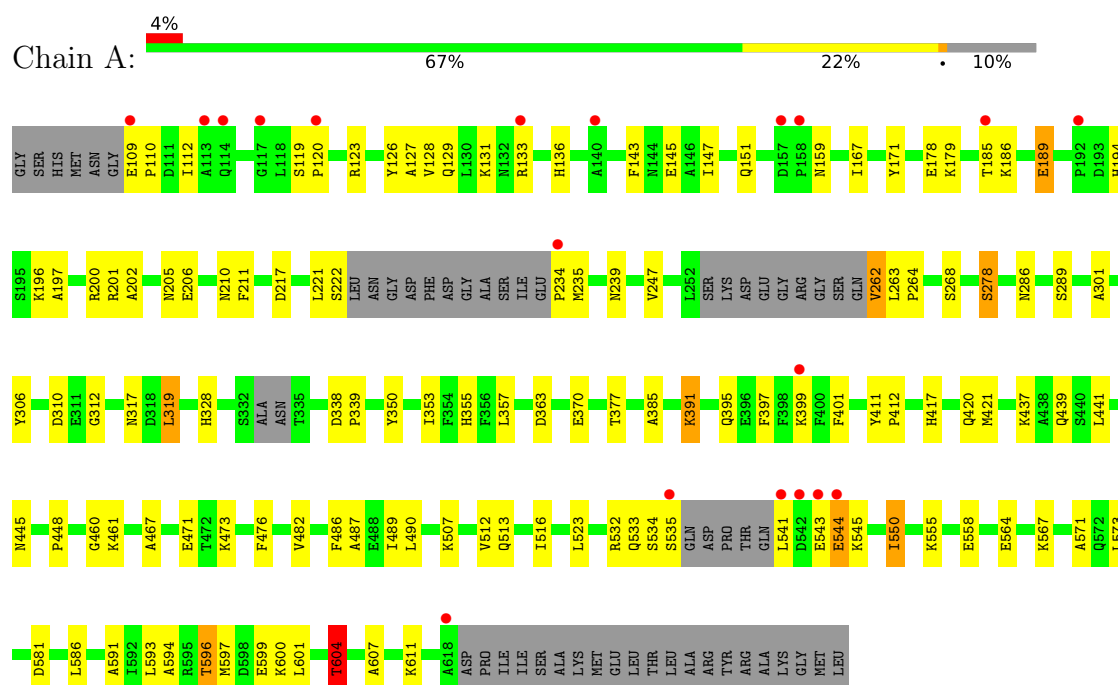
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	262	Total	O	0	0
			262	262		
6	Q	2	Total	O	0	0
			2	2		

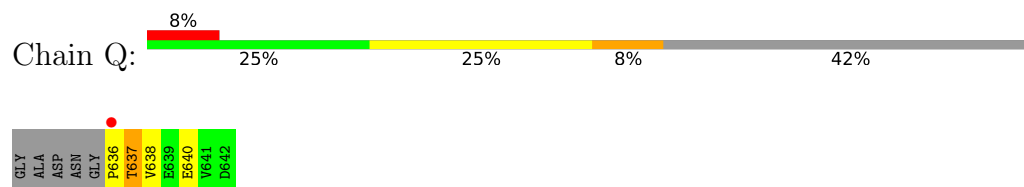
3 Residue-property plots [i](#)

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: TPR repeat-containing protein YHR117W



• Molecule 2: Ssa1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	47.82Å 116.03Å 150.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.14 8.00 – 2.14	Depositor EDS
% Data completeness (in resolution range)	89.4 (8.00-2.14) 87.5 (8.00-2.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.208 , 0.261 0.257 , 0.290	Depositor DCC
R_{free} test set	2100 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.467	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 25.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	4391	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, SO4, NA

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	1.28	14/4195 (0.3%)	1.25	15/5658 (0.3%)
2	Q	0.55	0/55	1.71	4/73 (5.5%)
All	All	1.27	14/4250 (0.3%)	1.26	19/5731 (0.3%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	412	PRO	CA-C	10.52	1.61	1.52
1	A	604	THR	CA-CB	6.94	1.64	1.53
1	A	550	ILE	CA-CB	6.51	1.61	1.54
1	A	461	LYS	CA-C	6.51	1.59	1.53
1	A	487	ALA	N-CA	6.09	1.54	1.46
1	A	467	ALA	CA-CB	6.03	1.62	1.53
1	A	591	ALA	CA-CB	5.99	1.62	1.53
1	A	247	VAL	CA-CB	5.90	1.61	1.54
1	A	127	ALA	CA-CB	5.78	1.62	1.53
1	A	516	ILE	CA-CB	5.61	1.60	1.54
1	A	353	ILE	CA-CB	5.61	1.62	1.54
1	A	489	ILE	CA-CB	5.27	1.61	1.54
1	A	385	ALA	CA-CB	5.13	1.61	1.53
1	A	350	TYR	C-O	-5.10	1.18	1.24

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	543	GLU	N-CA-C	18.97	135.53	112.38
1	A	543	GLU	CB-CA-C	-12.20	84.58	110.32
2	Q	637	THR	N-CA-C	-8.82	95.90	109.65
1	A	411[A]	TYR	CA-C-N	-8.19	111.95	120.38
1	A	411[A]	TYR	C-N-CA	-8.19	111.95	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	411[B]	TYR	CA-C-N	-8.19	111.95	120.38
1	A	411[B]	TYR	C-N-CA	-8.19	111.95	120.38
2	Q	637	THR	CB-CA-C	-7.60	96.71	112.44
1	A	412	PRO	N-CA-C	6.12	118.16	110.70
1	A	377	THR	CA-C-N	-5.97	112.43	119.05
1	A	377	THR	C-N-CA	-5.97	112.43	119.05
1	A	143	PHE	N-CA-C	5.83	118.58	111.82
1	A	604	THR	CB-CA-C	5.76	120.64	110.85
1	A	417	HIS	N-CA-C	5.33	117.17	111.36
1	A	126	TYR	N-CA-C	5.28	117.12	111.36
1	A	421	MET	N-CA-C	5.14	116.57	111.07
1	A	211	PHE	N-CA-C	5.11	116.92	111.36
2	Q	637	THR	CA-C-N	5.08	128.69	120.82
2	Q	637	THR	C-N-CA	5.08	128.69	120.82

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	4043	0	4096	88	0
2	Q	55	0	48	3	0
3	A	11	0	0	13	0
4	A	3	0	0	0	0
5	A	15	0	0	1	0
6	A	262	0	0	16	0
6	Q	2	0	0	0	0
All	All	4391	0	4144	89	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 11.

All (89) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391[A]:LYS:HD3	6:A:829:HOH:O	1.44	1.15
1:A:600:LYS:O	1:A:604:THR:HG22	1.69	0.93
1:A:185:THR:O	1:A:189:GLU:HG2	1.81	0.81
1:A:600:LYS:O	1:A:604:THR:CG2	2.33	0.77
1:A:301:ALA:HB2	1:A:319:LEU:HB3	1.67	0.76
1:A:235:MET:HE2	6:A:777:HOH:O	1.85	0.74
1:A:194:HIS:HD2	1:A:197:ALA:H	1.32	0.74
1:A:328:HIS:HE1	1:A:370:GLU:OE1	1.73	0.70
1:A:473[A]:LYS:HG3	1:A:482:VAL:HG11	1.76	0.67
1:A:221:LEU:O	1:A:222:SER:HB2	1.95	0.66
1:A:395:GLN:HE21	1:A:395:GLN:HA	1.61	0.65
1:A:234:PRO:N	6:A:665:HOH:O	2.32	0.62
1:A:262:VAL:O	1:A:262:VAL:CG1	2.47	0.62
1:A:278:SER:HB3	1:A:306:TYR:HB3	1.81	0.61
1:A:286:ASN:O	3:A:648:CL:CL	2.55	0.61
1:A:420:GLN:HG2	6:A:716:HOH:O	2.02	0.60
1:A:196:LYS:HE2	2:Q:637:THR:O	2.02	0.59
1:A:513:GLN:NE2	6:A:737:HOH:O	2.34	0.59
1:A:473[A]:LYS:HG3	1:A:482:VAL:CG1	2.33	0.57
1:A:312:GLY:HA3	3:A:649:CL:CL	2.43	0.56
1:A:486:PHE:CE2	1:A:490:LEU:HD11	2.41	0.56
1:A:202:ALA:HA	3:A:1:CL:CL	2.43	0.55
1:A:109:GLU:HG3	1:A:110:PRO:CD	2.36	0.55
1:A:201:ARG:HD2	1:A:217:ASP:OD2	2.07	0.55
1:A:558:GLU:HG3	6:A:58:HOH:O	2.06	0.55
1:A:201:ARG:CD	1:A:217:ASP:OD2	2.54	0.55
1:A:200:ARG:NH2	2:Q:638:VAL:O	2.29	0.55
1:A:507[B]:LYS:HD2	1:A:523:LEU:CD2	2.37	0.54
1:A:109:GLU:N	1:A:110:PRO:HD2	2.23	0.54
1:A:171:TYR:CD2	1:A:179:LYS:HB3	2.43	0.54
1:A:439[C]:GLN:HA	3:A:642:CL:CL	2.44	0.54
1:A:109:GLU:N	6:A:754:HOH:O	2.41	0.53
1:A:439[A]:GLN:HA	3:A:642:CL:CL	2.44	0.53
1:A:534:SER:HB3	1:A:545:LYS:HB3	1.89	0.53
1:A:596:THR:HG23	1:A:599:GLU:HB2	1.89	0.53
1:A:439[B]:GLN:HA	3:A:642:CL:CL	2.44	0.53
1:A:262:VAL:O	1:A:262:VAL:HG12	2.07	0.53
1:A:109:GLU:HG3	1:A:110:PRO:HD3	1.91	0.52
1:A:437:LYS:HE3	1:A:441:LEU:HD11	1.92	0.52
1:A:507[B]:LYS:HD2	1:A:523:LEU:HD21	1.93	0.51
1:A:533:GLN:C	1:A:535:SER:H	2.18	0.51
1:A:310:ASP:HB3	5:A:2:SO4:S	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:LEU:O	1:A:222:SER:CB	2.58	0.50
1:A:328:HIS:CE1	1:A:370:GLU:OE1	2.61	0.49
1:A:206:GLU:HB2	1:A:239:ASN:HD21	1.77	0.49
1:A:235:MET:CE	6:A:777:HOH:O	2.53	0.49
1:A:147:ILE:CD1	1:A:167:ILE:HG23	2.43	0.49
1:A:594:ALA:HB1	1:A:599:GLU:HB3	1.94	0.49
1:A:147:ILE:HD13	1:A:167:ILE:HG23	1.95	0.48
1:A:445:ASN:O	3:A:642:CL:CL	2.68	0.48
1:A:289:SER:HB2	1:A:339:PRO:HB2	1.96	0.47
1:A:420:GLN:NE2	6:A:716:HOH:O	2.38	0.47
1:A:571:ALA:HB2	1:A:586:LEU:HB3	1.97	0.47
1:A:264:PRO:HG3	1:A:357:LEU:O	2.15	0.47
1:A:263:LEU:HD21	1:A:317:ASN:CG	2.40	0.46
1:A:473[A]:LYS:NZ	6:A:860:HOH:O	2.35	0.46
1:A:391[A]:LYS:HA	1:A:391[A]:LYS:HD2	1.52	0.46
1:A:471[C]:GLU:CD	6:A:862:HOH:O	2.59	0.46
1:A:564[A]:GLU:HG3	1:A:593:LEU:HB3	1.98	0.46
1:A:397:PHE:CZ	1:A:401:PHE:CE1	3.04	0.46
1:A:601:LEU:HA	1:A:604:THR:HG23	1.97	0.45
1:A:217:ASP:OD2	3:A:1:CL:CL	2.70	0.45
1:A:210:ASN:HB3	3:A:640:CL:CL	2.53	0.45
1:A:289:SER:HB3	3:A:648:CL:CL	2.53	0.45
1:A:471[C]:GLU:OE2	6:A:862:HOH:O	2.21	0.45
1:A:581[B]:ASP:OD1	6:A:748:HOH:O	2.21	0.45
1:A:201:ARG:HD3	1:A:217:ASP:OD2	2.18	0.44
1:A:607:ALA:O	1:A:611:LYS:HG3	2.17	0.44
1:A:263:LEU:HD21	1:A:317:ASN:OD1	2.18	0.44
1:A:120:PRO:HD2	6:A:756:HOH:O	2.17	0.44
1:A:460:GLY:HA2	6:A:655:HOH:O	2.17	0.44
1:A:338:ASP:N	1:A:339:PRO:CD	2.80	0.43
1:A:186:LYS:HA	1:A:189:GLU:HG3	2.00	0.43
1:A:448:PRO:HG2	3:A:642:CL:CL	2.56	0.43
2:Q:636:PRO:HD2	2:Q:640:GLU:OE2	2.18	0.43
1:A:205:ASN:ND2	3:A:1:CL:CL	2.72	0.42
1:A:550:ILE:HD11	1:A:573:LEU:HB3	2.01	0.42
1:A:133:ARG:O	1:A:136:HIS:HB3	2.19	0.42
1:A:131:LYS:HE2	1:A:131:LYS:HB3	1.84	0.42
1:A:476:PHE:O	3:A:653:CL:CL	2.75	0.42
1:A:567:LYS:HE2	1:A:593:LEU:HD11	2.02	0.42
1:A:178:GLU:CD	1:A:178:GLU:H	2.27	0.41
1:A:355:HIS:CD2	1:A:363:ASP:HB3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:129:GLN:O	1:A:133:ARG:HG3	2.21	0.41
1:A:189:GLU:HG2	1:A:189:GLU:H	1.72	0.41
1:A:264:PRO:HB2	1:A:268[A]:SER:OG	2.20	0.41
1:A:119:SER:O	1:A:123:ARG:HG3	2.21	0.41
1:A:544:GLU:O	1:A:545:LYS:C	2.64	0.41
1:A:328:HIS:HD2	6:A:676:HOH:O	2.02	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	503/537 (94%)	485 (96%)	18 (4%)	0	100	100
2	Q	5/12 (42%)	3 (60%)	2 (40%)	0	100	100
All	All	508/549 (92%)	488 (96%)	20 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	452/463 (98%)	430 (95%)	22 (5%)	22	18
2	Q	7/9 (78%)	7 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	459/472 (97%)	437 (95%)	22 (5%)	25	18

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112[A]	ILE
1	A	112[B]	ILE
1	A	128	VAL
1	A	145	GLU
1	A	151	GLN
1	A	159	ASN
1	A	189	GLU
1	A	262	VAL
1	A	278	SER
1	A	319	LEU
1	A	391[A]	LYS
1	A	391[B]	LYS
1	A	399[A]	LYS
1	A	399[B]	LYS
1	A	512	VAL
1	A	532	ARG
1	A	541	LEU
1	A	544	GLU
1	A	555	LYS
1	A	596	THR
1	A	597	MET
1	A	604	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	GLN
1	A	159	ASN
1	A	194	HIS
1	A	239	ASN
1	A	279	HIS
1	A	328	HIS
1	A	355	HIS
1	A	359	ASN
1	A	369	GLN
1	A	375	HIS

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Mol	Chain	Res	Type
1	A	395	GLN
1	A	402	GLN
1	A	430	ASN
1	A	502	GLN
1	A	513	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 14 are monoatomic - leaving 3 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	SO4	A	3	-	4,4,4	0.34	0	6,6,6	0.37	0
5	SO4	A	647	-	4,4,4	0.25	0	6,6,6	0.15	0
5	SO4	A	2	-	4,4,4	0.27	0	6,6,6	0.44	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2	SO4	1	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	483/537 (89%)	0.20	19 (3%) 43 48	2, 17, 30, 48	28 (5%)
2	Q	7/12 (58%)	0.66	1 (14%) 6 7	6, 12, 25, 28	0
All	All	490/549 (89%)	0.20	20 (4%) 41 46	2, 17, 30, 48	28 (5%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	543	GLU	6.7
1	A	544	GLU	5.9
1	A	541	LEU	5.1
1	A	113	ALA	3.9
1	A	117	GLY	3.5
1	A	399[A]	LYS	3.4
1	A	114	GLN	3.2
1	A	109	GLU	3.1
1	A	158	PRO	2.8
1	A	234	PRO	2.8
1	A	157	ASP	2.5
1	A	133	ARG	2.5
1	A	192	PRO	2.4
1	A	618	ALA	2.4
1	A	120	PRO	2.4
1	A	535	SER	2.3
1	A	185	THR	2.3
1	A	542	ASP	2.2
2	Q	636	PRO	2.0
1	A	140	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
5	SO4	A	2	5/5	0.20	0.34	99,99,100,100	0
3	CL	A	640	1/1	0.62	0.40	38,38,38,38	0
5	SO4	A	647	5/5	0.73	0.17	95,95,96,96	0
5	SO4	A	3	5/5	0.75	0.19	43,44,45,46	0
3	CL	A	651	1/1	0.78	0.18	22,22,22,22	0
3	CL	A	652	1/1	0.81	0.15	18,18,18,18	0
4	NA	A	645	1/1	0.82	0.12	2,2,2,2	0
4	NA	A	643	1/1	0.83	0.05	17,17,17,17	0
4	NA	A	644	1/1	0.85	0.15	4,4,4,4	0
3	CL	A	646	1/1	0.86	0.15	24,24,24,24	0
3	CL	A	642	1/1	0.94	0.37	6,6,6,6	0
3	CL	A	1	1/1	0.97	0.29	20,20,20,20	0
3	CL	A	641	1/1	0.97	0.29	20,20,20,20	0
3	CL	A	649	1/1	0.97	0.32	3,3,3,3	0
3	CL	A	650	1/1	0.97	0.33	9,9,9,9	0
3	CL	A	648	1/1	0.98	0.35	5,5,5,5	0
3	CL	A	653	1/1	0.99	0.32	2,2,2,2	0

6.5 Other polymers [i](#)

There are no such residues in this entry.