



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:28 PM GMT

PDB ID : 1KGB  
Title : structure of ground-state bacteriorhodopsin  
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Deposited on : 2001-11-26  
Resolution : 1.65 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 (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

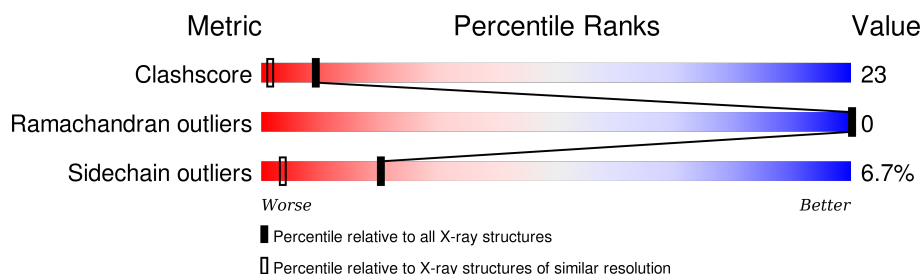
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.65 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	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	231	

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
3	LI1	A	601	X	-	-	-
3	LI1	A	611	X	-	-	-
3	LI1	A	613	X	-	-	-

## 2 Entry composition [i](#)

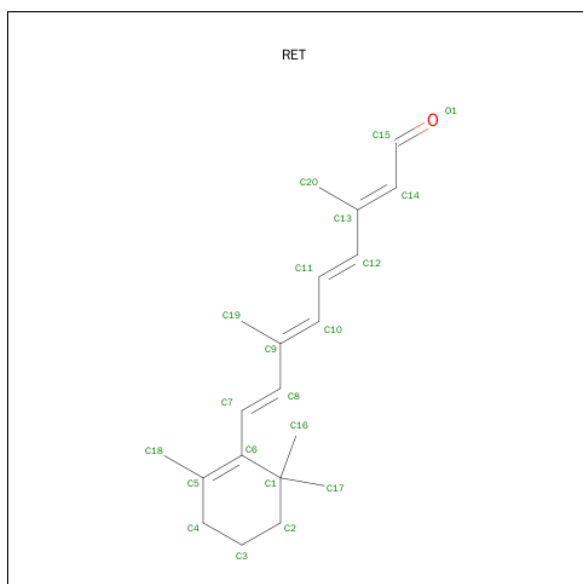
There are 4 unique types of molecules in this entry. The entry contains 2050 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 bacteriorhodopsin.

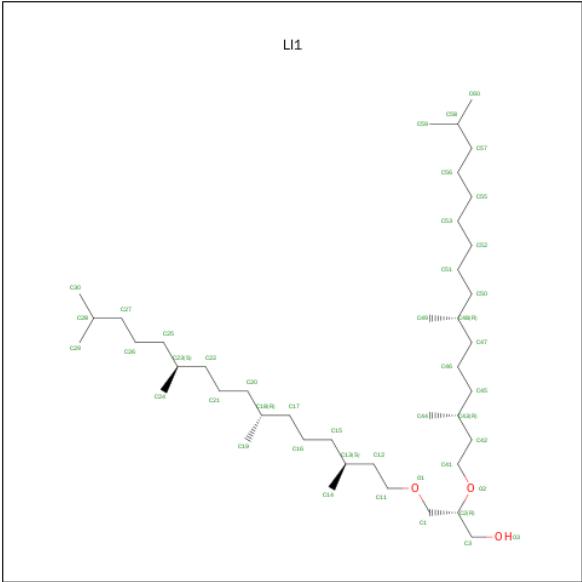
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	0	0
			1720	1159	262	290	9			

- Molecule 2 is RETINAL (three-letter code: RET) (formula: C<sub>20</sub>H<sub>28</sub>O).



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

- Molecule 3 is 1-[2,6,10,14-TETRAMETHYL-HEXADECAN-16-YL]-2-[2,10,14-TRIMETHYLHEXADECAN-16-YL]GLYCEROL (three-letter code: LI1) (formula: C<sub>42</sub>H<sub>86</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 32 29 3	0	0
3	A	1	Total C O 41 38 3	0	0
3	A	1	Total C 16 16	0	0
3	A	1	Total C O 40 37 3	0	0
3	A	1	Total C 17 17	0	0
3	A	1	Total C 18 18	0	0
3	A	1	Total C 18 18	0	0
3	A	1	Total C 13 13	0	0
3	A	1	Total C 16 16	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C 8 8	0	0
3	A	1	Total C O 38 35 3	0	0
3	A	1	Total C 18 18	0	0

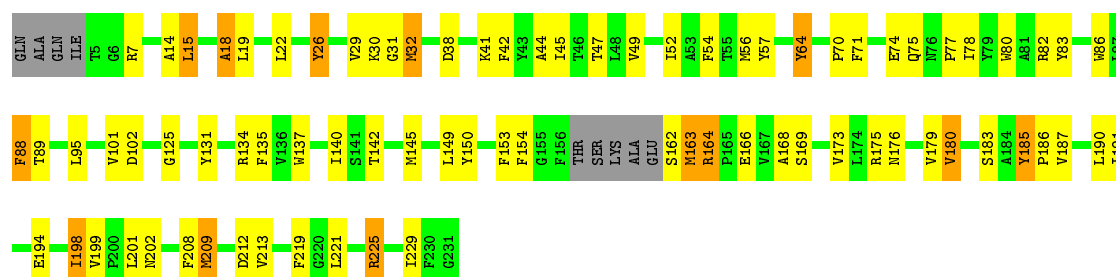
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	27	Total	O	0	0
			27	27		



Note EDS was not executed.

- Chain A:  61% 29% 6% .



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.99Å 60.99Å 109.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.65	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.65)	Depositor
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.130 , 0.188	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2050	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	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: LI1, RET

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	0.88	2/1767 (0.1%)	2.07	72/2413 (3.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	80	TRP	NE1-CE2	-5.12	1.30	1.37
1	A	137	TRP	CG-CD1	-5.03	1.29	1.36

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	83	TYR	CB-CG-CD1	-15.91	111.45	121.00
1	A	57	TYR	CB-CG-CD1	-12.35	113.59	121.00
1	A	83	TYR	CG-CD1-CE1	-12.13	111.59	121.30
1	A	82	ARG	NE-CZ-NH2	-11.84	114.38	120.30
1	A	82	ARG	NE-CZ-NH1	-11.38	114.61	120.30
1	A	7	ARG	NE-CZ-NH1	11.23	125.92	120.30
1	A	137	TRP	CE3-CZ3-CH2	-10.89	109.22	121.20
1	A	83	TYR	CB-CG-CD2	10.77	127.46	121.00
1	A	82	ARG	NH1-CZ-NH2	10.55	131.00	119.40
1	A	88	PHE	CB-CG-CD1	-9.88	113.89	120.80
1	A	164	ARG	NE-CZ-NH1	9.32	124.96	120.30
1	A	57	TYR	CD1-CG-CD2	9.08	127.89	117.90
1	A	219	PHE	CB-CG-CD1	8.87	127.01	120.80
1	A	57	TYR	CD1-CE1-CZ	-8.71	111.96	119.80
1	A	137	TRP	CZ3-CH2-CZ2	8.57	131.88	121.60
1	A	137	TRP	CD2-CE2-CZ2	-8.41	112.21	122.30
1	A	82	ARG	CD-NE-CZ	-8.35	111.92	123.60
1	A	57	TYR	CG-CD2-CE2	-8.24	114.71	121.30
1	A	135	PHE	CB-CG-CD1	-8.06	115.16	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	THR	CA-C-O	8.04	136.99	120.10
1	A	135	PHE	CB-CG-CD2	7.77	126.24	120.80
1	A	80	TRP	CE3-CZ3-CH2	-7.54	112.91	121.20
1	A	83	TYR	CD1-CE1-CZ	7.48	126.53	119.80
1	A	219	PHE	CZ-CE2-CD2	7.43	129.01	120.10
1	A	175	ARG	NE-CZ-NH2	-7.42	116.59	120.30
1	A	208	PHE	CG-CD1-CE1	-7.42	112.64	120.80
1	A	212	ASP	CB-CG-OD1	-7.25	111.77	118.30
1	A	88	PHE	CG-CD1-CE1	-7.21	112.86	120.80
1	A	175	ARG	NE-CZ-NH1	7.17	123.88	120.30
1	A	83	TYR	CZ-CE2-CD2	-7.13	113.39	119.80
1	A	145	MET	CA-CB-CG	-7.05	101.32	113.30
1	A	137	TRP	CE2-CD2-CG	-6.96	101.73	107.30
1	A	7	ARG	NE-CZ-NH2	-6.83	116.89	120.30
1	A	57	TYR	CE1-CZ-CE2	6.74	130.59	119.80
1	A	18	ALA	O-C-N	-6.54	112.24	122.70
1	A	150	TYR	CB-CG-CD2	6.53	124.92	121.00
1	A	137	TRP	NE1-CE2-CD2	6.46	113.75	107.30
1	A	208	PHE	CD1-CG-CD2	6.38	126.60	118.30
1	A	135	PHE	CG-CD2-CE2	6.36	127.79	120.80
1	A	135	PHE	CZ-CE2-CD2	-6.33	112.50	120.10
1	A	137	TRP	CE2-CD2-CE3	6.28	126.24	118.70
1	A	208	PHE	CZ-CE2-CD2	-6.26	112.59	120.10
1	A	137	TRP	CD1-NE1-CE2	-6.22	103.41	109.00
1	A	88	PHE	CD1-CG-CD2	6.17	126.32	118.30
1	A	208	PHE	CB-CG-CD1	-6.16	116.49	120.80
1	A	185	TYR	CB-CG-CD2	-6.15	117.31	121.00
1	A	164	ARG	CD-NE-CZ	6.04	132.06	123.60
1	A	142	THR	O-C-N	-5.90	113.27	122.70
1	A	83	TYR	CG-CD2-CE2	5.87	125.99	121.30
1	A	219	PHE	CG-CD1-CE1	5.86	127.25	120.80
1	A	134	ARG	O-C-N	-5.79	113.44	122.70
1	A	86	TRP	CG-CD2-CE3	5.78	139.10	133.90
1	A	47	THR	O-C-N	-5.77	113.47	122.70
1	A	80	TRP	CA-C-O	5.68	132.04	120.10
1	A	14	ALA	O-C-N	-5.65	113.66	122.70
1	A	64	TYR	CZ-CE2-CD2	-5.64	114.72	119.80
1	A	80	TRP	CZ3-CH2-CZ2	5.60	128.32	121.60
1	A	208	PHE	CB-CG-CD2	-5.57	116.90	120.80
1	A	213	VAL	O-C-N	-5.50	113.90	122.70
1	A	71	PHE	CB-CG-CD1	5.46	124.62	120.80
1	A	54	PHE	CB-CG-CD1	5.42	124.59	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	VAL	O-C-N	-5.38	114.09	122.70
1	A	212	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	86	TRP	CE2-CD2-CE3	-5.29	112.36	118.70
1	A	64	TYR	CB-CG-CD1	-5.28	117.83	121.00
1	A	209	MET	CG-SD-CE	-5.25	91.81	100.20
1	A	86	TRP	CH2-CZ2-CE2	5.20	122.60	117.40
1	A	26	TYR	O-C-N	-5.19	114.40	122.70
1	A	125	GLY	O-C-N	-5.14	114.48	122.70
1	A	54	PHE	CZ-CE2-CD2	5.10	126.22	120.10
1	A	31	GLY	O-C-N	5.10	130.86	122.70
1	A	183	SER	O-C-N	-5.02	114.67	122.70

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	1720	0	1776	67	0
2	A	20	0	27	1	0
3	A	283	0	457	68	0
4	A	27	0	0	4	0
All	All	2050	0	2260	98	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 23.

All (98) 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:149:LEU:HD22	1:A:179:VAL:HG22	1.38	1.02
1:A:154:PHE:HZ	3:A:609:LI1:H152	1.44	0.83
1:A:198:ILE:HG22	1:A:199:VAL:HG23	1.64	0.80
3:A:601:LI1:H302	3:A:608:LI1:H303	1.63	0.79
1:A:88:PHE:HB2	4:A:515:HOH:O	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:TYR:HD1	3:A:611:LI1:H152	1.47	0.78
1:A:89:THR:HG23	4:A:515:HOH:O	1.84	0.77
1:A:18:ALA:HA	3:A:606:LI1:H211	1.69	0.74
1:A:52:ILE:HG21	4:A:515:HOH:O	1.88	0.74
1:A:131:TYR:OH	3:A:602:LI1:H162	1.88	0.73
1:A:18:ALA:O	1:A:22:LEU:HD13	1.88	0.72
1:A:64:TYR:OH	3:A:607:LI1:H32	1.90	0.71
1:A:164:ARG:HE	1:A:166:GLU:HG3	1.55	0.70
3:A:602:LI1:H151	3:A:602:LI1:H443	1.74	0.70
1:A:29:VAL:O	1:A:32:MET:HB2	1.93	0.69
1:A:153:PHE:HE2	1:A:179:VAL:HG21	1.58	0.67
1:A:140:ILE:HG13	3:A:601:LI1:H272	1.75	0.67
1:A:190:LEU:HD23	3:A:603:LI1:H222	1.77	0.66
3:A:602:LI1:H593	3:A:608:LI1:H302	1.78	0.64
1:A:153:PHE:CE2	1:A:179:VAL:HG21	2.33	0.64
1:A:180:VAL:HG21	3:A:610:LI1:H521	1.79	0.63
3:A:610:LI1:H411	3:A:610:LI1:H122	1.80	0.63
1:A:26:TYR:CE1	3:A:611:LI1:H121	2.34	0.63
1:A:164:ARG:HG3	1:A:166:GLU:HG3	1.81	0.63
1:A:26:TYR:CD1	3:A:611:LI1:H152	2.33	0.61
1:A:187:VAL:HG21	3:A:610:LI1:H293	1.84	0.59
1:A:131:TYR:OH	3:A:602:LI1:H13	2.04	0.58
1:A:169:SER:O	1:A:173:VAL:HG23	2.03	0.58
3:A:610:LI1:H593	3:A:610:LI1:H303	1.85	0.57
1:A:140:ILE:CG1	3:A:601:LI1:H272	2.35	0.57
3:A:609:LI1:C28	3:A:603:LI1:H293	2.36	0.56
1:A:131:TYR:CE2	3:A:602:LI1:H13	2.41	0.56
3:A:602:LI1:H161	3:A:603:LI1:H141	1.88	0.56
1:A:221:LEU:O	1:A:225:ARG:HG2	2.05	0.56
3:A:610:LI1:H122	3:A:610:LI1:C41	2.36	0.55
1:A:202:ASN:H	1:A:202:ASN:HD22	1.54	0.55
1:A:15:LEU:HB3	1:A:209:MET:HE2	1.88	0.55
1:A:154:PHE:CZ	3:A:609:LI1:H152	2.33	0.54
1:A:131:TYR:CE2	3:A:602:LI1:H112	2.43	0.54
1:A:153:PHE:HE1	3:A:610:LI1:H112	1.72	0.53
1:A:180:VAL:HG11	3:A:610:LI1:H551	1.91	0.53
1:A:164:ARG:HE	1:A:166:GLU:CG	2.22	0.53
3:A:610:LI1:H272	3:A:610:LI1:H58	1.90	0.52
3:A:602:LI1:C15	3:A:602:LI1:H443	2.40	0.52
1:A:176:ASN:OD1	3:A:610:LI1:H121	2.09	0.52
1:A:180:VAL:CG2	3:A:610:LI1:H521	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:TYR:HE2	3:A:602:LI1:H112	1.75	0.50
1:A:164:ARG:CG	1:A:166:GLU:HG3	2.41	0.50
2:A:301:RET:H171	2:A:301:RET:H8	1.93	0.50
3:A:602:LI1:C44	3:A:602:LI1:H172	2.43	0.49
1:A:30:LYS:HE3	1:A:225:ARG:HD3	1.95	0.49
1:A:176:ASN:ND2	3:A:610:LI1:H412	2.28	0.48
3:A:610:LI1:H251	3:A:610:LI1:H562	1.96	0.48
1:A:56:MET:CE	3:A:607:LI1:H512	2.44	0.48
3:A:612:LI1:H143	4:A:512:HOH:O	2.13	0.48
1:A:180:VAL:HG13	3:A:610:LI1:H562	1.96	0.47
1:A:26:TYR:CD1	3:A:611:LI1:H121	2.48	0.47
3:A:610:LI1:C59	3:A:610:LI1:H303	2.44	0.47
3:A:608:LI1:H162	3:A:608:LI1:H193	1.71	0.47
3:A:603:LI1:H262	3:A:603:LI1:H303	1.50	0.47
3:A:610:LI1:C46	3:A:610:LI1:H152	2.45	0.46
1:A:164:ARG:NE	1:A:166:GLU:HG3	2.27	0.46
1:A:198:ILE:HD11	3:A:603:LI1:H151	1.97	0.46
3:A:602:LI1:H443	3:A:602:LI1:H172	1.97	0.46
3:A:602:LI1:H422	3:A:602:LI1:H2	1.43	0.46
3:A:607:LI1:H12	3:A:607:LI1:H122	1.59	0.46
1:A:154:PHE:CE1	3:A:609:LI1:H121	2.50	0.46
1:A:153:PHE:CE1	3:A:610:LI1:H112	2.51	0.45
1:A:22:LEU:HD11	3:A:611:LI1:C27	2.47	0.45
3:A:601:LI1:H191	3:A:601:LI1:H211	1.71	0.45
3:A:608:LI1:H262	3:A:608:LI1:H292	1.35	0.45
1:A:131:TYR:CZ	3:A:602:LI1:H13	2.53	0.44
1:A:45:ILE:O	1:A:49:VAL:HG23	2.18	0.44
1:A:190:LEU:CD2	3:A:603:LI1:H222	2.47	0.44
3:A:611:LI1:H262	3:A:611:LI1:H241	1.65	0.44
3:A:602:LI1:H593	3:A:608:LI1:C30	2.47	0.43
3:A:601:LI1:H152	3:A:601:LI1:O1	2.00	0.43
1:A:190:LEU:HD21	3:A:603:LI1:H202	2.00	0.43
1:A:70:PRO:HG2	1:A:70:PRO:O	2.19	0.43
1:A:154:PHE:CZ	3:A:609:LI1:H121	2.53	0.43
1:A:163:MET:HG3	1:A:168:ALA:HB2	1.99	0.43
1:A:190:LEU:CD2	3:A:603:LI1:H202	2.49	0.43
1:A:78:ILE:HD12	1:A:194:GLU:HG3	2.01	0.43
1:A:198:ILE:HD11	3:A:603:LI1:C15	2.49	0.42
1:A:42:PHE:CD2	1:A:229:ILE:HB	2.53	0.42
3:A:613:LI1:H191	3:A:613:LI1:H211	1.72	0.42
1:A:176:ASN:CG	3:A:610:LI1:H412	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ALA:HA	3:A:612:LI1:H13	2.01	0.42
1:A:77:PRO:HG2	1:A:201:LEU:HD22	2.02	0.42
1:A:56:MET:HE3	3:A:607:LI1:H512	2.01	0.42
1:A:185:TYR:N	1:A:186:PRO:HD2	2.35	0.41
1:A:101:VAL:O	1:A:102:ASP:HB3	2.20	0.41
3:A:602:LI1:H262	3:A:602:LI1:H241	1.78	0.41
3:A:607:LI1:H462	3:A:607:LI1:H441	1.48	0.41
1:A:202:ASN:H	1:A:202:ASN:ND2	2.17	0.41
3:A:613:LI1:H202	3:A:613:LI1:H162	1.53	0.41
1:A:15:LEU:HD22	1:A:19:LEU:CD1	2.51	0.40
3:A:610:LI1:H292	3:A:610:LI1:H261	1.65	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	218/231 (94%)	212 (97%)	6 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	178/185 (96%)	166 (93%)	12 (7%)	20 3

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	LEU
1	A	32	MET
1	A	38	ASP
1	A	41	LYS
1	A	74	GLU
1	A	75	GLN
1	A	95	LEU
1	A	162	SER
1	A	163	MET
1	A	191	ILE
1	A	198	ILE
1	A	225	ARG

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	105	GLN
1	A	202	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

14 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	RET	A	301	1	19,20,21	1.34	4 (21%)	27,27,28	2.48	11 (40%)
3	LI1	A	601	-	31,31,44	0.83	1 (3%)	33,33,51	1.13	3 (9%)
3	LI1	A	602	-	40,40,44	0.74	1 (2%)	41,45,51	1.04	0
3	LI1	A	603	-	17,17,44	0.50	0	18,18,51	1.06	0
3	LI1	A	604	-	15,15,44	0.53	0	14,14,51	1.13	0
3	LI1	A	605	-	7,7,44	0.49	0	6,6,51	0.81	0
3	LI1	A	606	-	7,7,44	0.47	0	6,6,51	0.78	0
3	LI1	A	607	-	37,37,44	0.72	1 (2%)	36,38,51	1.16	2 (5%)
3	LI1	A	608	-	17,17,44	0.50	0	18,18,51	1.15	0
3	LI1	A	609	-	15,15,44	0.51	0	14,14,51	0.98	0
3	LI1	A	610	-	39,39,44	0.74	1 (2%)	41,41,51	1.01	0
3	LI1	A	611	-	16,16,44	0.46	0	17,18,51	1.19	2 (11%)
3	LI1	A	612	-	17,17,44	0.51	0	18,18,51	0.95	0
3	LI1	A	613	-	12,12,44	0.50	0	12,12,51	1.62	2 (16%)

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	RET	A	301	1	-	0/13/30/31	0/1/1/1
3	LI1	A	601	-	2/2/3/8	0/32/32/49	0/0/0/0
3	LI1	A	602	-	-	0/44/44/49	0/0/0/0
3	LI1	A	603	-	-	0/16/16/49	0/0/0/0
3	LI1	A	604	-	-	0/13/13/49	0/0/0/0
3	LI1	A	605	-	-	0/5/5/49	0/0/0/0
3	LI1	A	606	-	-	0/5/5/49	0/0/0/0
3	LI1	A	607	-	-	0/38/38/49	0/0/0/0
3	LI1	A	608	-	-	0/16/16/49	0/0/0/0
3	LI1	A	609	-	-	0/13/13/49	0/0/0/0
3	LI1	A	610	-	-	0/39/39/49	0/0/0/0
3	LI1	A	611	-	1/1/3/8	0/17/17/49	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	LI1	A	612	-	-	0/16/16/49	0/0/0/0
3	LI1	A	613	-	1/1/1/8	0/11/11/49	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	RET	C20-C13	-2.64	1.45	1.50
2	A	301	RET	C5-C6	2.05	1.37	1.34
2	A	301	RET	C11-C12	2.06	1.39	1.34
2	A	301	RET	C17-C1	2.27	1.58	1.53
3	A	607	LI1	O3-C3	2.66	1.53	1.42
3	A	602	LI1	O3-C3	2.73	1.54	1.42
3	A	610	LI1	O3-C3	2.80	1.54	1.42
3	A	601	LI1	O3-C3	2.90	1.54	1.42

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	RET	C11-C10-C9	-3.99	121.44	127.20
3	A	613	LI1	C16-C17-C18	-3.82	102.83	115.49
2	A	301	RET	C10-C11-C12	-3.80	111.54	123.13
2	A	301	RET	C11-C12-C13	-3.19	116.93	126.32
2	A	301	RET	C8-C9-C10	-3.15	113.91	118.98
3	A	613	LI1	C21-C20-C18	-3.11	105.17	115.49
2	A	301	RET	C12-C13-C14	-3.10	108.84	118.92
2	A	301	RET	C4-C5-C6	-2.89	119.10	122.78
3	A	611	LI1	C16-C17-C18	-2.78	106.28	115.49
3	A	607	LI1	C46-C45-C43	-2.49	107.22	115.49
3	A	601	LI1	C16-C17-C18	-2.41	107.48	115.49
3	A	601	LI1	C21-C20-C18	-2.20	108.20	115.49
3	A	601	LI1	O3-C3-C2	-2.07	105.61	111.66
3	A	611	LI1	C21-C20-C18	-2.01	108.82	115.49
3	A	607	LI1	O1-C1-C2	2.09	112.24	108.71
2	A	301	RET	C1-C6-C7	2.40	122.53	115.82
2	A	301	RET	C17-C1-C6	2.59	114.37	110.30
2	A	301	RET	C2-C1-C6	4.02	116.73	110.36
2	A	301	RET	C19-C9-C8	4.66	125.85	118.10
2	A	301	RET	C20-C13-C12	4.90	126.25	118.10

All (4) chirality outliers are listed below:



Mol	Chain	Res	Type	Atom
3	A	611	LI1	C13
3	A	601	LI1	C2
3	A	601	LI1	C18
3	A	613	LI1	C18

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 69 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	RET	1	0
3	A	601	LI1	5	0
3	A	602	LI1	15	0
3	A	603	LI1	9	0
3	A	606	LI1	1	0
3	A	607	LI1	5	0
3	A	608	LI1	5	0
3	A	609	LI1	5	0
3	A	610	LI1	18	0
3	A	611	LI1	6	0
3	A	612	LI1	2	0
3	A	613	LI1	2	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](#)

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

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

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

### 6.4 Ligands [i](#)

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

### 6.5 Other polymers [i](#)

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