



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:30 PM GMT

PDB ID : 1PCX
Title : Crystal structure of the COPII coat subunit, Sec24, complexed with a peptide from the SNARE protein Bet1
Authors : Mossessova, E.; Bickford, L.C.; Goldberg, J.
Deposited on : 2003-05-18
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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

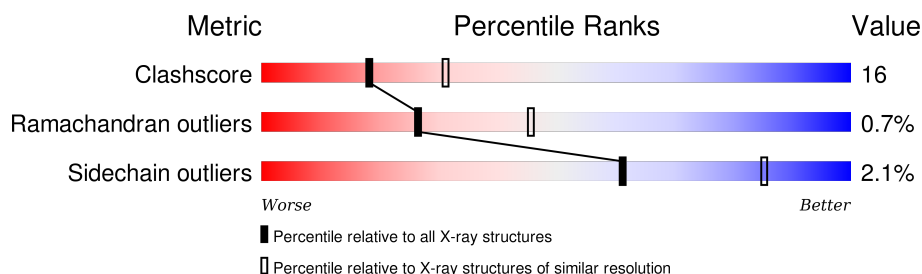
1 Overall quality at a glance

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	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	810	
2	B	8	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6116 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 Protein transport protein Sec24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	745	Total	C	N	O	S	0	0	0
			5893	3751	1006	1099	37			

- Molecule 2 is a protein called COPII-binding peptide of the protein transport protein BET1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	8	Total	C	N	O	0	0	0
			58	34	9	15			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	164	Total	O	0	0
			164	164		

Note EDS was not executed.

- Chain A: 63% 28% 8%

Sequence logo for Chain A, showing amino acid conservation across 40 positions. The logo is divided into four horizontal sections, each with a different background color (grey, light green, light orange, and light blue). The top section (positions 1-10) shows high conservation, with large letters indicating high probability. The second section (positions 11-20) shows moderate conservation. The third section (positions 21-30) shows low conservation. The bottom section (positions 31-40) shows very low conservation. The color scale at the top indicates the probability of each amino acid at each position, with a legend showing '63%', '28%', and '8%'.

- Chain B:  50% 38% 13%
- 
- L483
A484
S485
L486
E487
S488
Q489
S490

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	94.93 Å 94.93 Å 198.57 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.78 – 2.50	Depositor
% Data completeness (in resolution range)	84.6 (19.78-2.50)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	0.10	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.217 , 0.259	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6116	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.38	0/6014	0.64	0/8157
2	B	0.39	0/57	0.61	0/74
All	All	0.38	0/6071	0.64	0/8231

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

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	5893	0	5921	186	0
2	B	58	0	55	7	0
3	A	1	0	0	0	0
4	A	164	0	0	6	0
All	All	6116	0	5976	186	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 16.

All (186) 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:373:ILE:HD12	1:A:409:LYS:HD2	1.41	1.00
1:A:827:THR:HG22	1:A:829:ASP:H	1.26	1.00
1:A:582:LEU:HD22	2:B:484:ALA:HB2	1.39	0.99
1:A:235:ARG:HH21	2:B:489:GLN:HB3	1.27	0.98
1:A:810:LEU:HD22	1:A:840:ILE:HD11	1.53	0.89
1:A:373:ILE:HD11	1:A:406:LEU:HA	1.56	0.88
1:A:444:VAL:HB	1:A:499:LEU:HD23	1.59	0.85
1:A:375:MET:HE1	1:A:413:ILE:HG21	1.61	0.82
1:A:672:ARG:HH21	1:A:725:SER:HA	1.44	0.81
1:A:525:PHE:CE2	1:A:527:PRO:HG3	2.19	0.78
1:A:215:ASP:O	1:A:219:PRO:HG3	1.85	0.75
1:A:238:MET:SD	1:A:242:VAL:HG21	2.27	0.73
1:A:919:ILE:O	1:A:923:ARG:HG3	1.90	0.72
1:A:672:ARG:NH2	1:A:725:SER:HA	2.05	0.70
1:A:359:ILE:HB	1:A:394:VAL:HG11	1.73	0.70
1:A:708:ARG:O	1:A:708:ARG:HG2	1.90	0.70
1:A:827:THR:HG22	1:A:829:ASP:N	2.05	0.70
1:A:619:LEU:HD23	1:A:621:ASN:ND2	2.08	0.68
1:A:874:VAL:HG22	1:A:894:LEU:HB3	1.76	0.68
1:A:410:ILE:HB	1:A:411:PRO:HD3	1.76	0.67
1:A:279:ASP:HA	1:A:284:LYS:HE3	1.77	0.67
1:A:880:SER:O	1:A:882:PRO:HD3	1.95	0.67
1:A:669:ASP:HA	1:A:672:ARG:NH1	2.10	0.66
1:A:831:PHE:CE2	1:A:882:PRO:HD2	2.30	0.66
1:A:324:THR:OG1	1:A:537:ILE:HD12	1.96	0.66
1:A:621:ASN:OD1	1:A:623:GLN:HB2	1.96	0.65
1:A:141:ILE:HG12	1:A:703:LEU:O	1.96	0.65
1:A:827:THR:HG22	1:A:828:GLN:N	2.12	0.64
1:A:895:ARG:O	1:A:899:SER:HB2	1.97	0.64
1:A:138:LEU:CD2	1:A:704:CYS:HB3	2.29	0.63
1:A:419:ILE:HG22	1:A:421:ASN:H	1.66	0.61
1:A:380:ASP:OD2	1:A:383:GLU:HB2	2.01	0.61
1:A:682:ILE:HD12	1:A:710:PHE:CE2	2.36	0.61
1:A:759:LEU:O	1:A:762:MET:HB2	2.00	0.61
1:A:701:LEU:HA	4:A:1086:HOH:O	2.01	0.59
1:A:147:LEU:HA	1:A:148:PRO:C	2.22	0.59
1:A:302:PRO:HB3	1:A:438:VAL:HG12	1.83	0.59
1:A:299:ARG:HH12	1:A:438:VAL:HA	1.68	0.59
1:A:662:LYS:O	1:A:666:SER:HB3	2.01	0.59
1:A:720:HIS:O	1:A:724:ARG:HG3	2.04	0.58
1:A:239:ASN:O	1:A:242:VAL:HG22	2.03	0.58
1:A:559:ARG:HD2	2:B:487:GLU:OE1	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:667:SER:HB3	1:A:670:ASP:OD1	2.03	0.58
1:A:825:PHE:CD2	1:A:834:PRO:HD2	2.39	0.57
1:A:840:ILE:HD12	1:A:856:ILE:CD1	2.35	0.57
1:A:297:THR:HG22	1:A:624:ARG:CD	2.35	0.57
1:A:733:ARG:HD2	4:A:1060:HOH:O	2.04	0.57
1:A:282:GLU:HB3	1:A:288:MET:HE3	1.85	0.57
1:A:390:ASN:O	1:A:391:SER:HB2	2.05	0.56
1:A:710:PHE:HB3	1:A:711:PRO:HD3	1.87	0.56
1:A:571:PHE:CZ	1:A:581:ASP:HA	2.40	0.56
1:A:352:ASN:HD22	1:A:352:ASN:N	2.02	0.56
1:A:199:SER:O	1:A:200:LYS:HB2	2.05	0.56
1:A:553:CYS:O	1:A:587:THR:HA	2.06	0.56
1:A:582:LEU:HD22	2:B:484:ALA:CB	2.25	0.56
1:A:136:ASN:OD1	1:A:160:PRO:HD2	2.06	0.56
1:A:429:LYS:HE3	1:A:482:PHE:HE1	1.71	0.55
1:A:145:THR:O	1:A:145:THR:HG22	2.05	0.55
1:A:205:LEU:O	1:A:595:LEU:HA	2.07	0.55
1:A:672:ARG:HH21	1:A:725:SER:CA	2.16	0.55
1:A:334:ASP:CG	1:A:400:ARG:HH12	2.10	0.55
1:A:169:LEU:HD11	1:A:242:VAL:HG23	1.90	0.54
1:A:322:LEU:HB3	4:A:1050:HOH:O	2.07	0.54
1:A:567:ARG:HA	4:A:1048:HOH:O	2.06	0.54
1:A:765:GLU:CD	1:A:765:GLU:H	2.11	0.54
1:A:352:ASN:H	1:A:352:ASN:HD22	1.56	0.53
1:A:519:THR:O	1:A:520:ALA:HB3	2.08	0.53
1:A:352:ASN:HD22	1:A:353:ALA:N	2.06	0.53
1:A:816:ALA:HB3	1:A:830:ILE:HD12	1.91	0.53
1:A:218:ASP:N	1:A:219:PRO:HD3	2.24	0.53
1:A:138:LEU:HD23	1:A:704:CYS:HB3	1.91	0.53
1:A:817:VAL:HG12	1:A:819:ALA:H	1.74	0.53
1:A:191:LYS:HG3	1:A:635:THR:HB	1.91	0.53
1:A:279:ASP:CA	1:A:284:LYS:HE3	2.38	0.52
1:A:874:VAL:CG2	1:A:894:LEU:HB3	2.39	0.52
1:A:373:ILE:HD12	1:A:409:LYS:CD	2.28	0.52
1:A:255:PHE:CZ	1:A:612:GLN:HB2	2.45	0.52
1:A:250:ARG:HA	1:A:262:VAL:HG23	1.91	0.51
1:A:373:ILE:CD1	1:A:406:LEU:HA	2.34	0.51
1:A:154:LEU:HG	1:A:709:MET:CE	2.41	0.51
1:A:297:THR:HG22	1:A:624:ARG:HG2	1.90	0.51
1:A:781:ILE:HD12	1:A:781:ILE:N	2.26	0.51
1:A:840:ILE:HD12	1:A:856:ILE:HD11	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:669:ASP:O	1:A:673:VAL:HG23	2.11	0.51
1:A:266:MET:O	1:A:277:ARG:HB3	2.11	0.51
1:A:297:THR:CG2	1:A:624:ARG:HG2	2.41	0.50
1:A:505:ASP:HA	4:A:1100:HOH:O	2.10	0.50
1:A:151:ILE:HA	1:A:709:MET:HE1	1.93	0.50
1:A:344:ARG:HH22	1:A:438:VAL:HG21	1.77	0.50
1:A:449:LEU:HD12	1:A:450:PRO:HD2	1.93	0.50
1:A:457:LEU:CD2	1:A:480:ASP:HB2	2.42	0.50
1:A:803:ASP:OD1	1:A:869:GLN:OE1	2.29	0.49
1:A:874:VAL:HG22	1:A:894:LEU:HD13	1.93	0.49
1:A:352:ASN:H	1:A:352:ASN:ND2	2.10	0.49
1:A:639:LEU:HD23	1:A:689:GLU:HB3	1.93	0.49
1:A:823:ASP:O	1:A:849:ASN:HB2	2.12	0.49
1:A:668:LEU:O	1:A:671:ALA:HB3	2.12	0.49
1:A:312:VAL:HG11	1:A:349:CYS:HB3	1.94	0.49
1:A:138:LEU:HD11	1:A:690:ILE:HD13	1.93	0.49
1:A:297:THR:HG22	1:A:624:ARG:CG	2.43	0.49
1:A:151:ILE:HA	1:A:709:MET:CE	2.43	0.49
1:A:827:THR:HG22	1:A:828:GLN:H	1.78	0.49
1:A:847:GLU:O	1:A:851:ARG:HG3	2.13	0.49
1:A:149:PRO:HG3	1:A:913:TYR:HE2	1.78	0.49
1:A:907:ILE:HG22	1:A:908:LEU:HG	1.95	0.49
1:A:356:TYR:CD2	1:A:392:MET:HE3	2.48	0.48
1:A:765:GLU:N	1:A:765:GLU:CD	2.67	0.48
1:A:911:GLU:HB2	1:A:915:GLU:OE1	2.12	0.48
1:A:876:GLY:O	1:A:895:ARG:NH2	2.40	0.48
1:A:539:LYS:HA	1:A:868:TYR:CD2	2.48	0.48
1:A:483:TYR:O	1:A:487:THR:HG23	2.14	0.47
1:A:309:LEU:HB3	1:A:444:VAL:HG22	1.97	0.47
1:A:138:LEU:HD21	1:A:704:CYS:HB3	1.96	0.47
1:A:141:ILE:HD12	1:A:146:GLU:OE1	2.14	0.47
1:A:352:ASN:HB3	1:A:421:ASN:HB2	1.97	0.47
1:A:279:ASP:C	1:A:284:LYS:HE3	2.35	0.46
1:A:280:ARG:NE	1:A:282:GLU:OE1	2.49	0.46
1:A:309:LEU:HD13	1:A:428:LEU:HD12	1.98	0.46
1:A:827:THR:CG2	1:A:828:GLN:N	2.77	0.46
1:A:230:ARG:NH2	2:B:489:GLN:HB2	2.31	0.46
1:A:504:GLU:HG2	1:A:528:GLY:HA2	1.98	0.45
1:A:789:ALA:O	1:A:904:GLU:HB2	2.17	0.45
1:A:756:VAL:HG12	1:A:787:ILE:HD11	1.98	0.45
1:A:352:ASN:ND2	1:A:352:ASN:N	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:551:ASP:O	1:A:590:ARG:HG2	2.17	0.45
1:A:345:ILE:HG12	1:A:346:SER:N	2.32	0.45
1:A:849:ASN:OD1	1:A:853:ARG:HD3	2.16	0.45
1:A:357:PHE:CD2	1:A:406:LEU:HD11	2.52	0.45
1:A:147:LEU:HD21	1:A:917:LEU:HD12	1.99	0.45
1:A:783:LEU:HD22	1:A:855:ILE:HG23	1.99	0.45
1:A:292:ALA:HA	1:A:293:PRO:HD3	1.90	0.45
1:A:621:ASN:OD1	1:A:623:GLN:CB	2.65	0.44
1:A:559:ARG:HB2	1:A:582:LEU:HD12	1.98	0.44
1:A:154:LEU:HG	1:A:709:MET:HE2	1.98	0.44
1:A:162:VAL:O	1:A:634:PRO:HG3	2.17	0.44
1:A:410:ILE:CB	1:A:411:PRO:HD3	2.45	0.44
1:A:767:GLY:O	1:A:854:ASN:ND2	2.49	0.44
1:A:149:PRO:HG3	1:A:913:TYR:CE2	2.52	0.44
1:A:607:ASP:HA	1:A:635:THR:OG1	2.17	0.44
1:A:582:LEU:CD2	2:B:484:ALA:HB2	2.29	0.44
1:A:424:LEU:HD12	1:A:428:LEU:HD13	1.99	0.44
1:A:595:LEU:HD23	1:A:596:PHE:N	2.33	0.44
1:A:715:HIS:NE2	1:A:719:LYS:HE3	2.32	0.43
1:A:837:LYS:HE2	1:A:872:TYR:OH	2.17	0.43
1:A:686:TYR:CD1	1:A:690:ILE:HD12	2.54	0.43
1:A:829:ASP:HB3	1:A:832:ASP:HB2	2.00	0.43
1:A:230:ARG:HD2	1:A:235:ARG:O	2.18	0.43
1:A:853:ARG:O	1:A:857:ASN:ND2	2.52	0.43
1:A:162:VAL:O	1:A:163:ILE:HD13	2.19	0.43
1:A:762:MET:HG2	1:A:766:ALA:HB3	2.00	0.43
1:A:802:ILE:O	1:A:808:LEU:HA	2.19	0.43
1:A:842:VAL:HG22	1:A:853:ARG:NE	2.34	0.42
1:A:684:ALA:HB2	1:A:924:ILE:HG22	2.01	0.42
1:A:781:ILE:HG22	1:A:782:VAL:N	2.33	0.42
1:A:149:PRO:HA	1:A:150:PRO:HD3	1.78	0.42
1:A:633:MET:HA	1:A:634:PRO:HD3	1.85	0.42
1:A:669:ASP:HA	1:A:672:ARG:HH12	1.83	0.42
1:A:494:GLN:HG3	1:A:555:GLU:HG2	2.01	0.42
1:A:303:PRO:HG3	1:A:342:ARG:CZ	2.48	0.42
1:A:711:PRO:HD2	4:A:961:HOH:O	2.19	0.42
1:A:864:ASP:N	1:A:864:ASP:OD1	2.53	0.42
1:A:457:LEU:HD21	1:A:480:ASP:HB2	2.01	0.42
1:A:901:THR:O	1:A:903:VAL:HG13	2.19	0.42
1:A:810:LEU:CD2	1:A:840:ILE:HD11	2.37	0.41
1:A:229:VAL:HG21	1:A:266:MET:SD	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:763:ALA:O	1:A:851:ARG:NH2	2.52	0.41
1:A:302:PRO:HA	1:A:303:PRO:HD3	1.81	0.41
1:A:263:PRO:HD2	1:A:266:MET:HG3	2.01	0.41
1:A:252:ARG:HH11	1:A:252:ARG:HG3	1.86	0.41
1:A:619:LEU:HD23	1:A:621:ASN:HD21	1.82	0.41
1:A:533:ASN:O	1:A:535:ASN:N	2.53	0.41
1:A:663:ALA:C	1:A:665:ASN:H	2.24	0.41
1:A:595:LEU:HD11	1:A:654:PHE:HA	2.01	0.41
1:A:719:LYS:NZ	1:A:905:ASP:O	2.49	0.41
1:A:677:LYS:HE2	1:A:681:ASP:OD2	2.21	0.41
1:A:835:ILE:HA	1:A:835:ILE:HD13	1.96	0.41
1:A:208:ARG:HH11	1:A:208:ARG:HG3	1.85	0.41
1:A:373:ILE:HD13	1:A:406:LEU:CD1	2.51	0.41
1:A:449:LEU:O	1:A:450:PRO:C	2.59	0.40
1:A:298:LEU:HG	2:B:486:LEU:HD11	2.03	0.40
1:A:390:ASN:O	1:A:391:SER:CB	2.69	0.40
1:A:593:SER:HB2	1:A:744:PRO:HA	2.02	0.40
1:A:424:LEU:CD1	1:A:428:LEU:HD13	2.51	0.40
1:A:639:LEU:CD2	1:A:689:GLU:HB3	2.51	0.40
1:A:142:ASP:OD1	1:A:700:PRO:HB2	2.22	0.40
1:A:179:PRO:O	1:A:183:ARG:HG3	2.21	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	731/810 (90%)	672 (92%)	54 (7%)	5 (1%)	26	46
2	B	6/8 (75%)	6 (100%)	0	0	100	100
All	All	737/818 (90%)	678 (92%)	54 (7%)	5 (1%)	26	46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	903	VAL
1	A	151	ILE
1	A	664	LEU
1	A	575	PHE
1	A	162	VAL

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	667/720 (93%)	654 (98%)	13 (2%)	65	87
2	B	7/7 (100%)	6 (86%)	1 (14%)	4	7
All	All	674/727 (93%)	660 (98%)	14 (2%)	61	85

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	138	LEU
1	A	265	GLN
1	A	330	LEU
1	A	352	ASN
1	A	482	PHE
1	A	610	TYR
1	A	636	THR
1	A	733	ARG
1	A	792	SER
1	A	832	ASP
1	A	847	GLU
1	A	861	ASN
1	A	909	ASN
2	B	489	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	212	HIS
1	A	352	ASN
1	A	365	ASN
1	A	401	GLN
1	A	412	GLN
1	A	421	ASN
1	A	732	HIS
1	A	857	ASN
1	A	861	ASN
1	A	869	GLN
2	B	489	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.