



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2017 – 10:03 AM EDT

PDB ID : 3AYM  
Title : Crystal structure of the batho intermediate of squid rhodopsin  
Authors : Murakami, M.; Kouyama, T.  
Deposited on : unknown  
Resolution : 2.80 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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-20030345

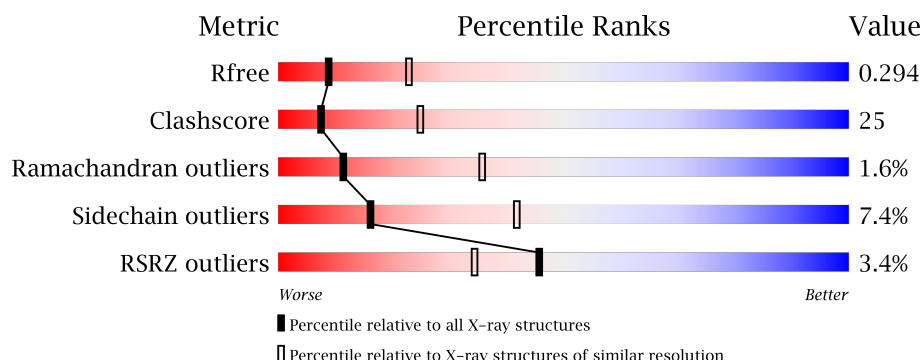
# 1 Overall quality at a glance

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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (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  $\geq 3$ , 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	448	<div> <div>3%</div> <div>38%</div> <div>36%</div> <div>•</div> <div>22%</div> </div>
1	B	448	<div> <div>3%</div> <div>45%</div> <div>29%</div> <div>•</div> <div>23%</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	PLM	A	1001	-	-	-	X
3	BOG	B	1005	-	-	-	X
6	PC1	B	1004	-	-	-	X

## 2 Entry composition [i](#)

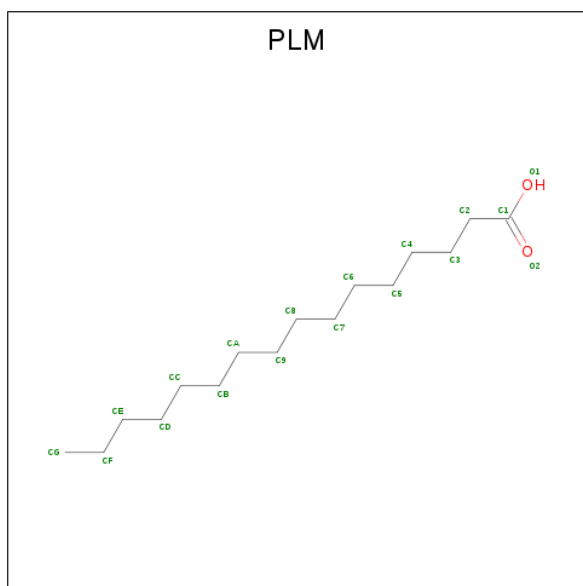
There are 7 unique types of molecules in this entry. The entry contains 5742 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

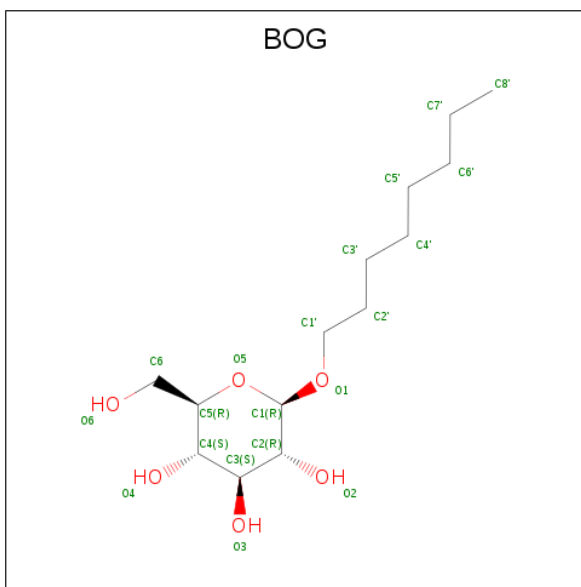
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2780	1838	443	473	26			
1	B	347	Total	C	N	O	S	0	0	0
			2762	1828	440	468	26			

- Molecule 2 is PALMITIC ACID (three-letter code: PLM) (formula:  $C_{16}H_{32}O_2$ ).



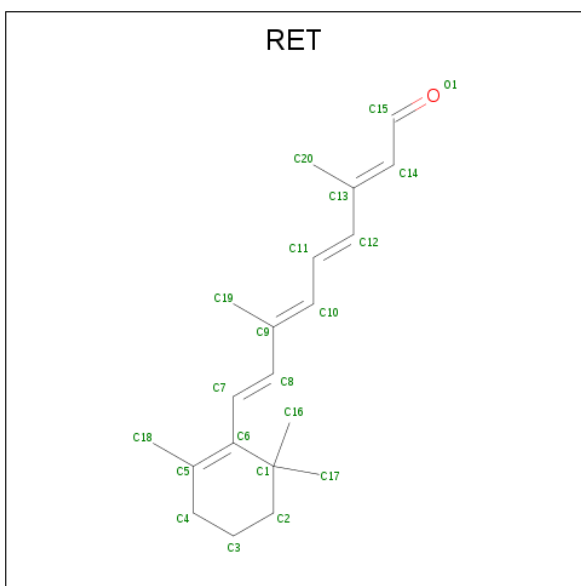
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			17	16	1		

- Molecule 3 is 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:  $C_{20}H_{28}O$ ).



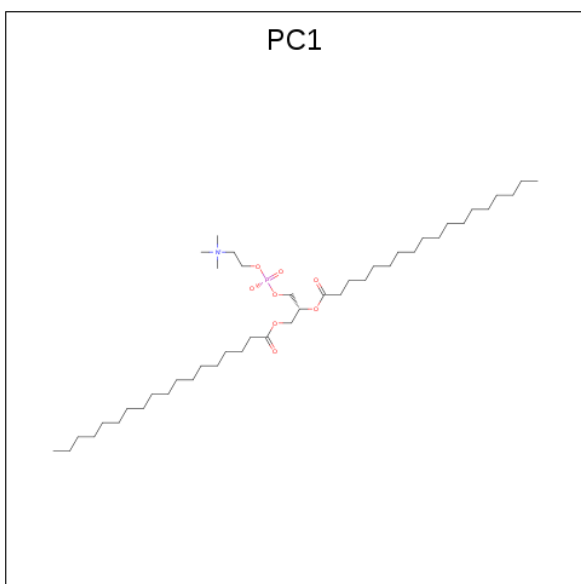
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	C	0	0
			20	20		
4	B	1	Total	C	0	0
			20	20		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 6 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PC1) (formula: C<sub>44</sub>H<sub>88</sub>NO<sub>8</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	O	P	0	0
			39	30	8	1		

- Molecule 7 is water.

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

These plots are drawn for all protein, RNA and DNA 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 ( $\text{RSRZ} > 2$ ). 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.

[illegible]

Chain B:

3% 45% 29% 23%

MET GLY ARG ASP ASP ASN E9 T10 W11 W12 Y13 P21 R24 E26 D27 Q28 V29 P30 D31 A32 V33 Y34 Y35 I39 F40 I41 G42 I43 G51 N52 V55 I56 T60 K61 T62 K63 Q66 T67 N70 I73 I74 H75 L76 A77 F78 S79 I86

V86 N87 G88 I102 F105 K109 W110 Y111 G112 F113 I114 I117 F118 M121 S122 I123 M124 A127 M128 I131 D132 R133 V136 I137 G138 R139 P140 M141 K145 S148 H149 R150 R151 I156 I157 A167 I168 G169 P170 M174 Y177 V182 S195 H198

T197 R198 S199 N200 I201 F209 P212 W224 V225 S226 V227 S228 N229 H230 E231 K232 E233 M234 A235 A236 M237 A238 R239 K240 L241 M242 A243 K244 E245 L246 R247 K248 A251 E256 M257 K261 K262 S263 I266 Q269 F270 P276 A284 T292



[illegible]

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.56 (at 2.81Å)	Xtriage
Refinement program	CNS	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 <sup>2</sup> )	46.1	Xtriage
Anisotropy	0.441	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 71.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.088 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	5742	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 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(°)	Ideal(°)
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 [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	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.

All (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
1:A:67:THR:HG21	3:A:1005:BOG:H5	1.52	0.89
1:A:117:ILE:HD11	1:A:164:VAL:HG22	1.57	0.84
1:A:284:ALA:HB2	1:A:292:VAL:HG21	1.58	0.84
1:B:284:ALA:HB2	1:B:292:VAL:HG21	1.60	0.82
1:B:21:PRO:HA	1:B:24:ARG:HG3	1.63	0.81
1:A:21:PRO:CA	1:A:24:ARG:HD3	2.09	0.80
1:A:354:ILE:O	1:A:354:ILE:HD12	1.83	0.79
1:B:148:SER:HB2	1:B:150:ARG:HH21	1.49	0.77
1:A:193:ARG:HD2	7:A:516:HOH:O	1.86	0.75
1:A:29:VAL:HG22	7:A:523:HOH:O	1.85	0.75
1:A:327:SER:O	1:A:331:PRO:HB3	1.87	0.75
1:B:113:PHE:O	1:B:117:ILE:HG23	1.89	0.73
1:B:319:HIS:HB3	1:B:322:PHE:HB3	1.70	0.73
1:A:298:GLN:O	1:A:301:VAL:HG12	1.88	0.72
1:A:170:PRO:HB3	1:A:176:ALA:CA	2.22	0.69
1:A:137:ILE:HD11	1:A:256:GLU:HB2	1.74	0.69
1:B:237:MET:O	1:B:242:ASN:HB2	1.93	0.68
1:B:276:PRO:HB2	7:B:511:HOH:O	1.93	0.68
1:A:77:ALA:HA	7:A:508:HOH:O	1.92	0.68
1:B:182:VAL:HG22	1:B:298:GLN:OE1	1.93	0.68
1:B:298:GLN:O	1:B:301:VAL:HG12	1.91	0.68
1:B:73:ILE:HD11	3:B:1005:BOG:H7'2	1.75	0.67
1:A:248:LYS:HE2	1:A:353:GLU:OE1	1.95	0.67
1:A:218:PHE:O	1:A:222:ASN:HB2	1.94	0.67
1:A:182:VAL:HG22	1:A:298:GLN:OE1	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:TRP:CD2	1:A:28:GLN:HB2	2.31	0.66
1:B:136:VAL:HG23	1:B:137:ILE:HG12	1.77	0.65
1:A:19:VAL:HG21	1:A:183:LEU:HD13	1.78	0.65
1:A:340:ASP:OD2	1:A:342:LYS:HB2	1.98	0.64
1:B:306:ALA:O	1:B:309:ILE:HG12	1.97	0.64
1:B:41:ILE:HG13	1:B:88:GLY:HA2	1.79	0.63
1:A:324:GLU:HG3	1:A:339:PHE:CZ	2.33	0.63
1:A:133:ARG:NH2	1:A:136:VAL:HG11	2.13	0.63
1:B:145:LYS:HD3	1:B:151:ARG:NH2	2.14	0.63
1:B:52:ASN:HA	1:B:55:VAL:CG1	2.29	0.62
1:A:243:ALA:HB3	1:A:245:GLU:HG2	1.82	0.62
1:A:95:SER:OG	1:A:101:TRP:HA	2.00	0.62
1:A:19:VAL:O	1:A:24:ARG:HD2	2.00	0.61
1:A:20:HIS:ND1	1:A:21:PRO:CD	2.61	0.61
1:A:283:LEU:HD23	1:A:291:TRP:HE3	1.65	0.61
1:B:137:ILE:O	1:B:139:ARG:N	2.33	0.61
4:B:1000:RET:H181	4:B:1000:RET:H8	1.83	0.60
1:A:240:ARG:HA	1:A:240:ARG:HE	1.65	0.60
1:B:199:SER:HA	6:B:1004:PC1:H361	1.82	0.60
1:B:67:THR:HB	3:B:1005:BOG:O6	2.01	0.60
1:A:27:ASP:OD1	1:B:11:TRP:HD1	1.84	0.60
1:B:137:ILE:HD11	1:B:256:GLU:HB3	1.84	0.60
1:A:240:ARG:NE	1:A:240:ARG:HA	2.17	0.59
1:B:197:THR:O	1:B:201:ILE:HG13	2.02	0.59
1:A:170:PRO:HB3	1:A:176:ALA:HA	1.82	0.59
1:A:20:HIS:CE1	1:A:21:PRO:HD2	2.38	0.59
1:A:177:TYR:HA	1:A:187:SER:O	2.02	0.59
1:A:19:VAL:HG12	1:A:24:ARG:HG3	1.84	0.58
1:A:306:ALA:O	1:A:309:ILE:HG12	2.04	0.58
1:B:354:ILE:HD13	1:B:354:ILE:H	1.69	0.58
1:A:293:THR:N	1:A:296:ALA:HB3	2.19	0.58
1:A:133:ARG:HA	1:A:133:ARG:NE	2.17	0.58
1:A:185:ASN:OD1	7:A:500:HOH:O	2.17	0.57
1:A:19:VAL:CG1	1:A:24:ARG:HG3	2.34	0.57
1:A:50:GLY:O	1:A:54:ILE:HG13	2.05	0.57
1:B:311:ASN:HB2	1:B:312:PRO:HD3	1.87	0.57
1:B:197:THR:HG22	1:B:201:ILE:HD11	1.87	0.57
1:A:233:GLU:HG2	1:A:237:MET:HE3	1.87	0.56
1:A:320:PRO:HG2	7:A:521:HOH:O	2.04	0.56
1:B:316:SER:O	1:B:323:ARG:NH1	2.36	0.56
1:A:21:PRO:HA	1:A:24:ARG:CD	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ILE:O	1:A:117:ILE:HG22	2.05	0.56
1:A:259:LEU:HD13	1:A:262:ILE:HD12	1.87	0.56
1:B:141:MET:CE	1:B:141:MET:HA	2.36	0.56
1:A:41:ILE:HG13	1:A:88:GLY:HA2	1.87	0.56
1:A:311:ASN:HB2	1:A:312:PRO:HD3	1.89	0.55
1:A:291:TRP:O	1:A:293:THR:N	2.38	0.55
1:A:356:ALA:C	1:A:358:GLU:H	2.09	0.55
1:A:12:TRP:CE3	1:A:24:ARG:HG2	2.42	0.55
1:B:52:ASN:HA	1:B:55:VAL:HG12	1.88	0.55
1:B:62:THR:O	1:B:66:GLN:OE1	2.23	0.55
1:A:19:VAL:CG2	1:A:183:LEU:HD13	2.37	0.55
1:A:293:THR:H	1:A:296:ALA:HB3	1.72	0.54
1:B:12:TRP:CZ2	1:B:24:ARG:HD3	2.43	0.54
1:B:322:PHE:CE2	1:B:326:ILE:HD11	2.42	0.54
1:A:240:ARG:O	1:A:242:ASN:N	2.40	0.54
1:B:12:TRP:CE2	1:B:24:ARG:HB3	2.43	0.54
1:B:60:THR:HG22	1:B:74:ILE:HD13	1.88	0.54
1:A:257:MET:HE3	1:A:261:LYS:HG3	1.90	0.54
1:B:87:ASN:HA	1:B:111:TYR:CE1	2.43	0.53
1:A:34:TYR:CD1	1:A:99:LYS:HG2	2.44	0.53
1:B:296:ALA:O	1:B:300:PRO:HG2	2.07	0.53
1:B:12:TRP:CH2	1:B:24:ARG:HD3	2.44	0.53
1:B:247:ARG:O	1:B:251:ALA:HB2	2.08	0.53
1:A:353:GLU:CD	1:A:354:ILE:H	2.11	0.53
1:B:26:PHE:CE1	1:B:293:THR:HG22	2.44	0.53
1:A:206:ILE:HA	1:A:210:PHE:CD2	2.44	0.53
1:A:330:PHE:N	1:A:331:PRO:CD	2.72	0.53
1:A:65:LEU:HD23	1:A:321:LYS:HB3	1.91	0.52
1:B:238:ALA:HA	1:B:246:LEU:HD13	1.91	0.52
1:A:224:VAL:O	1:A:227:VAL:HG23	2.10	0.52
1:A:69:ALA:HB3	3:A:1005:BOG:H2'2	1.91	0.52
1:A:276:PRO:HB2	7:A:510:HOH:O	2.10	0.52
1:A:37:LEU:HD22	1:A:302:MET:CE	2.39	0.52
1:A:345:GLU:HA	1:A:348:LYS:HD2	1.91	0.52
1:A:291:TRP:O	1:A:293:THR:HG23	2.09	0.52
1:A:52:ASN:HA	1:A:55:VAL:CG1	2.40	0.52
1:A:257:MET:HG3	1:A:261:LYS:HZ2	1.75	0.51
1:A:65:LEU:CD2	1:A:321:LYS:HB3	2.40	0.51
1:B:117:ILE:HD11	1:B:118:PHE:CE1	2.46	0.51
1:A:17:ILE:HD11	1:A:108:CYS:HB2	1.93	0.51
1:B:299:LEU:HB2	1:B:300:PRO:HD3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:LYS:NZ	1:B:353:GLU:HA	2.26	0.51
1:B:340:ASP:OD1	1:B:342:LYS:HB2	2.11	0.51
1:A:170:PRO:HB3	1:A:176:ALA:N	2.25	0.50
1:B:297:ALA:O	1:B:300:PRO:HD2	2.11	0.50
1:B:113:PHE:CZ	1:B:168:ILE:HD12	2.47	0.50
1:B:170:PRO:HB2	1:B:177:TYR:CD2	2.46	0.50
1:B:293:THR:HB	1:B:294:PRO:CD	2.41	0.50
1:A:206:ILE:HA	1:A:210:PHE:HD2	1.75	0.50
1:A:207:LEU:N	1:A:207:LEU:HD22	2.26	0.50
1:B:156:ILE:HG13	1:B:157:ILE:N	2.25	0.50
1:A:243:ALA:HB3	1:A:245:GLU:OE2	2.11	0.50
1:B:79:SER:HB2	1:B:121:MET:HE2	1.93	0.50
1:A:139:ARG:HB3	1:A:140:PRO:HD2	1.93	0.49
1:B:195:SER:HA	6:B:1004:PC1:H321	1.94	0.49
1:A:355:PRO:HD2	1:A:358:GLU:HG2	1.94	0.49
1:B:117:ILE:HD11	1:B:118:PHE:CZ	2.47	0.49
1:A:209:PHE:CE1	1:A:213:ILE:HD11	2.48	0.49
1:A:342:LYS:HA	1:A:345:GLU:HG3	1.94	0.49
1:B:124:MET:O	1:B:128:MET:HG2	2.12	0.49
1:A:324:GLU:HG3	1:A:339:PHE:HZ	1.77	0.49
1:A:132:ASP:O	1:A:136:VAL:HG12	2.13	0.49
1:B:293:THR:HB	1:B:294:PRO:HD2	1.93	0.49
1:B:325:ALA:O	1:B:329:THR:OG1	2.28	0.49
1:B:56:ILE:HD11	1:B:78:PHE:HA	1.94	0.49
1:A:11:TRP:CE3	1:A:11:TRP:O	2.66	0.48
1:B:29:VAL:HG23	1:B:33:VAL:HB	1.94	0.48
1:A:189:ASP:HA	7:A:517:HOH:O	2.13	0.48
1:A:255:ALA:O	1:A:259:LEU:HD23	2.13	0.48
1:A:283:LEU:O	1:A:287:GLY:N	2.40	0.48
1:B:137:ILE:C	1:B:139:ARG:H	2.16	0.48
1:A:114:ILE:HA	1:A:117:ILE:HG22	1.95	0.48
1:A:134:TYR:O	1:A:139:ARG:HG3	2.13	0.48
1:B:317:VAL:HG12	1:B:317:VAL:O	2.13	0.48
1:B:327:SER:O	1:B:331:PRO:HB3	2.14	0.48
1:A:297:ALA:O	1:A:300:PRO:HD2	2.14	0.48
1:A:23:TRP:HZ2	1:A:190:TYR:HH	1.60	0.48
1:A:219:CYS:O	1:A:223:ILE:HG13	2.14	0.48
1:B:35:TYR:O	1:B:39:ILE:HG12	2.14	0.48
1:B:137:ILE:HD11	1:B:256:GLU:CB	2.44	0.47
1:A:357:GLY:O	1:A:358:GLU:CB	2.62	0.47
1:B:29:VAL:CG2	1:B:33:VAL:HB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:ASP:OD1	1:B:133:ARG:NH1	2.46	0.47
1:A:37:LEU:HD22	1:A:302:MET:HE1	1.97	0.47
1:A:351:GLU:O	1:A:353:GLU:N	2.46	0.47
1:A:63:LYS:O	1:A:66:GLN:HB2	2.15	0.47
3:B:1005:BOG:H3'2	7:B:525:HOH:O	2.14	0.47
1:A:338:GLN:NE2	1:A:338:GLN:HA	2.29	0.47
1:B:10:THR:OG1	1:B:11:TRP:N	2.46	0.47
1:B:63:LYS:HA	1:B:66:GLN:NE2	2.29	0.47
1:A:198:ARG:O	1:A:202:LEU:HG	2.14	0.47
1:A:330:PHE:N	1:A:331:PRO:HD3	2.30	0.47
1:B:244:LYS:HD3	1:B:247:ARG:HB2	1.97	0.47
1:A:178:THR:OG1	1:A:179:LEU:N	2.48	0.46
1:A:293:THR:HB	1:A:294:PRO:HD2	1.96	0.46
1:A:168:ILE:O	1:A:171:ILE:HB	2.15	0.46
1:B:28:GLN:HE21	1:B:34:TYR:HE2	1.58	0.46
1:B:248:LYS:HZ2	1:B:353:GLU:HA	1.79	0.46
1:B:67:THR:O	1:B:70:ASN:HB2	2.14	0.46
1:B:133:ARG:NH2	1:B:136:VAL:HG21	2.31	0.46
1:A:27:ASP:OD2	1:B:9:GLU:O	2.34	0.46
1:A:62:THR:CG2	1:A:64:SER:OG	2.63	0.46
1:A:80:ASP:HB3	1:A:308:ALA:O	2.15	0.45
1:B:248:LYS:HE3	1:B:350:ALA:O	2.16	0.45
1:A:161:LEU:HD13	1:A:161:LEU:HA	1.63	0.45
1:A:210:PHE:O	1:A:213:ILE:HB	2.17	0.45
1:A:293:THR:HB	1:A:294:PRO:CD	2.46	0.45
1:B:105:PHE:O	1:B:109:LYS:HG3	2.16	0.45
1:B:29:VAL:HB	1:B:295:TYR:OH	2.16	0.45
1:A:348:LYS:O	1:A:352:THR:HG23	2.16	0.45
1:A:49:CYS:HA	1:A:81:PHE:CD1	2.51	0.45
1:B:301:VAL:O	1:B:305:LYS:HG3	2.16	0.45
1:A:263:SER:O	1:A:267:VAL:HG23	2.17	0.45
1:A:293:THR:H	1:A:296:ALA:CB	2.30	0.45
1:B:293:THR:H	1:B:296:ALA:HB3	1.82	0.45
1:A:11:TRP:O	1:A:11:TRP:HE3	1.99	0.45
1:A:140:PRO:O	1:A:143:ALA:N	2.42	0.45
1:B:150:ARG:CD	1:B:150:ARG:H	2.11	0.45
1:B:319:HIS:O	1:B:323:ARG:HG3	2.16	0.45
1:A:19:VAL:HG12	1:A:24:ARG:CG	2.47	0.45
1:A:209:PHE:O	1:A:213:ILE:HG13	2.16	0.45
1:A:205:PHE:HE1	1:A:278:ALA:HB1	1.82	0.44
1:A:288:PRO:HG2	1:A:291:TRP:CZ2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:MET:HG3	1:B:261:LYS:NZ	2.31	0.44
1:B:235:ALA:C	1:B:237:MET:H	2.21	0.44
1:A:258:ARG:O	1:A:262:ILE:HG13	2.17	0.44
1:A:160:TRP:O	1:A:164:VAL:HG23	2.17	0.44
1:A:16:SER:CB	1:A:104:GLY:HA2	2.48	0.44
1:A:124:MET:O	1:A:127:ALA:HB3	2.18	0.44
1:A:141:MET:HG3	1:A:233:GLU:OE1	2.18	0.44
1:A:103:PHE:O	1:A:107:ALA:HB3	2.18	0.44
1:A:52:ASN:O	1:A:56:ILE:HG13	2.18	0.44
1:B:39:ILE:O	1:B:43:ILE:HG13	2.18	0.44
1:A:229:ASN:N	1:A:229:ASN:HD22	2.16	0.44
1:A:60:THR:HG23	1:A:74:ILE:HD13	2.00	0.44
1:B:138:GLY:HA2	1:B:223:ILE:HA	2.00	0.44
1:A:269:GLN:NE2	1:A:307:SER:OG	2.38	0.43
1:A:266:ILE:HG22	1:A:314:ILE:HD12	2.00	0.43
1:B:56:ILE:O	1:B:60:THR:HG23	2.18	0.43
1:A:240:ARG:C	1:A:242:ASN:N	2.72	0.43
1:A:12:TRP:CD2	1:A:24:ARG:HG2	2.52	0.43
1:A:28:GLN:HG3	1:A:34:TYR:OH	2.18	0.43
1:B:263:SER:O	1:B:266:ILE:HG12	2.18	0.43
1:A:319:HIS:HB3	1:A:322:PHE:HB3	1.99	0.43
1:B:174:TRP:CD1	1:B:200:ASN:HB2	2.53	0.43
1:A:216:ILE:HG23	1:A:220:TYR:CE2	2.52	0.43
1:A:243:ALA:C	1:A:245:GLU:H	2.22	0.43
1:A:237:MET:O	1:A:240:ARG:HB3	2.19	0.43
1:A:357:GLY:O	1:A:358:GLU:HB2	2.18	0.43
1:B:117:ILE:HG22	1:B:167:ALA:HB3	2.01	0.43
1:B:79:SER:HB2	1:B:121:MET:CE	2.49	0.43
1:A:273:SER:HB3	1:A:307:SER:HB2	2.01	0.43
1:B:117:ILE:HD12	1:B:117:ILE:C	2.38	0.43
1:B:117:ILE:HG22	1:B:167:ALA:CB	2.49	0.43
1:A:137:ILE:HD11	1:A:256:GLU:CB	2.45	0.43
1:B:141:MET:HA	1:B:141:MET:HE3	1.99	0.43
1:B:209:PHE:O	1:B:212:PRO:HG2	2.18	0.43
1:B:31:ASP:HB3	1:B:35:TYR:CE1	2.54	0.43
1:A:263:SER:O	1:A:266:ILE:HG12	2.19	0.43
1:B:86:VAL:HG21	1:B:114:ILE:HG21	2.01	0.43
1:A:220:TYR:OH	1:A:263:SER:HB3	2.19	0.43
1:B:51:GLY:O	1:B:55:VAL:HG12	2.19	0.43
1:A:355:PRO:HG2	1:A:358:GLU:HA	2.00	0.42
1:B:223:ILE:O	1:B:224:VAL:C	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:324:GLU:HG3	1:B:339:PHE:CE2	2.53	0.42
1:B:242:ASN:OD1	1:B:246:LEU:HD13	2.19	0.42
1:A:339:PHE:CG	1:A:340:ASP:N	2.87	0.42
1:A:341:ASP:N	1:A:341:ASP:OD2	2.52	0.42
1:A:52:ASN:O	1:A:55:VAL:HG13	2.19	0.42
1:A:60:THR:CG2	1:A:74:ILE:HD13	2.50	0.42
1:B:209:PHE:CE1	4:B:1000:RET:H31	2.55	0.42
1:A:294:PRO:O	1:A:298:GLN:HB2	2.20	0.42
1:A:334:LEU:HD13	1:A:339:PHE:HB2	2.00	0.42
1:A:349:ASP:HA	1:A:352:THR:OG1	2.19	0.42
1:B:117:ILE:HG13	1:B:118:PHE:N	2.35	0.42
1:B:340:ASP:OD2	1:B:341:ASP:N	2.51	0.42
1:B:228:SER:O	1:B:231:GLU:HG2	2.19	0.42
1:A:187:SER:HA	4:A:1000:RET:H203	2.00	0.42
1:A:62:THR:HG22	1:A:64:SER:OG	2.20	0.42
1:B:133:ARG:NH2	1:B:256:GLU:OE1	2.53	0.42
1:B:127:ALA:O	1:B:131:ILE:HG13	2.20	0.42
1:B:294:PRO:O	1:B:298:GLN:HB2	2.20	0.42
1:A:242:ASN:HD22	1:A:242:ASN:HA	1.68	0.42
1:A:29:VAL:HG21	1:A:182:VAL:HG11	2.02	0.42
1:B:229:ASN:O	1:B:233:GLU:HG3	2.19	0.42
1:B:28:GLN:NE2	1:B:34:TYR:OH	2.52	0.42
1:B:298:GLN:O	1:B:302:MET:HG2	2.19	0.42
1:A:279:VAL:O	1:A:283:LEU:HD13	2.20	0.41
1:A:39:ILE:O	1:A:43:ILE:HG13	2.19	0.41
1:B:145:LYS:HD3	1:B:151:ARG:CZ	2.50	0.41
1:B:216:ILE:HG23	1:B:220:TYR:CE2	2.55	0.41
1:A:17:ILE:HD13	1:A:108:CYS:SG	2.60	0.41
1:A:121:MET:HG3	1:A:159:VAL:HG12	2.02	0.41
1:A:252:GLY:O	1:A:256:GLU:HG2	2.20	0.41
1:B:11:TRP:CE3	1:B:28:GLN:OE1	2.73	0.41
1:B:123:ILE:HG12	1:B:270:PHE:CZ	2.56	0.41
1:A:62:THR:HG22	1:A:64:SER:H	1.85	0.41
1:A:243:ALA:C	1:A:245:GLU:N	2.73	0.41
1:B:12:TRP:CE3	1:B:13:TYR:HA	2.56	0.41
1:B:269:GLN:HE21	1:B:310:HIS:HD2	1.68	0.41
1:A:123:ILE:HG12	1:A:270:PHE:CZ	2.56	0.41
1:B:299:LEU:N	1:B:300:PRO:CD	2.84	0.41
1:B:235:ALA:O	1:B:239:LYS:HE3	2.20	0.40
1:B:41:ILE:HA	1:B:41:ILE:HD12	1.99	0.40
1:A:117:ILE:HG23	1:A:118:PHE:CD1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:THR:O	1:A:129:ILE:HG13	2.21	0.40
1:A:344:THR:O	1:A:348:LYS:HG3	2.22	0.40
1:B:269:GLN:NE2	1:B:310:HIS:HD2	2.19	0.40
1:B:30:PRO:O	1:B:31:ASP:C	2.60	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	348/448 (78%)	308 (88%)	33 (10%)	7 (2%)	9	28
1	B	345/448 (77%)	317 (92%)	24 (7%)	4 (1%)	15	44
All	All	693/896 (77%)	625 (90%)	57 (8%)	11 (2%)	11	36

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	241	LEU
1	A	243	ALA
1	A	292	VAL
1	B	138	GLY
1	A	352	THR
1	B	226	SER
1	A	335	THR
1	A	141	MET
1	A	331	PRO
1	B	320	PRO
1	B	223	ILE

### 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	296/369 (80%)	275 (93%)	21 (7%)	17	44
1	B	295/369 (80%)	272 (92%)	23 (8%)	15	39
All	All	591/738 (80%)	547 (93%)	44 (7%)	16	42

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	SER
1	A	55	VAL
1	A	58	LEU
1	A	63	LYS
1	A	65	LEU
1	A	76	LEU
1	A	85	LEU
1	A	90	PRO
1	A	105	PHE
1	A	123	ILE
1	A	150	ARG
1	A	190	TYR
1	A	192	SER
1	A	193	ARG
1	A	234	MET
1	A	242	ASN
1	A	294	PRO
1	A	337	CYS
1	A	338	GLN
1	A	346	ASP
1	A	358	GLU
1	B	10	THR
1	B	29	VAL
1	B	63	LYS
1	B	66	GLN
1	B	67	THR
1	B	76	LEU

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Mol	Chain	Res	Type
1	B	85	LEU
1	B	102	ILE
1	B	105	PHE
1	B	117	ILE
1	B	123	ILE
1	B	133	ARG
1	B	150	ARG
1	B	225	MET
1	B	240	ARG
1	B	242	ASN
1	B	245	GLU
1	B	247	ARG
1	B	329	THR
1	B	335	THR
1	B	337	CYS
1	B	349	ASP
1	B	354	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	87	ASN
1	A	229	ASN
1	A	254	ASN
1	A	269	GLN
1	A	285	GLN
1	A	328	GLN
1	A	338	GLN
1	B	28	GLN
1	B	70	ASN
1	B	222	ASN
1	B	269	GLN
1	B	328	GLN

### 5.3.3 RNA ⓘ

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	1.83	2 (10%)	27,27,28	1.76	6 (22%)
2	PLM	A	1001	-	16,16,17	0.38	0	15,15,17	0.69	0
3	BOG	A	1005	-	20,20,20	1.74	4 (20%)	25,25,25	2.65	10 (40%)
4	RET	B	1000	1	19,20,21	1.93	4 (21%)	27,27,28	2.04	8 (29%)
6	PC1	B	1004	-	38,38,53	1.86	4 (10%)	40,43,61	1.02	2 (5%)
3	BOG	B	1005	-	20,20,20	1.77	5 (25%)	25,25,25	2.70	10 (40%)
5	SO4	B	449	-	4,4,4	0.41	0	6,6,6	0.25	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

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1000	RET	C2-C3	-3.74	1.42	1.52
4	B	1000	RET	C2-C3	-3.57	1.43	1.52
3	B	1005	BOG	C4-C5	-2.95	1.46	1.53
4	B	1000	RET	C8-C9	-2.40	1.40	1.45
6	B	1004	PC1	O31-C3	2.01	1.49	1.45
3	B	1005	BOG	C4-C3	2.03	1.57	1.52
6	B	1004	PC1	C1-C2	2.09	1.56	1.50
3	B	1005	BOG	O6-C6	2.34	1.52	1.42
3	A	1005	BOG	C6-C5	2.50	1.60	1.51
3	A	1005	BOG	O6-C6	2.72	1.53	1.42
3	B	1005	BOG	O2-C2	2.86	1.49	1.43
3	A	1005	BOG	O2-C2	3.00	1.49	1.43
4	B	1000	RET	C5-C6	3.77	1.40	1.34
3	B	1005	BOG	O5-C1	4.01	1.51	1.41
3	A	1005	BOG	O5-C1	4.01	1.51	1.41
6	B	1004	PC1	O31-C31	5.13	1.48	1.33
4	B	1000	RET	C1-C6	5.25	1.61	1.53
4	A	1000	RET	C1-C6	6.25	1.62	1.53
6	B	1004	PC1	O21-C21	8.18	1.58	1.34

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1005	BOG	C1'-O1-C1	-8.34	99.56	113.87
3	B	1005	BOG	C1'-O1-C1	-7.88	100.34	113.87
4	B	1000	RET	C8-C9-C10	-6.31	109.25	118.94
4	A	1000	RET	C8-C9-C10	-5.15	111.04	118.94
3	B	1005	BOG	C1-C2-C3	-4.98	100.73	109.98
3	A	1005	BOG	C1-C2-C3	-4.60	101.43	109.98
3	B	1005	BOG	O3-C3-C2	-3.80	102.08	110.36
3	A	1005	BOG	O5-C5-C4	-3.69	102.86	109.66
3	B	1005	BOG	O1-C1-C2	-3.67	102.25	108.23
3	A	1005	BOG	O3-C3-C2	-3.49	102.77	110.36
3	B	1005	BOG	O5-C5-C4	-3.42	103.36	109.66
4	B	1000	RET	C7-C8-C9	-3.37	121.14	126.21
3	A	1005	BOG	O1-C1-C2	-3.29	102.87	108.23
3	B	1005	BOG	C6'-C5'-C4'	-2.95	99.28	114.45
4	A	1000	RET	C10-C11-C12	-2.91	114.30	123.23
3	B	1005	BOG	O4-C4-C5	-2.79	102.24	109.28
3	A	1005	BOG	O4-C4-C5	-2.48	103.03	109.28
3	A	1005	BOG	C4'-C3'-C2'	-2.41	102.05	114.45
3	B	1005	BOG	C4'-C3'-C2'	-2.41	102.05	114.45

*Continued on next page...*

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1005	BOG	C3'-C2'-C1'	-2.38	102.76	113.48
3	A	1005	BOG	C6'-C5'-C4'	-2.32	102.49	114.45
4	A	1000	RET	C8-C7-C6	-2.24	120.99	127.25
3	B	1005	BOG	O1-C1'-C2'	-2.21	101.81	109.68
3	B	1005	BOG	C3'-C2'-C1'	-2.20	103.58	113.48
4	B	1000	RET	C11-C10-C9	-2.19	124.19	127.31
4	B	1000	RET	C1-C6-C7	-2.06	109.95	115.73
4	A	1000	RET	C18-C5-C6	2.01	126.76	124.51
3	A	1005	BOG	O2-C2-C1	2.01	114.24	110.03
4	B	1000	RET	C2-C3-C4	2.04	116.20	111.34
6	B	1004	PC1	C2-O21-C21	2.14	122.94	117.88
4	B	1000	RET	C7-C6-C5	2.53	127.56	121.54
6	B	1004	PC1	O21-C21-C22	2.90	117.58	111.55
4	A	1000	RET	C11-C10-C9	2.98	131.56	127.31
4	B	1000	RET	C19-C9-C10	3.20	127.40	122.92
4	B	1000	RET	C18-C5-C6	3.26	128.15	124.51
4	A	1000	RET	C19-C9-C10	3.28	127.51	122.92

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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	350/448 (78%)	0.03	12 (3%) 46 34	28, 54, 115, 135	0
1	B	347/448 (77%)	0.10	12 (3%) 44 33	29, 49, 95, 124	0
All	All	697/896 (77%)	0.07	24 (3%) 46 34	28, 52, 108, 135	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	246	LEU	4.7
1	B	241	LEU	4.3
1	B	238	ALA	4.0
1	B	239	LYS	4.0
1	A	241	LEU	3.9
1	B	236	ALA	3.6
1	A	248	LYS	3.2
1	A	240	ARG	3.2
1	A	234	MET	3.1
1	B	232	LYS	3.0
1	B	237	MET	3.0
1	B	234	MET	2.9
1	B	229	ASN	2.8
1	B	233	GLU	2.7
1	B	240	ARG	2.6
1	A	236	ALA	2.6
1	B	230	HIS	2.5
1	B	246	LEU	2.4
1	A	242	ASN	2.3
1	A	153	PHE	2.3
1	A	244	LYS	2.2
1	A	245	GLU	2.2
1	A	150	ARG	2.1
1	A	249	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 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	PLM	A	1001	17/18	0.85	0.34	5.54	45,66,73,74	0
6	PC1	B	1004	39/54	0.82	0.36	5.29	44,65,119,120	0
3	BOG	B	1005	20/20	0.81	0.38	2.28	70,109,111,112	0
4	RET	A	1000	20/21	0.95	0.25	1.61	30,45,51,53	0
3	BOG	A	1005	20/20	0.87	0.32	1.54	50,92,97,100	0
5	SO4	B	449	5/5	0.95	0.22	0.83	85,86,87,88	0
4	RET	B	1000	20/21	0.96	0.18	-0.45	20,24,31,37	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.