



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:23 PM UTC

PDB ID : 2PFT / pdb_00002pft
Title : The Crystal Structure of Mouse Exo70 Reveals Unique Features of the Mammalian Exocyst
Authors : Moore, B.A.; Xu, Z.
Deposited on : 2007-04-05
Resolution : 2.25 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
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

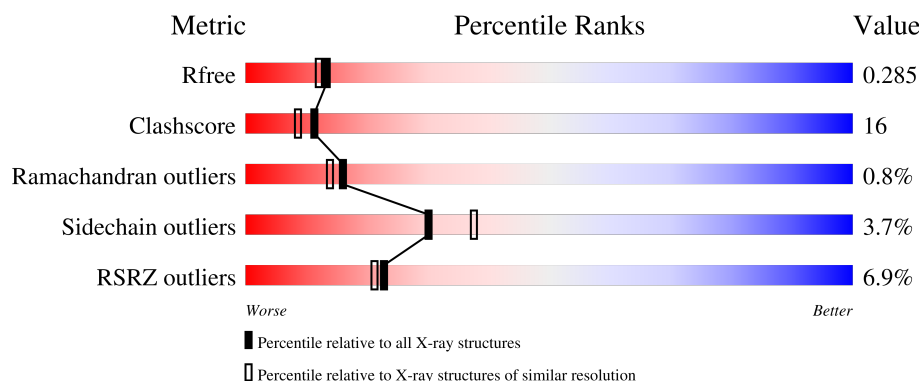
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	571	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4268 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 Exocytosis Protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	519	Total	C	N	O	S	0	0	0
			4098	2621	694	770	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	83	GLY	-	cloning artifact	UNP Q3TIP4
A	84	SER	-	cloning artifact	UNP Q3TIP4

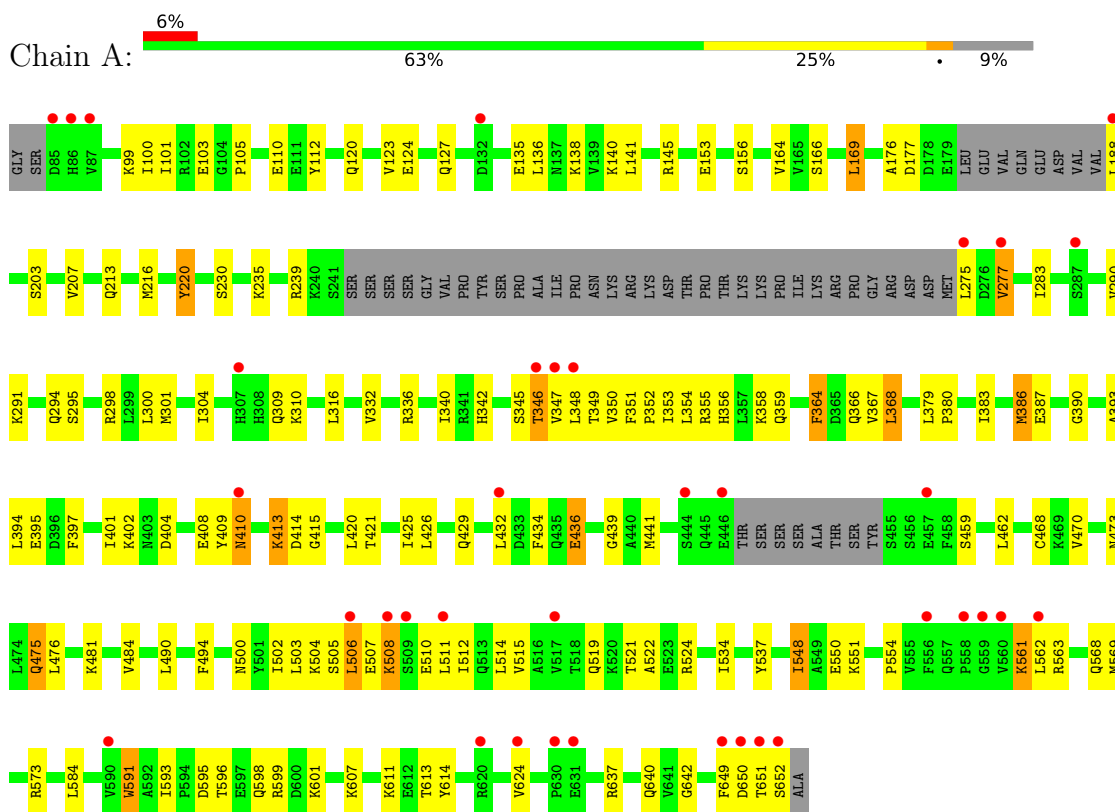
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	170	Total	O	0	0
			170	170		

3 Residue-property plots

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: Exocytosis Protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	61.52Å 61.52Å 294.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.84 – 2.25 46.84 – 2.25	Depositor EDS
% Data completeness (in resolution range)	90.0 (46.84-2.25) 89.9 (46.84-2.25)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.52 (at 2.18Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.235 , 0.285 0.235 , 0.285	Depositor DCC
R_{free} test set	1555 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	46.2	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.037 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4268	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.08% 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	0.47	0/4173	0.89	7/5638 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	593	ILE	CA-C-N	5.76	125.88	119.32
1	A	593	ILE	C-N-CA	5.76	125.88	119.32
1	A	508	LYS	N-CA-C	-5.45	106.68	113.38
1	A	548	ILE	N-CA-C	5.27	117.25	111.77
1	A	408	GLU	N-CA-C	5.26	117.42	111.11
1	A	309	GLN	N-CA-C	5.04	116.47	111.07
1	A	506	LEU	N-CA-C	-5.04	107.28	112.93

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	4098	0	4038	132	0
2	A	170	0	0	8	1
All	All	4268	0	4038	132	1

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 16.

All (132) 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:500:ASN:HD21	1:A:504:LYS:HE3	1.27	0.98
1:A:561:LYS:HZ2	1:A:563:ARG:HD3	1.39	0.86
1:A:110:GLU:HG3	2:A:792:HOH:O	1.84	0.77
1:A:166:SER:OG	1:A:169:LEU:HB2	1.85	0.76
1:A:350:VAL:HG13	1:A:386:MET:HE2	1.68	0.76
1:A:345:SER:C	1:A:347:VAL:H	1.97	0.72
1:A:506:LEU:O	1:A:512:ILE:HB	1.89	0.71
1:A:500:ASN:ND2	1:A:504:LYS:HE3	2.06	0.69
1:A:569:MET:HG2	1:A:573:ARG:NH1	2.07	0.68
1:A:235:LYS:HE2	1:A:239:ARG:NH2	2.08	0.68
1:A:561:LYS:O	1:A:561:LYS:HD2	1.94	0.67
1:A:426:LEU:HA	1:A:429:GLN:HG3	1.76	0.66
1:A:354:LEU:HD23	1:A:441:MET:HE2	1.78	0.66
1:A:345:SER:O	1:A:348:LEU:HG	1.95	0.66
1:A:404:ASP:OD2	1:A:420:LEU:HD13	1.97	0.65
1:A:145:ARG:HD3	2:A:746:HOH:O	1.96	0.64
1:A:283:ILE:HD11	1:A:353:ILE:HA	1.79	0.64
1:A:401:ILE:HD12	1:A:470:VAL:HG13	1.79	0.64
1:A:213:GLN:HG3	1:A:216:MET:HE3	1.80	0.64
1:A:120:GLN:O	1:A:124:GLU:HG3	1.97	0.63
1:A:562:LEU:HD11	1:A:624:VAL:CG2	2.29	0.63
1:A:481:LYS:O	1:A:484:VAL:HG23	2.00	0.61
1:A:379:LEU:HB3	1:A:380:PRO:HD3	1.82	0.61
1:A:203:SER:O	1:A:207:VAL:HG23	2.01	0.60
1:A:220:TYR:C	1:A:220:TYR:CD1	2.80	0.59
1:A:346:THR:HG22	1:A:346:THR:O	2.03	0.59
1:A:410:ASN:H	1:A:410:ASN:HD22	1.49	0.59
1:A:350:VAL:HG13	1:A:386:MET:CE	2.31	0.59
1:A:188:LEU:HD23	1:A:295:SER:OG	2.02	0.58
1:A:637:ARG:HB2	1:A:640:GLN:HG3	1.84	0.58
1:A:554:PRO:HD3	1:A:569:MET:HE2	1.86	0.58
1:A:521:THR:HG21	1:A:524:ARG:NH2	2.19	0.57
1:A:476:LEU:HD23	1:A:476:LEU:O	2.05	0.57
1:A:135:GLU:H	1:A:135:GLU:CD	2.14	0.56
1:A:413:LYS:HD2	1:A:414:ASP:N	2.20	0.56
1:A:136:LEU:O	1:A:140:LYS:HG3	2.04	0.56
1:A:599:ARG:HD2	1:A:649:PHE:HB2	1.88	0.55
1:A:573:ARG:HG3	1:A:573:ARG:HH11	1.70	0.55
1:A:432:LEU:HD23	1:A:510:GLU:HG2	1.87	0.55
1:A:336:ARG:HH11	1:A:336:ARG:HG3	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:GLN:HB2	2:A:802:HOH:O	2.07	0.55
1:A:283:ILE:HD12	1:A:356:HIS:CB	2.38	0.54
1:A:502:ILE:O	1:A:506:LEU:HD13	2.06	0.54
1:A:550:GLU:OE2	1:A:550:GLU:HA	2.08	0.54
1:A:99:LYS:O	1:A:103:GLU:HG3	2.08	0.54
1:A:145:ARG:HH11	1:A:145:ARG:HG3	1.73	0.54
1:A:551:LYS:HE2	2:A:799:HOH:O	2.08	0.53
1:A:421:THR:O	1:A:425:ILE:HG12	2.09	0.53
1:A:515:VAL:HG12	1:A:519:GLN:HB2	1.90	0.53
1:A:548:ILE:HD12	1:A:614:TYR:HA	1.89	0.53
1:A:562:LEU:HD11	1:A:624:VAL:HG21	1.91	0.53
1:A:607:LYS:O	1:A:611:LYS:HB2	2.09	0.53
1:A:316:LEU:C	1:A:316:LEU:HD23	2.34	0.53
1:A:439:GLY:C	1:A:459:SER:HB2	2.34	0.52
1:A:355:ARG:HD3	1:A:359:GLN:NE2	2.25	0.52
1:A:504:LYS:O	1:A:508:LYS:HG3	2.10	0.52
1:A:436:GLU:OE1	1:A:436:GLU:N	2.35	0.52
1:A:584:LEU:HD23	1:A:584:LEU:C	2.35	0.51
1:A:100:ILE:HG23	1:A:101:ILE:N	2.24	0.51
1:A:432:LEU:CD2	1:A:510:GLU:HG2	2.40	0.51
1:A:345:SER:C	1:A:347:VAL:N	2.66	0.51
1:A:510:GLU:HA	2:A:805:HOH:O	2.12	0.50
1:A:348:LEU:C	1:A:348:LEU:HD12	2.36	0.50
1:A:347:VAL:HG11	1:A:393:ALA:HB1	1.93	0.50
1:A:599:ARG:HD2	1:A:649:PHE:O	2.12	0.49
1:A:490:LEU:HD13	1:A:591:TRP:CE2	2.48	0.49
1:A:468:CYS:SG	1:A:519:GLN:HG2	2.53	0.49
1:A:348:LEU:HD12	1:A:349:THR:N	2.27	0.49
1:A:598:GLN:HE22	1:A:601:LYS:NZ	2.10	0.49
1:A:573:ARG:NH1	1:A:573:ARG:HG3	2.28	0.49
1:A:397:PHE:CE2	1:A:401:ILE:HD11	2.48	0.48
1:A:554:PRO:HD3	1:A:569:MET:CE	2.42	0.48
1:A:598:GLN:HE22	1:A:601:LYS:HZ3	1.60	0.48
1:A:105:PRO:HB3	1:A:112:TYR:CG	2.48	0.48
1:A:390:GLY:O	1:A:394:LEU:HD13	2.13	0.48
1:A:351:PHE:HZ	1:A:394:LEU:HD11	1.79	0.47
1:A:300:LEU:HG	1:A:304:ILE:HG13	1.96	0.47
1:A:503:LEU:O	1:A:503:LEU:HD13	2.15	0.47
1:A:548:ILE:HG13	1:A:613:THR:HG22	1.96	0.47
1:A:358:LYS:HZ1	1:A:387:GLU:CD	2.24	0.46
1:A:123:VAL:O	1:A:127:GLN:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:432:LEU:HD11	1:A:511:LEU:CD2	2.45	0.46
1:A:290:VAL:O	1:A:294:GLN:HG3	2.15	0.46
1:A:275:LEU:HB2	1:A:277:VAL:HG23	1.97	0.46
1:A:332:VAL:HG22	1:A:386:MET:HE3	1.97	0.46
1:A:432:LEU:HD11	1:A:511:LEU:HD23	1.96	0.46
1:A:367:VAL:HG23	1:A:368:LEU:HD13	1.96	0.46
1:A:355:ARG:CD	1:A:359:GLN:NE2	2.79	0.45
1:A:504:LYS:NZ	1:A:595:ASP:OD2	2.38	0.45
1:A:507:GLU:HA	2:A:807:HOH:O	2.16	0.45
1:A:475:GLN:HE21	1:A:475:GLN:HB3	1.57	0.45
1:A:138:LYS:HG3	2:A:821:HOH:O	2.16	0.45
1:A:164:VAL:HG13	1:A:230:SER:HA	1.99	0.45
1:A:390:GLY:HA3	1:A:441:MET:SD	2.58	0.44
1:A:650:ASP:O	1:A:652:SER:N	2.51	0.44
1:A:548:ILE:HG13	1:A:613:THR:CG2	2.48	0.44
1:A:345:SER:O	1:A:347:VAL:N	2.49	0.44
1:A:354:LEU:HD21	1:A:387:GLU:HG2	2.00	0.44
1:A:347:VAL:HG11	1:A:393:ALA:CB	2.49	0.43
1:A:354:LEU:HD11	1:A:358:LYS:HE2	2.00	0.43
1:A:426:LEU:CA	1:A:429:GLN:HG3	2.46	0.43
1:A:591:TRP:H	1:A:591:TRP:CD1	2.35	0.43
1:A:176:ALA:O	1:A:177:ASP:HB3	2.19	0.43
1:A:100:ILE:CG2	1:A:101:ILE:N	2.81	0.43
1:A:355:ARG:HG2	1:A:359:GLN:HE21	1.85	0.42
1:A:402:LYS:HB2	1:A:473:ASN:ND2	2.35	0.42
1:A:415:GLY:O	1:A:494:PHE:HA	2.19	0.42
1:A:561:LYS:HZ2	1:A:563:ARG:CD	2.18	0.42
1:A:468:CYS:SG	1:A:515:VAL:HG13	2.60	0.42
1:A:355:ARG:HD3	1:A:359:GLN:HE22	1.85	0.42
1:A:637:ARG:NH1	1:A:640:GLN:HG3	2.35	0.42
1:A:434:PHE:HA	2:A:757:HOH:O	2.19	0.42
1:A:519:GLN:HB3	1:A:522:ALA:HB2	2.02	0.42
1:A:349:THR:C	1:A:352:PRO:HD2	2.45	0.42
1:A:291:LYS:O	1:A:294:GLN:HB2	2.20	0.42
1:A:213:GLN:N	1:A:213:GLN:CD	2.79	0.41
1:A:364:PHE:CG	1:A:379:LEU:HD22	2.55	0.41
1:A:425:ILE:O	1:A:429:GLN:CG	2.69	0.41
1:A:394:LEU:HD12	1:A:394:LEU:N	2.36	0.41
1:A:410:ASN:HD22	1:A:410:ASN:N	2.14	0.41
1:A:505:SER:C	1:A:507:GLU:H	2.29	0.41
1:A:153:GLU:HA	1:A:156:SER:OG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:534:ILE:O	1:A:537:TYR:HB3	2.21	0.41
1:A:310:LYS:HD3	1:A:310:LYS:HA	1.91	0.41
1:A:468:CYS:SG	1:A:519:GLN:CG	3.09	0.41
1:A:611:LYS:HE2	1:A:642:GLY:HA3	2.03	0.41
1:A:340:ILE:C	1:A:342:HIS:H	2.29	0.40
1:A:409:TYR:CD1	1:A:410:ASN:N	2.90	0.40
1:A:145:ARG:HG3	1:A:145:ARG:NH1	2.36	0.40
1:A:298:ARG:HA	1:A:301:MET:HE2	2.02	0.40
1:A:383:ILE:O	1:A:387:GLU:HG3	2.22	0.40
1:A:596:THR:HG22	1:A:599:ARG:HH12	1.87	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:809:HOH:O	2:A:809:HOH:O[5_795]	1.46	0.74

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	511/571 (90%)	482 (94%)	25 (5%)	4 (1%)	16 14

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	561	LYS
1	A	591	TRP
1	A	651	THR
1	A	346	THR

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	436/517 (84%)	420 (96%)	16 (4%)	30	37

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	141	LEU
1	A	169	LEU
1	A	220	TYR
1	A	277	VAL
1	A	364	PHE
1	A	366	GLN
1	A	368	LEU
1	A	386	MET
1	A	395	GLU
1	A	410	ASN
1	A	413	LYS
1	A	436	GLU
1	A	462	LEU
1	A	475	GLN
1	A	514	LEU
1	A	568	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	221	GLN
1	A	294	GLN
1	A	308	HIS
1	A	309	GLN
1	A	356	HIS
1	A	359	GLN
1	A	377	ASN
1	A	410	ASN

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Mol	Chain	Res	Type
1	A	423	ASN
1	A	430	GLN
1	A	475	GLN
1	A	500	ASN
1	A	538	GLN
1	A	552	ASN
1	A	557	GLN
1	A	588	GLN
1	A	598	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](#)

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	519/571 (90%)	0.61	36 (6%) 23 21	31, 53, 79, 98	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	652	SER	4.4
1	A	275	LEU	4.0
1	A	558	PRO	4.0
1	A	346	THR	3.9
1	A	560	VAL	3.8
1	A	86	HIS	3.5
1	A	347	VAL	3.4
1	A	446	GLU	3.3
1	A	277	VAL	3.2
1	A	624	VAL	3.1
1	A	509	SER	3.1
1	A	457	GLU	3.0
1	A	590	VAL	2.8
1	A	506	LEU	2.8
1	A	132	ASP	2.6
1	A	556	PHE	2.6
1	A	651	THR	2.5
1	A	85	ASP	2.5
1	A	631	GLU	2.4
1	A	508	LYS	2.4
1	A	410	ASN	2.4
1	A	559	GLY	2.4
1	A	307	HIS	2.3
1	A	188	LEU	2.2
1	A	444	SER	2.2
1	A	562	LEU	2.2
1	A	87	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	432	LEU	2.1
1	A	517	VAL	2.1
1	A	630	PRO	2.1
1	A	650	ASP	2.1
1	A	620	ARG	2.1
1	A	348	LEU	2.1
1	A	287	SER	2.0
1	A	649	PHE	2.0
1	A	511	LEU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.