



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 21, 2017 – 04:47 PM EST

PDB ID : 5M3B
Title : Structure of cobinamide-bound BtuF mutant W66L, the periplasmic vitamin B12 binding protein in E.coli
Authors : Mireku, S.A.; Ruetz, M.; Zhou, T.; Korkhov, V.M.; Kraeutler, B.; Locher, K.P.
Deposited on : 2016-10-14
Resolution : 1.50 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : rb-20028442

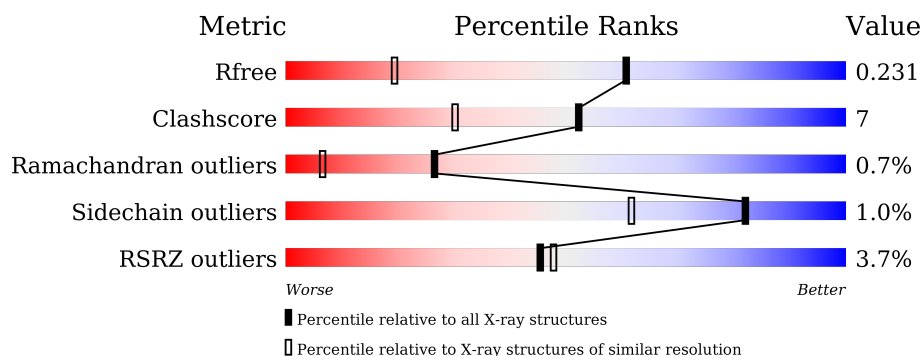
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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))
R_{free}	91344	2072 (1.50-1.50)
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)
RSRZ outliers	91569	2075 (1.50-1.50)

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.

Mol	Chain	Length	Quality of chain
1	A	289	<div> <div>3%</div> <div>71%</div> <div>7%</div> <div>21%</div> </div>
1	B	289	<div> <div>2%</div> <div>70%</div> <div>9%</div> <div>20%</div> </div>

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
2	CYN	A	301	-	-	X	-
4	GOL	A	304	-	-	-	X
4	GOL	B	303[A]	-	-	-	X
4	GOL	B	303[B]	-	-	-	X
4	GOL	B	304	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4266 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 Vitamin B12-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	0
			1762	1120	308	330	4			
1	B	230	Total	C	N	O	S	0	1	0
			1783	1133	313	332	5			

There are 90 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	initiating methionine	UNP P37028
A	-1	LYS	-	expression tag	UNP P37028
A	0	LYS	-	expression tag	UNP P37028
A	1	THR	-	expression tag	UNP P37028
A	2	ALA	-	expression tag	UNP P37028
A	3	ILE	-	expression tag	UNP P37028
A	4	ALA	-	expression tag	UNP P37028
A	5	ILE	-	expression tag	UNP P37028
A	6	ALA	-	expression tag	UNP P37028
A	7	VAL	-	expression tag	UNP P37028
A	8	ALA	-	expression tag	UNP P37028
A	9	LEU	-	expression tag	UNP P37028
A	10	ALA	-	expression tag	UNP P37028
A	11	GLY	-	expression tag	UNP P37028
A	12	PHE	-	expression tag	UNP P37028
A	13	ALA	-	expression tag	UNP P37028
A	14	THR	-	expression tag	UNP P37028
A	15	VAL	-	expression tag	UNP P37028
A	16	ALA	-	expression tag	UNP P37028
A	17	GLN	-	expression tag	UNP P37028
A	18	ALA	-	expression tag	UNP P37028
A	19	ALA	-	expression tag	UNP P37028
A	20	SER	-	expression tag	UNP P37028
A	21	MET	-	expression tag	UNP P37028
A	66	LEU	TRP	engineered mutation	UNP P37028

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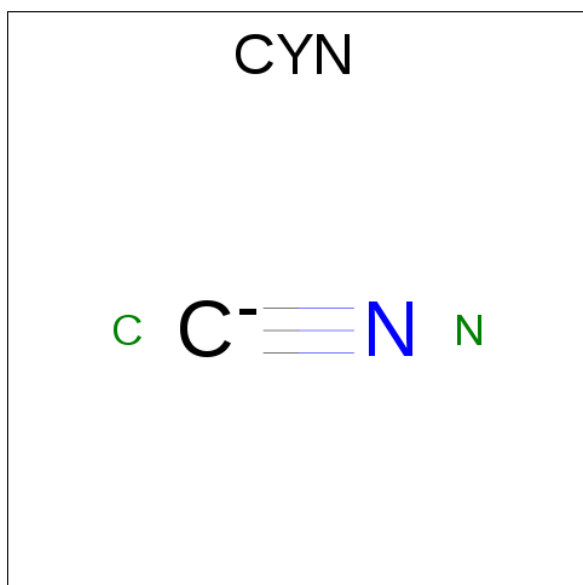
Chain	Residue	Modelled	Actual	Comment	Reference
A	267	SER	-	expression tag	UNP P37028
A	268	GLY	-	expression tag	UNP P37028
A	269	SER	-	expression tag	UNP P37028
A	270	LEU	-	expression tag	UNP P37028
A	271	GLU	-	expression tag	UNP P37028
A	272	VAL	-	expression tag	UNP P37028
A	273	LEU	-	expression tag	UNP P37028
A	274	PHE	-	expression tag	UNP P37028
A	275	GLN	-	expression tag	UNP P37028
A	276	GLY	-	expression tag	UNP P37028
A	277	PRO	-	expression tag	UNP P37028
A	278	GLY	-	expression tag	UNP P37028
A	279	GLY	-	expression tag	UNP P37028
A	280	SER	-	expression tag	UNP P37028
A	281	HIS	-	expression tag	UNP P37028
A	282	HIS	-	expression tag	UNP P37028
A	283	HIS	-	expression tag	UNP P37028
A	284	HIS	-	expression tag	UNP P37028
A	285	HIS	-	expression tag	UNP P37028
A	286	HIS	-	expression tag	UNP P37028
B	-2	MET	-	initiating methionine	UNP P37028
B	-1	LYS	-	expression tag	UNP P37028
B	0	LYS	-	expression tag	UNP P37028
B	1	THR	-	expression tag	UNP P37028
B	2	ALA	-	expression tag	UNP P37028
B	3	ILE	-	expression tag	UNP P37028
B	4	ALA	-	expression tag	UNP P37028
B	5	ILE	-	expression tag	UNP P37028
B	6	ALA	-	expression tag	UNP P37028
B	7	VAL	-	expression tag	UNP P37028
B	8	ALA	-	expression tag	UNP P37028
B	9	LEU	-	expression tag	UNP P37028
B	10	ALA	-	expression tag	UNP P37028
B	11	GLY	-	expression tag	UNP P37028
B	12	PHE	-	expression tag	UNP P37028
B	13	ALA	-	expression tag	UNP P37028
B	14	THR	-	expression tag	UNP P37028
B	15	VAL	-	expression tag	UNP P37028
B	16	ALA	-	expression tag	UNP P37028
B	17	GLN	-	expression tag	UNP P37028
B	18	ALA	-	expression tag	UNP P37028
B	19	ALA	-	expression tag	UNP P37028

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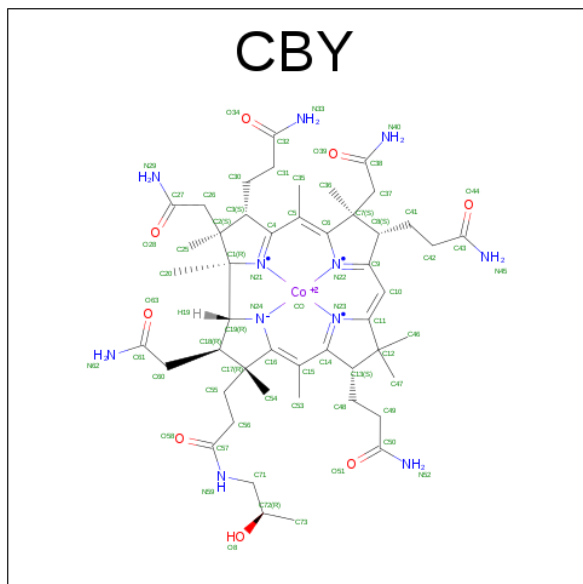
Chain	Residue	Modelled	Actual	Comment	Reference
B	20	SER	-	expression tag	UNP P37028
B	21	MET	-	expression tag	UNP P37028
B	66	LEU	TRP	engineered mutation	UNP P37028
B	267	SER	-	expression tag	UNP P37028
B	268	GLY	-	expression tag	UNP P37028
B	269	SER	-	expression tag	UNP P37028
B	270	LEU	-	expression tag	UNP P37028
B	271	GLU	-	expression tag	UNP P37028
B	272	VAL	-	expression tag	UNP P37028
B	273	LEU	-	expression tag	UNP P37028
B	274	PHE	-	expression tag	UNP P37028
B	275	GLN	-	expression tag	UNP P37028
B	276	GLY	-	expression tag	UNP P37028
B	277	PRO	-	expression tag	UNP P37028
B	278	GLY	-	expression tag	UNP P37028
B	279	GLY	-	expression tag	UNP P37028
B	280	SER	-	expression tag	UNP P37028
B	281	HIS	-	expression tag	UNP P37028
B	282	HIS	-	expression tag	UNP P37028
B	283	HIS	-	expression tag	UNP P37028
B	284	HIS	-	expression tag	UNP P37028
B	285	HIS	-	expression tag	UNP P37028
B	286	HIS	-	expression tag	UNP P37028

- Molecule 2 is CYANIDE ION (three-letter code: CYN) (formula: CN).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			2	1	1		
2	A	1	Total	C	N	0	0
			2	1	1		
2	B	1	Total	C	N	0	0
			2	1	1		

- Molecule 3 is COB(II)INAMIDE (three-letter code: CBY) (formula: $C_{48}H_{72}CoN_{11}O_8$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	1
			12	6	6		
4	B	1	Total	C	O	0	0
			6	3	3		

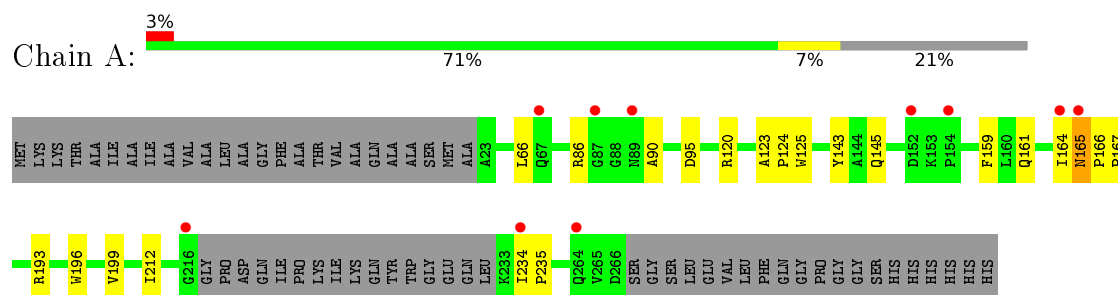
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	275	Total	O	0	0
			275	275		
5	B	280	Total	O	0	0
			280	280		

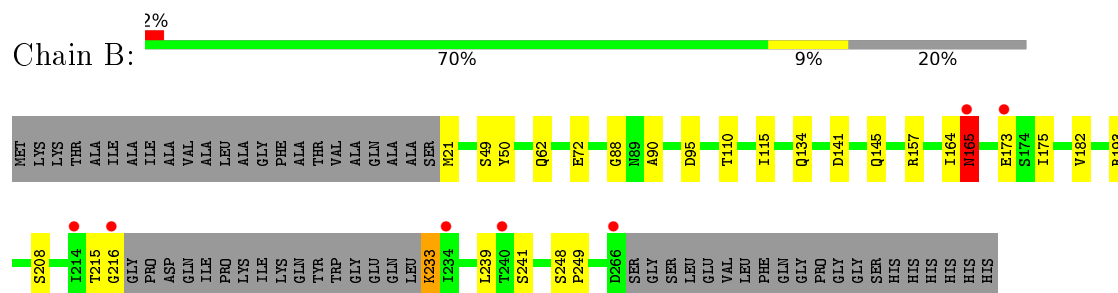
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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: Vitamin B12-binding protein



• Molecule 1: Vitamin B12-binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	136.28 Å 90.46 Å 50.81 Å 90.00° 110.74° 90.00°	Depositor
Resolution (Å)	19.67 – 1.50 19.67 – 1.50	Depositor EDS
% Data completeness (in resolution range)	96.8 (19.67-1.50) 91.5 (19.67-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.50 Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.196 , 0.229 0.201 , 0.231	Depositor DCC
R_{free} test set	4454 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.068 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4266	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.52% 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: GOL, CBY, CYN

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	1.07	2/1798 (0.1%)	1.02	4/2450 (0.2%)
1	B	1.02	1/1822 (0.1%)	0.99	1/2481 (0.0%)
All	All	1.04	3/3620 (0.1%)	1.01	5/4931 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	125	TRP	CB-CG	5.90	1.60	1.50
1	A	125	TRP	CE3-CZ3	-5.89	1.28	1.38
1	B	72	GLU	CG-CD	5.39	1.60	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	95	ASP	CB-CG-OD2	-7.39	111.65	118.30
1	A	86	ARG	NE-CZ-NH1	-5.45	117.58	120.30
1	A	120	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	A	95	ASP	CB-CG-OD2	-5.39	113.44	118.30
1	A	193	ARG	NE-CZ-NH2	-5.06	117.77	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	165	ASN	Peptide
1	B	165	ASN	Peptide

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	1762	0	1787	12	0
1	B	1783	0	1814	20	0
2	A	4	0	0	8	0
2	B	2	0	0	0	0
3	A	68	0	72	15	0
3	B	68	0	72	5	0
4	A	6	0	8	0	0
4	B	18	0	24	6	0
5	A	275	0	0	2	1
5	B	280	0	0	5	0
All	All	4266	0	3777	50	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 7.

All (50) 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:90:ALA:HB1	5:B:621:HOH:O	1.47	1.13
2:A:301:CYN:C	3:A:302:CBY:N22	2.16	1.08
1:B:50:TYR:H	4:B:304:GOL:H2	1.21	1.04
1:B:62:GLN:HE22	4:B:304:GOL:H32	1.35	0.91
2:A:301:CYN:C	3:A:302:CBY:CO	1.49	0.89
2:A:301:CYN:C	3:A:302:CBY:N21	2.38	0.87
1:B:62:GLN:NE2	4:B:304:GOL:H32	2.00	0.76
1:A:143:TYR:OH	5:A:401:HOH:O	2.03	0.76
2:A:301:CYN:C	3:A:302:CBY:N23	2.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:THR:HB	1:B:241:SER:HA	1.72	0.71
1:A:212:ILE:HG13	1:A:234:ILE:HD11	1.73	0.71
3:A:302:CBY:H20B	2:A:303:CYN:C	2.24	0.67
1:B:193:ARG:NH2	5:B:407:HOH:O	2.31	0.64
3:B:301:CBY:C35	3:B:301:CBY:H36	2.29	0.63
1:B:208:SER:HB2	5:B:431:HOH:O	1.98	0.62
1:A:145:GLN:NE2	5:A:404:HOH:O	2.34	0.61
1:B:216:GLY:N	1:B:239:LEU:O	2.32	0.61
1:A:234:ILE:HD12	1:A:235:PRO:O	2.00	0.60
1:A:164:ILE:HD12	1:A:165:ASN:N	2.17	0.60
3:A:302:CBY:H36	3:A:302:CBY:H35A	1.84	0.60
3:A:302:CBY:C35	3:A:302:CBY:H36	2.32	0.59
1:A:123:ALA:HB3	1:A:124:PRO:HD3	1.86	0.58
3:B:301:CBY:H36	3:B:301:CBY:H35A	1.86	0.57
2:A:301:CYN:C	3:A:302:CBY:N24	2.68	0.57
1:B:62:GLN:HE22	4:B:304:GOL:C3	2.12	0.56
1:A:212:ILE:CG1	1:A:234:ILE:HD11	2.35	0.56
1:A:234:ILE:C	1:A:234:ILE:HD12	2.26	0.55
2:A:301:CYN:C	3:A:302:CBY:C6	2.85	0.55
3:B:301:CBY:H3	3:B:301:CBY:O28	2.06	0.55
1:B:157[B]:ARG:NH2	5:B:401:HOH:O	2.20	0.54
1:B:110:THR:HB	1:B:173:GLU:O	2.08	0.54
1:B:233:LYS:HE2	1:B:233:LYS:HA	1.97	0.47
1:B:62:GLN:OE1	4:B:304:GOL:C3	2.63	0.46
3:B:301:CBY:C36	3:B:301:CBY:C35	2.92	0.46
1:A:159:PHE:CE2	1:A:161:GLN:HB2	2.52	0.44
1:B:141:ASP:O	1:B:145:GLN:HG3	2.17	0.44
1:B:115:ILE:HD11	1:B:175:ILE:CD1	2.47	0.44
1:B:49:SER:HA	4:B:304:GOL:H31	2.00	0.43
3:A:302:CBY:C36	3:A:302:CBY:C35	2.97	0.43
1:A:196:TRP:CG	3:A:302:CBY:H49A	2.53	0.42
1:B:164:ILE:O	1:B:165:ASN:C	2.58	0.42
1:B:88:GLY:C	5:B:465:HOH:O	2.59	0.41
1:A:167:PRO:HG2	1:A:199:VAL:O	2.20	0.41
1:A:66:LEU:HB2	3:A:302:CBY:N33	2.36	0.41
3:B:301:CBY:C36	3:B:301:CBY:H35A	2.50	0.41
2:A:301:CYN:C	3:A:302:CBY:C4	2.99	0.41
3:A:302:CBY:C36	3:A:302:CBY:H35A	2.51	0.41
1:B:215:THR:HB	1:B:241:SER:CA	2.44	0.41
1:B:248:SER:HB2	1:B:249:PRO:CD	2.51	0.40
3:A:302:CBY:H20	3:A:302:CBY:H30	2.03	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)
5:A:446:HOH:O	5:A:542:HOH:O[2_454]	2.02	0.18

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	224/289 (78%)	219 (98%)	3 (1%)	2 (1%)	21	4
1	B	227/289 (78%)	220 (97%)	6 (3%)	1 (0%)	39	14
All	All	451/578 (78%)	439 (97%)	9 (2%)	3 (1%)	26	6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	ALA
1	B	165	ASN
1	A	166	PRO

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	191/235 (81%)	191 (100%)	0	100	100
1	B	193/235 (82%)	189 (98%)	4 (2%)	61	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	384/470 (82%)	380 (99%)	4 (1%)	82	62

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	21	MET
1	B	134	GLN
1	B	182	VAL
1	B	233	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	GLN
1	A	161	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](#)

9 ligands are modelled in this entry.

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
2	CYN	A	301	3	0,1,1	0.00	-	0,0,0	0.00	-
3	CBY	A	302	2	51,75,75	1.27	4 (7%)	80,125,125	1.61	15 (18%)
2	CYN	A	303	3	0,1,1	0.00	-	0,0,0	0.00	-
4	GOL	A	304	-	5,5,5	0.36	0	5,5,5	0.75	0
3	CBY	B	301	2	51,75,75	1.27	4 (7%)	80,125,125	1.53	13 (16%)
2	CYN	B	302	3	0,1,1	0.00	-	0,0,0	0.00	-
4	GOL	B	303[A]	-	5,5,5	0.33	0	5,5,5	0.73	0
4	GOL	B	303[B]	-	5,5,5	0.27	0	5,5,5	0.18	0
4	GOL	B	304	-	5,5,5	0.72	0	5,5,5	1.28	1 (20%)

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
2	CYN	A	301	3	-	0/0/0/0	0/0/0/0
3	CBY	A	302	2	-	0/39/191/191	0/0/8/8
2	CYN	A	303	3	-	0/0/0/0	0/0/0/0
4	GOL	A	304	-	-	0/4/4/4	0/0/0/0
3	CBY	B	301	2	-	0/39/191/191	0/0/8/8
2	CYN	B	302	3	-	0/0/0/0	0/0/0/0
4	GOL	B	303[A]	-	-	0/4/4/4	0/0/0/0
4	GOL	B	303[B]	-	-	0/4/4/4	0/0/0/0
4	GOL	B	304	-	-	0/4/4/4	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	CBY	C11-C10	-6.15	1.30	1.41
3	B	301	CBY	C48-C13	-4.72	1.46	1.54
3	B	301	CBY	C11-C10	-4.34	1.33	1.41
3	A	302	CBY	C55-C17	-2.81	1.47	1.54
3	A	302	CBY	C48-C13	-2.60	1.50	1.54
3	B	301	CBY	C36-C7	-2.55	1.50	1.54
3	B	301	CBY	C2-C3	-2.09	1.54	1.58
3	A	302	CBY	C17-C18	2.63	1.58	1.54

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	CBY	C56-C57-N59	-3.23	110.84	116.46
3	A	302	CBY	C35-C5-C4	-3.21	113.39	117.81
3	B	301	CBY	C9-C10-C11	-2.94	125.20	132.31
3	B	301	CBY	C25-C2-C3	-2.87	112.43	115.90
3	A	302	CBY	C25-C2-C3	-2.82	112.49	115.90
3	A	302	CBY	C48-C49-C50	-2.76	103.72	112.64
3	A	302	CBY	C13-C14-C15	-2.71	123.56	132.12
3	B	301	CBY	C13-C14-C15	-2.67	123.69	132.12
3	B	301	CBY	C48-C49-C50	-2.41	104.86	112.64
3	A	302	CBY	C3-C4-C5	-2.37	124.64	132.12
3	B	301	CBY	C20-C1-N21	-2.35	101.35	108.03
3	A	302	CBY	C20-C1-C19	-2.34	107.04	109.36
3	A	302	CBY	C54-C17-C18	-2.26	109.53	112.94
3	B	301	CBY	C55-C17-C18	-2.20	107.08	111.03
3	B	301	CBY	C56-C57-N59	-2.12	112.77	116.46
3	B	301	CBY	C25-C2-C1	2.04	117.00	113.84
3	A	302	CBY	C7-C37-C38	2.21	121.26	114.24
3	A	302	CBY	C18-C17-C16	2.21	103.39	100.57
3	B	301	CBY	O58-C57-N59	2.35	127.62	122.96
4	B	304	GOL	O3-C3-C2	2.57	122.98	109.97
3	A	302	CBY	C19-C1-N21	2.88	105.20	102.16
3	B	301	CBY	C35-C5-C6	3.02	121.95	117.81
3	B	301	CBY	C2-C1-C19	3.10	121.56	118.62
3	A	302	CBY	C1-C2-C3	3.13	105.59	101.69
3	A	302	CBY	O58-C57-N59	3.23	129.37	122.96
3	B	301	CBY	C18-C17-C16	4.00	105.67	100.57
3	A	302	CBY	C35-C5-C6	4.33	123.77	117.81
3	A	302	CBY	C2-C1-C19	4.61	122.98	118.62
3	B	301	CBY	C19-C1-N21	4.92	107.37	102.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	CYN	7	0
3	A	302	CBY	15	0
2	A	303	CYN	1	0
3	B	301	CBY	5	0
4	B	304	GOL	6	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	228/289 (78%)	0.05	10 (4%) 38 40	12, 20, 44, 68	0
1	B	230/289 (79%)	0.11	7 (3%) 54 57	12, 22, 45, 71	0
All	All	458/578 (79%)	0.08	17 (3%) 45 48	12, 21, 45, 71	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	165	ASN	6.4
1	A	216	GLY	4.3
1	B	266	ASP	4.0
1	B	234	ILE	3.8
1	A	164	ILE	3.3
1	A	89	ASN	3.3
1	B	216	GLY	3.2
1	A	165	ASN	3.1
1	A	67	GLN	3.0
1	A	264	GLN	3.0
1	A	234	ILE	2.5
1	A	152	ASP	2.4
1	B	214	ILE	2.4
1	B	173	GLU	2.3
1	B	240	THR	2.2
1	A	87	GLY	2.1
1	A	154	PRO	2.1

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
4	GOL	B	303[A]	6/6	0.78	0.21	6.55	27,34,37,39	6
4	GOL	B	303[B]	6/6	0.78	0.21	5.21	51,62,67,69	6
4	GOL	A	304	6/6	0.80	0.17	3.42	40,42,43,51	0
3	CBY	A	302	68/68	0.97	0.10	0.35	13,19,46,57	0
3	CBY	B	301	68/68	0.96	0.10	-0.02	16,22,53,85	0
2	CYN	A	301	2/2	0.99	0.16	-	23,23,23,25	2
4	GOL	B	304	6/6	0.87	0.17	-	23,35,37,41	0
2	CYN	B	302	2/2	0.97	0.23	-	26,26,26,31	0
2	CYN	A	303	2/2	0.85	0.22	-	23,23,23,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.