W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:28 AM GMT

PDB ID	:	3AYM
Title	:	Crystal structure of the batho intermediate of squid rhodopsin
Authors	:	Murakami, M.; Kouyama, T.
Deposited on	:	2011-05-09
Resolution	:	2.80 Å(reported)

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)	:	1.9-1692
EDS	:	rb-20026688
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)	:	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 2.80 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	Percentile Ranks	Value
Rfree		0.294
Clashscore		25
Ramachandran outliers		1.6%
Sidechain outliers		7.4%
RSRZ outliers		0.3%

Worse ← → *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution
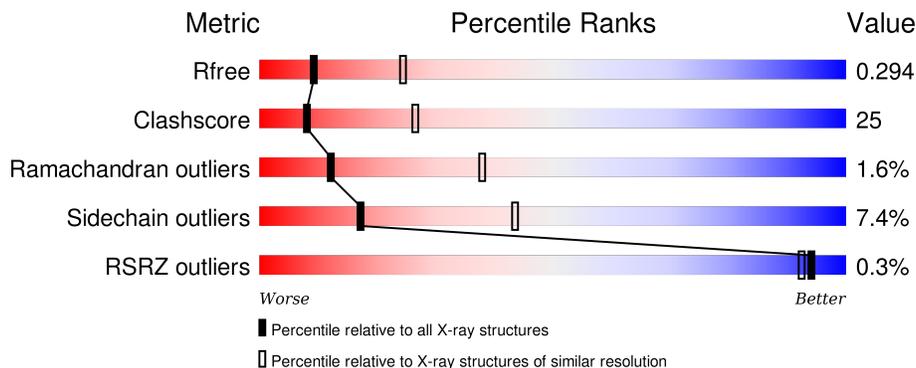
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 <=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	448	38% 36% • 22%
1	B	448	45% 29% • 23%

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	PLM	A	1001	-	-	-	X
3	BOG	B	1005	-	-	-	X
4	RET	B	1000	-	-	-	X
6	PC1	B	1004	-	-	-	X

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 5742 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 Rhodopsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2780	1838	443	473	26			
1	B	347	Total	C	N	O	S	0	0	0
			2762	1828	440	468	26			

- Molecule 2 is PALMITIC ACID (three-letter code: PLM) (formula: $C_{16}H_{32}O_2$).
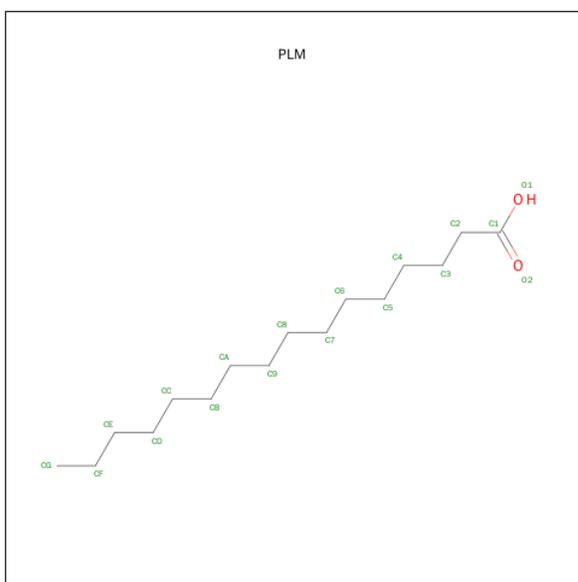
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			17	16	1		

- Molecule 3 is SUGAR (B-OCTYLGLUCOSIDE) (three-letter code: BOG) (formula: $C_{14}H_{28}O_6$).
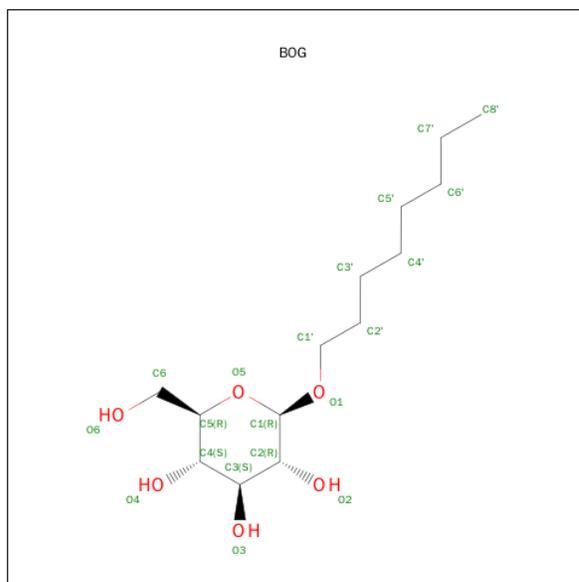
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			20	14	6		
3	B	1	Total	C	O	0	0
			20	14	6		

- Molecule 4 is RETINAL (three-letter code: RET) (formula: $C_{20}H_{28}O$).
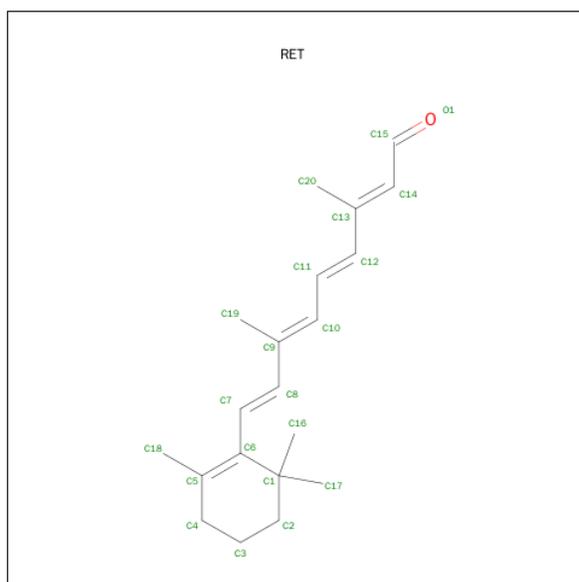
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	C	0	0
			20	20		
4	B	1	Total	C	0	0
			20	20		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).
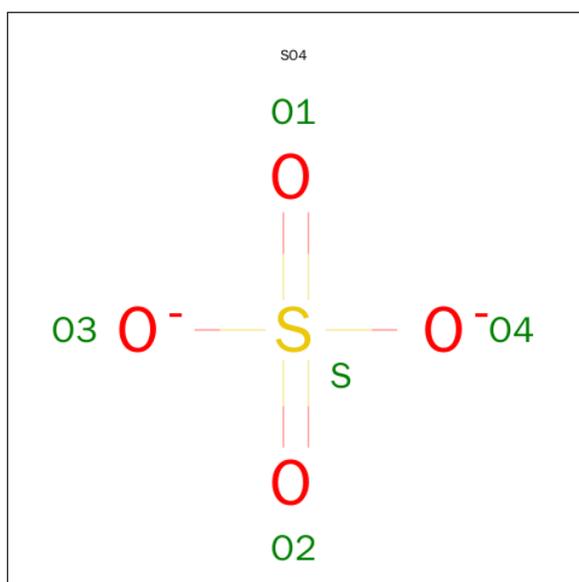
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
5	B	1	5	4	1	0	0

- Molecule 6 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: $C_{44}H_{88}NO_8P$).
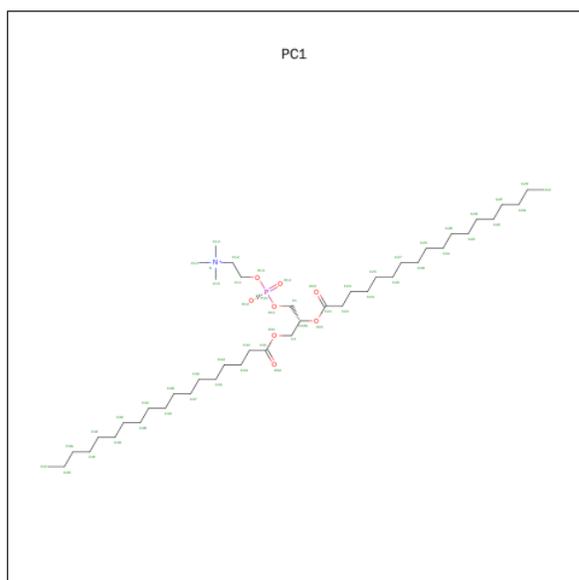
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
6	B	1	39	30	8	1	0	0

• Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	29	Total O 29 29	0	0
7	B	30	Total O 30 30	0	0

3 Residue-property plots ⓘ

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 (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: Rhodopsin

- Molecule 1: Rhodopsin

T293 P294 Y295 A296 A297 Q298 L299 P300 V301 M302 K305 A306 I309 H310 N311 P312 S316 V317 S318 H319 P320 K321 F322 R323 E324 A325 I326 S327 Q328 T329 F330 P331 T335 C336 C337 Q338 F339 D340 D341 K342 D349 A350 E353 I354 P355 ALA GLY GLU SER SER ASP ALA ALA PRO

SER ALA ASP ALA ALA GLN MET LYS GLU MET MET ALA MET MET GLN LYS MET GLN GLN GLN ALA ALA TYR PRO PRO GLN GLY TYR ALA PRO PRO PRO GLN GLY TYR PRO PRO GLN GLY TYR PRO PRO GLN GLY TYR PRO PRO GLN GLY TYR PRO PRO GLN GLY TYR PRO PRO PRO

GLN GLY ALA PRO PRO GLN GLY ALA PRO PRO ALA ALA PRO PRO GLN GLY VAL ASP ASN GLN ALA TYR GLN ALA

4   Data and refinement statistics (i)

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, α, β, γ	122.36Å 122.36Å 158.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	15.00 – 2.80 44.02 – 2.80	Depositor EDS
% Data completeness (in resolution range)	67.7 (15.00-2.80) 67.6 (44.02-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.56 (at 2.81Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.295 , 0.345 0.301 , 0.294	Depositor DCC
R_{free} test set	1085 reflections (4.88%)	DCC
Wilson B-factor (Å^2)	46.1	Xtriage
Anisotropy	0.441	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 47.9	EDS
Estimated twinning fraction	0.088 for h,-h-k,-l	Xtriage
L-test for twinning[2]	$< |L| > = 0.47, < L^2 > = 0.30$	Xtriage
Outliers	3 of 22333 reflections (0.013%)	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	5742	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.22% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: PLM, PC1, SO4, RET, BOG

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	0.73	0/2865	0.73	1/3889 (0.0%)
1	B	0.75	0/2847	0.74	0/3865
All	All	0.74	0/5712	0.73	1/7754 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	27	ASP	CB-CG-OD2	-9.35	109.88	118.30

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	2780	0	2766	161	0
1	B	2762	0	2752	119	0
2	A	17	0	31	0	0
3	A	20	0	28	2	0
3	B	20	0	28	4	0
4	A	20	0	27	1	0
4	B	20	0	27	2	0
5	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	39	0	49	2	0
7	A	29	0	0	7	0
7	B	30	0	0	2	0
All	All	5742	0	5708	280	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 25.

The worst 5 of 280 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:21:PRO:HA	1:A:24:ARG:HD3	1.30	1.11
1:B:67:THR:HG21	3:B:1005:BOG:H5	1.43	1.00
1:A:20:HIS:ND1	1:A:21:PRO:HD2	1.81	0.94
1:A:332:TRP:O	1:A:335:THR:HG23	1.67	0.93
1:B:150:ARG:HD2	1:B:150:ARG:H	1.32	0.93

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	348/448 (78%)	308 (88%)	33 (10%)	7 (2%)	9	30
1	B	345/448 (77%)	317 (92%)	24 (7%)	4 (1%)	16	47
All	All	693/896 (77%)	625 (90%)	57 (8%)	11 (2%)	12	38

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	241	LEU

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Mol	Chain	Res	Type
1	A	243	ALA
1	A	292	VAL
1	B	138	GLY
1	A	352	THR

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	296/369 (80%)	275 (93%)	21 (7%)	18	46
1	B	295/369 (80%)	272 (92%)	23 (8%)	16	41
All	All	591/738 (80%)	547 (93%)	44 (7%)	17	43

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	346	ASP
1	B	66	GLN
1	B	335	THR
1	A	358	GLU
1	B	29	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	285	GLN
1	A	328	GLN
1	B	222	ASN
1	A	269	GLN
1	B	70	ASN

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)

7 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	#$|Z| > 2$
4	RET	A	1000	1	19,20,21	1.77	2 (10%)	27,27,28	1.76	8 (29%)
2	PLM	A	1001	-	16,16,17	0.38	0	14,15,17	0.60	0
3	BOG	A	1005	-	20,20,20	1.69	4 (20%)	25,25,25	2.64	9 (36%)
4	RET	B	1000	1	19,20,21	1.93	4 (21%)	27,27,28	2.03	8 (29%)
6	PC1	B	1004	-	38,38,53	1.82	4 (10%)	39,43,61	1.01	2 (5%)
3	BOG	B	1005	-	20,20,20	1.73	4 (20%)	25,25,25	2.70	10 (40%)
5	SO4	B	449	-	4,4,4	0.40	0	6,6,6	0.26	0

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
4	RET	A	1000	1	-	0/13/30/31	0/1/1/1
2	PLM	A	1001	-	-	0/13/14/15	0/0/0/0
3	BOG	A	1005	-	-	0/11/31/31	0/1/1/1
4	RET	B	1000	1	-	0/13/30/31	0/1/1/1
6	PC1	B	1004	-	-	0/42/42/57	0/0/0/0
3	BOG	B	1005	-	-	0/11/31/31	0/1/1/1
5	SO4	B	449	-	-	0/0/0/0	0/0/0/0

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1000	RET	C2-C3	-3.59	1.42	1.52
4	B	1000	RET	C2-C3	-3.43	1.43	1.52
3	B	1005	BOG	C4-C5	-2.95	1.46	1.53
4	B	1000	RET	C8-C9	-2.35	1.40	1.45
6	B	1004	PC1	O31-C3	2.00	1.49	1.45

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1005	BOG	C1'-O1-C1	-8.23	99.56	113.94
3	B	1005	BOG	C1'-O1-C1	-7.78	100.34	113.94
4	B	1000	RET	C8-C9-C10	-6.04	109.25	118.98
4	A	1000	RET	C8-C9-C10	-4.93	111.04	118.98
3	B	1005	BOG	C1-C2-C3	-4.69	100.73	109.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1000	RET	1	0
3	A	1005	BOG	2	0
4	B	1000	RET	2	0
6	B	1004	PC1	2	0
3	B	1005	BOG	4	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	350/448 (78%)	-0.21	2 (0%)	90	86	28, 54, 115, 135	0
1	B	347/448 (77%)	-0.19	0	100	100	29, 49, 95, 124	0
All	All	697/896 (77%)	-0.20	2 (0%)	94	92	28, 52, 108, 135	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	248	LYS	2.2
1	A	241	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 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(Å^2)	Q<0.9
2	PLM	A	1001	17/18	0.91	0.39	5.83	45,66,73,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å²)	Q<0.9
3	BOG	B	1005	20/20	0.87	0.37	4.00	70,109,111,112	0
6	PC1	B	1004	39/54	0.90	0.31	3.31	44,65,119,120	0
4	RET	B	1000	20/21	0.98	0.22	2.01	20,24,31,37	0
4	RET	A	1000	20/21	0.98	0.23	1.66	30,45,51,53	0
3	BOG	A	1005	20/20	0.91	0.24	0.79	50,92,97,100	0
5	SO4	B	449	5/5	0.96	0.16	-0.81	85,86,87,88	0

6.5 Other polymers (i)

There are no such residues in this entry.