



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:17 AM GMT

PDB ID : 3A7K  
Title : Crystal structure of halorhodopsin from Natronomonas pharaonis  
Authors : Kouyama, T.  
Deposited on : 2009-09-27  
Resolution : 2.00 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.

---

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

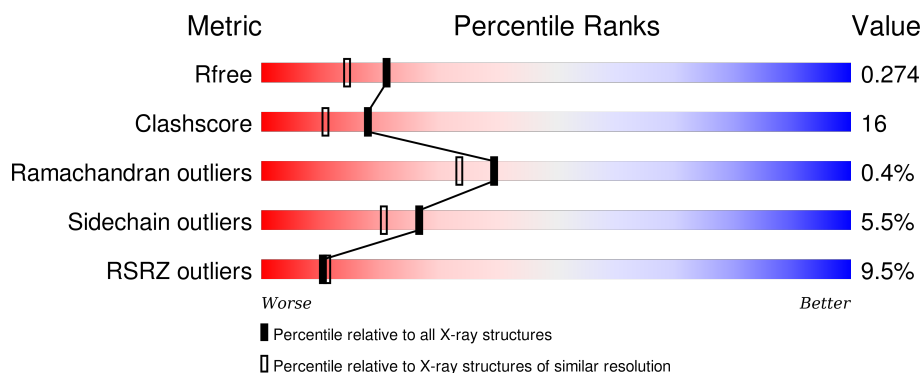
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	291	<div> <div>7%</div> <div>65%</div> <div>21%</div> <div>•</div> <div>11%</div> </div>
1	B	291	<div> <div>3%</div> <div>64%</div> <div>22%</div> <div>•</div> <div>11%</div> </div>
1	D	291	<div> <div>16%</div> <div>53%</div> <div>33%</div> <div>•</div> <div>11%</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
3	22B	A	300	-	-	-	X
3	22B	B	300	-	-	-	X
3	22B	D	300	-	-	-	X
4	L1P	A	293	-	-	-	X
4	L1P	B	293	-	-	-	X
4	L1P	B	294	-	-	-	X
5	L2P	A	294	-	-	-	X
5	L2P	A	295	-	-	-	X
5	L2P	B	295	-	-	-	X
5	L2P	B	296	-	-	-	X
5	L2P	D	293	-	-	-	X
5	L2P	D	294	-	-	-	X
6	L3P	A	296	-	-	-	X
6	L3P	A	297	-	-	-	X
6	L3P	A	301	-	-	-	X
6	L3P	A	331	-	-	-	X
6	L3P	A	333	-	-	-	X
6	L3P	B	331	-	-	-	X
6	L3P	D	330	-	-	-	X
7	CL	D	402	-	-	-	X

## 2 Entry composition [i](#)

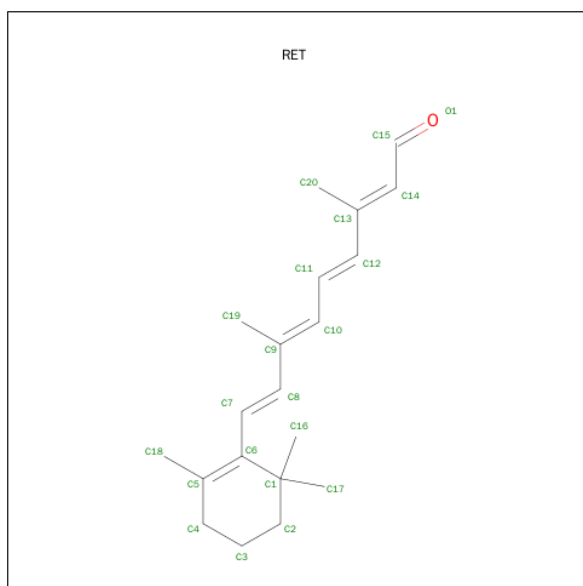
There are 8 unique types of molecules in this entry. The entry contains 6678 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Halorhodopsin.

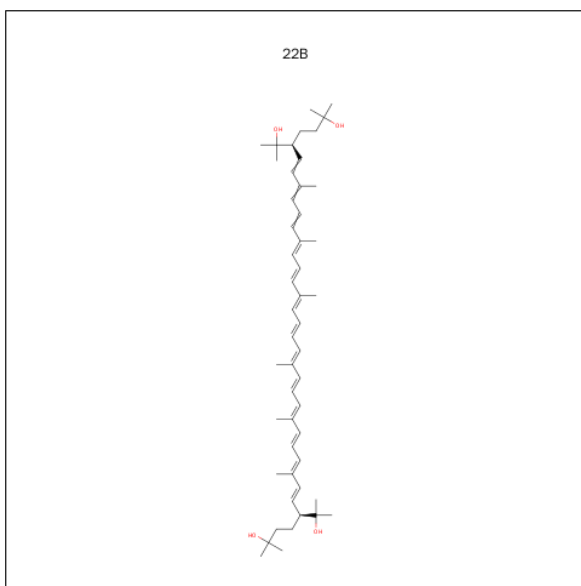
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	0	0
			1958	1299	298	350	11			
1	B	258	Total	C	N	O	S	0	0	0
			1952	1296	297	348	11			
1	D	259	Total	C	N	O	S	0	0	0
			1958	1299	298	350	11			

- Molecule 2 is RETINAL (three-letter code: RET) (formula:  $C_{20}H_{28}O$ ).



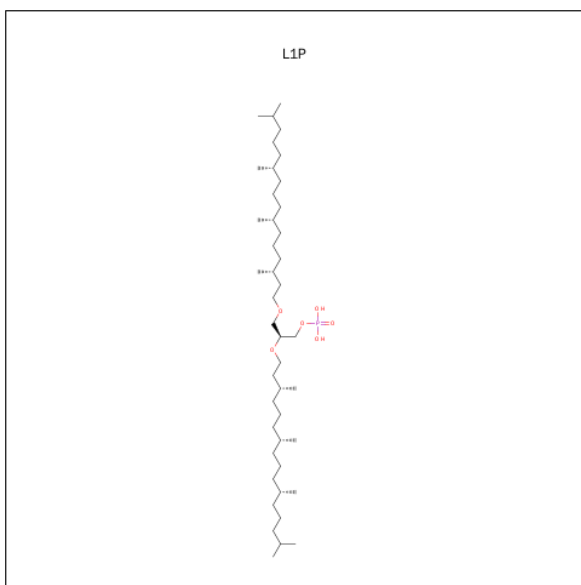
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	C	0	0
			20	20		
2	B	1	Total	C	0	0
			20	20		
2	D	1	Total	C	0	0
			20	20		

- Molecule 3 is BACTERIORUBERIN (three-letter code: 22B) (formula:  $C_{50}H_{76}O_4$ ).



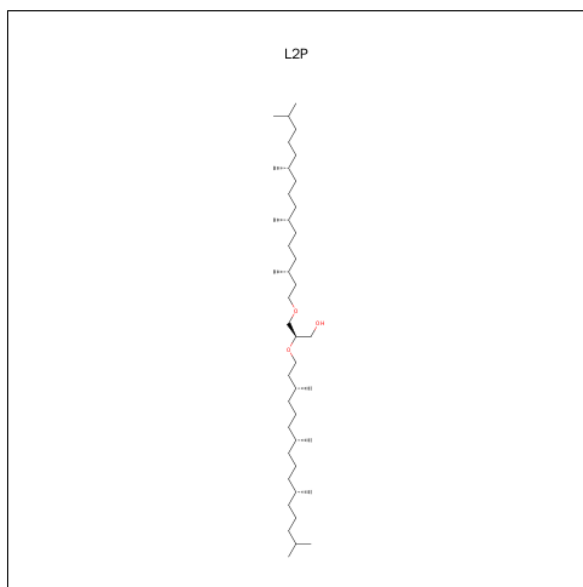
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			54	50	4		
3	B	1	Total	C	O	0	0
			54	50	4		
3	D	1	Total	C	O	0	0
			54	50	4		

- Molecule 4 is 3-PHOSPHORYL-[1,2-DI-PHYTANYL]GLYCEROL (three-letter code: L1P) (formula:  $C_{43}H_{89}O_6P$ ).



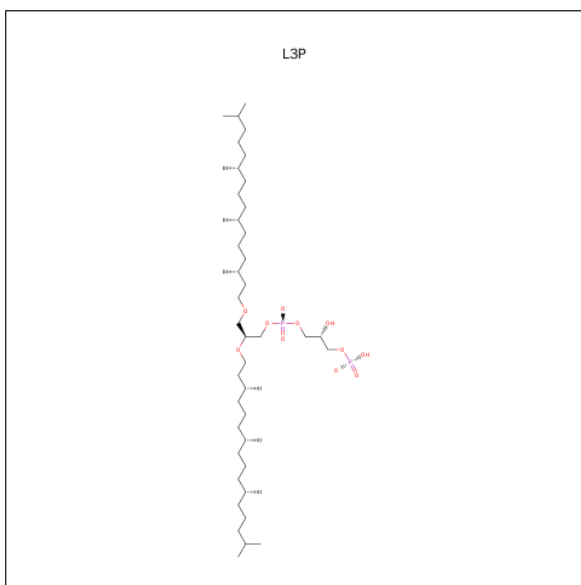
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			46	43	3		
4	B	1	Total	C	O	0	0
			46	43	3		
4	B	1	Total	C	O	0	0
			46	43	3		

- Molecule 5 is 2,3-DI-PHYTANYL-GLYCEROL (three-letter code: L2P) (formula:  $C_{43}H_{88}O_3$ ).



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

- Molecule 6 is 2,3-DI-O-PHYTANYL-3'-SN-GLYCERO-1-PHOSPHORYL-3'-SN-GLYCEROL-1'-PHOSPHATE (three-letter code: L3P) (formula:  $C_{46}H_{94}O_{11}P_2$ ).



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

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	2	Total Cl 2 2	0	0
7	A	2	Total Cl 2 2	0	0
7	D	2	Total Cl 2 2	0	0

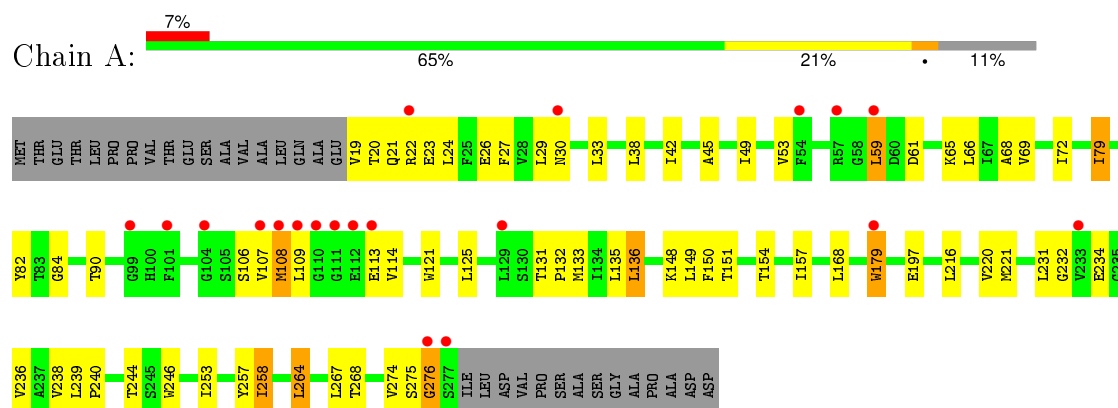
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	51	Total 51	O 51	0	0
8	B	60	Total 60	O 60	0	0
8	D	33	Total 33	O 33	0	0

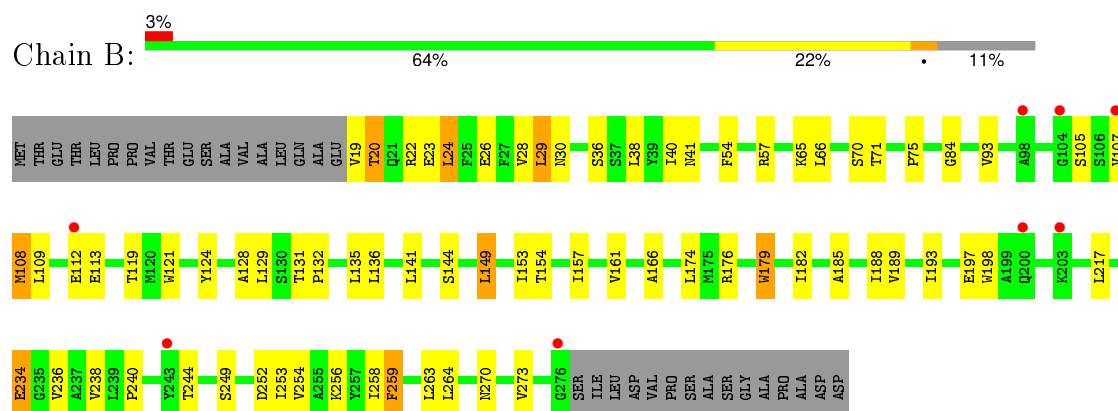
### 3 Residue-property plots [i](#)

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.

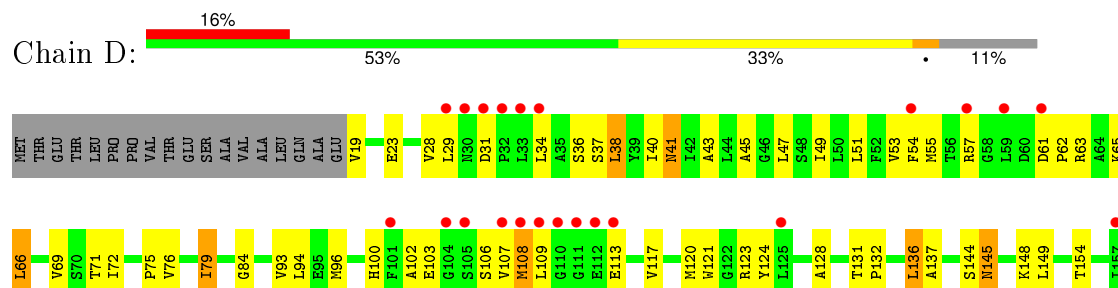
#### • Molecule 1: Halorhodopsin

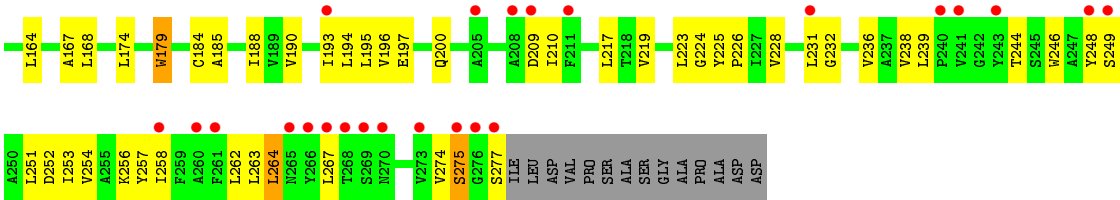


#### • Molecule 1: Halorhodopsin



#### • Molecule 1: Halorhodopsin





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	151.83Å 99.77Å 99.27Å 90.00° 127.67° 90.00°	Depositor
Resolution (Å)	15.00 – 2.00 46.57 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (15.00-2.00) 99.4 (46.57-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.249 , 0.274 0.249 , 0.274	Depositor DCC
$R_{free}$ test set	3975 reflections (5.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.0	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 78.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 78618 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6678	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CL, L1P, 22B, RET, L2P, L3P

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	0.40	0/2004	0.59	0/2744
1	B	0.37	0/1998	0.57	1/2736 (0.0%)
1	D	0.32	0/2004	0.52	0/2744
All	All	0.37	0/6006	0.56	1/8224 (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	B	29	LEU	N-CA-C	-5.30	96.68	111.00

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	1958	0	2012	58	0
1	B	1952	0	2007	67	0
1	D	1958	0	2012	89	0
2	A	20	0	27	0	0
2	B	20	0	27	1	0
2	D	20	0	27	0	0
3	A	54	0	76	0	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	54	0	76	2	0
3	D	54	0	76	0	0
4	A	46	0	87	3	0
4	B	92	0	174	4	0
5	A	40	0	78	8	0
5	B	40	0	78	7	0
5	D	40	0	78	5	0
6	A	140	0	273	2	0
6	B	20	0	39	0	0
6	D	20	0	39	0	0
7	A	2	0	0	0	0
7	B	2	0	0	0	0
7	D	2	0	0	0	0
8	A	51	0	0	1	1
8	B	60	0	0	3	0
8	D	33	0	0	3	0
All	All	6678	0	7186	215	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 16.

All (215) 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:238:VAL:HG23	1:A:239:LEU:HD13	1.51	0.92
1:A:45:ALA:HB3	1:A:79:ILE:HG23	1.60	0.83
1:A:238:VAL:HG23	1:A:239:LEU:CD1	2.14	0.78
1:A:108:MET:HA	1:A:113:GLU:HA	1.64	0.77
1:D:108:MET:HB2	1:D:113:GLU:HG3	1.68	0.76
1:D:254:VAL:HA	1:D:258:ILE:HG22	1.68	0.75
1:D:45:ALA:HB3	1:D:79:ILE:HG23	1.72	0.71
1:D:185:ALA:O	1:D:188:ILE:HG12	1.91	0.71
1:D:154:THR:HG22	5:D:294:L2P:H262	1.71	0.71
1:A:234:GLU:HG3	8:A:507:HOH:O	1.91	0.70
1:B:179:TRP:HH2	1:D:84:GLY:HA2	1.56	0.70
1:D:131:THR:OG1	1:D:132:PRO:HD3	1.92	0.70
1:D:190:VAL:O	1:D:193:ILE:HG13	1.92	0.69
1:B:254:VAL:HA	1:B:258:ILE:HG12	1.74	0.69
1:B:136:LEU:HG	5:B:295:L2P:H212	1.75	0.69
1:A:22:ARG:HG3	1:A:23:GLU:N	2.07	0.68
1:B:29:LEU:O	1:B:30:ASN:HB2	1.94	0.68

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:270:ASN:HB3	1:B:273:VAL:HG12	1.73	0.68
1:B:236:VAL:HG13	1:B:238:VAL:HG13	1.76	0.67
1:A:253:ILE:O	1:A:258:ILE:HG23	1.95	0.67
5:A:294:L2P:H201	5:B:295:L2P:H251	1.75	0.67
1:B:270:ASN:HB3	1:B:273:VAL:CG1	2.25	0.67
1:B:20:THR:HG22	1:B:23:GLU:H	1.59	0.66
1:A:150:PHE:HD2	5:A:294:L2P:H152	1.58	0.66
1:A:29:LEU:O	1:A:30:ASN:HB2	1.95	0.66
1:D:108:MET:HA	1:D:113:GLU:HA	1.80	0.64
1:B:19:VAL:HG21	1:B:93:VAL:HG11	1.79	0.63
1:D:238:VAL:HG23	1:D:239:LEU:HD13	1.81	0.63
1:B:108:MET:HA	1:B:113:GLU:HA	1.81	0.62
1:D:149:LEU:HG	5:D:294:L2P:H151	1.80	0.62
1:D:145:ASN:C	1:D:145:ASN:HD22	2.03	0.62
1:B:270:ASN:O	1:B:273:VAL:HG12	1.99	0.62
1:D:167:ALA:HB2	8:D:519:HOH:O	1.99	0.62
1:A:236:VAL:HG13	1:A:238:VAL:HG13	1.83	0.61
1:D:43:ALA:O	1:D:47:LEU:HD13	2.00	0.61
1:A:20:THR:HG22	1:A:22:ARG:H	1.65	0.61
1:D:36:SER:O	1:D:40:ILE:HG12	2.00	0.60
1:A:84:GLY:HA2	1:D:179:TRP:HH2	1.64	0.60
1:D:123:ARG:HD2	8:D:506:HOH:O	2.01	0.60
1:D:253:ILE:HA	1:D:257:TYR:CD2	2.37	0.59
1:D:164:LEU:O	1:D:168:LEU:HD23	2.02	0.59
1:D:195:LEU:HD21	1:D:219:VAL:HG21	1.84	0.59
1:B:254:VAL:HG13	1:B:258:ILE:HD11	1.84	0.59
1:D:254:VAL:HA	1:D:258:ILE:CG2	2.33	0.59
1:A:157:ILE:HG21	5:A:294:L2P:H241	1.84	0.59
1:A:179:TRP:HH2	1:B:84:GLY:HA2	1.67	0.59
1:A:121:TRP:HZ3	1:A:125:LEU:HD22	1.67	0.59
1:A:133:MET:HE1	5:A:295:L2P:H251	1.85	0.59
1:B:179:TRP:CH2	1:D:84:GLY:HA2	2.37	0.58
1:A:20:THR:CG2	1:A:22:ARG:HG2	2.33	0.58
1:A:151:THR:HG21	3:B:300:22B:H243	1.85	0.58
1:D:23:GLU:HB3	1:D:109:LEU:HB3	1.84	0.58
1:A:264:LEU:O	1:A:268:THR:HG22	2.04	0.58
1:D:51:LEU:O	1:D:55:MET:HG3	2.03	0.58
1:B:20:THR:HG21	8:B:535:HOH:O	2.04	0.58
1:B:36:SER:O	1:B:40:ILE:HG12	2.04	0.58
1:D:66:LEU:HD11	5:D:293:L2P:H192	1.85	0.57
1:D:217:LEU:HD11	1:D:254:VAL:HG12	1.87	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:ILE:HG13	1:B:259:PHE:N	2.20	0.56
1:D:193:ILE:HD12	1:D:194:LEU:N	2.21	0.56
1:A:22:ARG:HG3	1:A:23:GLU:H	1.69	0.56
1:A:20:THR:HG22	1:A:21:GLN:N	2.19	0.55
1:A:26:GLU:O	1:A:29:LEU:O	2.25	0.55
1:D:19:VAL:HG21	1:D:93:VAL:HG11	1.88	0.55
1:D:29:LEU:C	1:D:31:ASP:H	2.10	0.55
1:D:71:THR:HG21	1:D:264:LEU:HD13	1.89	0.55
1:B:166:ALA:HB2	1:B:179:TRP:HB3	1.88	0.55
1:A:84:GLY:HA2	1:D:179:TRP:CH2	2.42	0.55
4:A:293:L1P:H493	1:D:164:LEU:HD21	1.89	0.55
1:B:144:SER:OG	1:B:149:LEU:HD22	2.07	0.55
1:D:100:HIS:CD2	1:D:102:ALA:H	2.25	0.54
1:B:185:ALA:O	1:B:188:ILE:HG12	2.06	0.54
1:D:106:SER:HB3	1:D:113:GLU:HG2	1.88	0.54
1:D:28:VAL:HG13	1:D:34:LEU:HD12	1.90	0.54
1:D:54:PHE:HB3	1:D:57:ARG:NH1	2.23	0.54
1:A:33:LEU:HD22	1:A:246:TRP:HD1	1.73	0.54
1:D:65:LYS:O	1:D:69:VAL:HG23	2.08	0.53
1:B:70:SER:OG	1:B:136:LEU:HD12	2.09	0.53
1:D:196:VAL:O	1:D:200:GLN:HG2	2.08	0.53
1:A:20:THR:HG21	1:A:22:ARG:HG2	1.91	0.52
1:D:63:ARG:HH11	1:D:63:ARG:HG2	1.75	0.52
1:A:133:MET:HE1	5:A:295:L2P:H271	1.92	0.52
1:A:136:LEU:HD21	5:A:295:L2P:H201	1.92	0.52
1:B:240:PRO:O	1:B:244:THR:HG22	2.10	0.51
1:B:54:PHE:O	1:B:57:ARG:HG2	2.09	0.51
1:D:128:ALA:O	1:D:132:PRO:HG2	2.10	0.51
1:D:148:LYS:HE2	1:D:197:GLU:OE1	2.11	0.51
1:B:129:LEU:HA	5:B:295:L2P:H293	1.92	0.51
1:A:275:SER:O	1:A:276:GLY:C	2.49	0.51
1:D:154:THR:HG22	5:D:294:L2P:C26	2.39	0.51
1:D:38:LEU:HD11	1:D:120:MET:HE1	1.91	0.51
1:A:20:THR:HG21	1:A:22:ARG:NH1	2.25	0.50
1:D:145:ASN:ND2	1:D:148:LYS:H	2.09	0.50
1:B:93:VAL:HG13	1:B:93:VAL:O	2.10	0.50
1:B:29:LEU:O	1:B:30:ASN:CB	2.59	0.50
1:D:49:ILE:O	1:D:53:VAL:HG23	2.12	0.50
1:D:144:SER:HB3	1:D:149:LEU:CD2	2.41	0.50
1:B:109:LEU:N	1:B:109:LEU:HD22	2.26	0.50
1:B:182:ILE:HG13	8:D:532:HOH:O	2.12	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:61:ASP:OD2	1:D:275:SER:HA	2.12	0.50
1:D:238:VAL:HG23	1:D:239:LEU:CD1	2.42	0.49
1:D:29:LEU:C	1:D:31:ASP:N	2.66	0.49
1:B:19:VAL:CG2	1:B:93:VAL:HG11	2.43	0.49
1:D:232:GLY:CA	1:D:244:THR:HG21	2.43	0.49
1:A:240:PRO:O	1:A:244:THR:HG23	2.13	0.49
1:D:232:GLY:HA2	1:D:244:THR:HG21	1.94	0.49
1:A:107:VAL:HG12	1:A:114:VAL:O	2.13	0.49
1:B:108:MET:HA	1:B:112:GLU:O	2.13	0.48
1:B:141:LEU:HD22	1:B:263:LEU:HD13	1.96	0.48
1:A:20:THR:CG2	1:A:21:GLN:N	2.76	0.48
6:A:298:L3P:H222	1:D:174:LEU:HD23	1.96	0.48
1:A:29:LEU:O	1:A:30:ASN:CB	2.59	0.48
1:D:108:MET:HB2	1:D:113:GLU:CG	2.42	0.48
1:D:76:VAL:O	1:D:79:ILE:HG13	2.14	0.48
1:A:49:ILE:O	1:A:53:VAL:HG23	2.14	0.48
1:D:109:LEU:N	1:D:109:LEU:HD22	2.29	0.47
1:D:62:PRO:HG2	1:D:277:SER:HB3	1.96	0.47
1:B:249:SER:O	1:B:253:ILE:HG13	2.14	0.47
1:D:121:TRP:HA	1:D:124:TYR:CD2	2.49	0.47
1:D:184:CYS:O	1:D:188:ILE:HG23	2.14	0.47
1:A:231:LEU:HD22	1:A:238:VAL:HG21	1.97	0.47
1:B:217:LEU:C	1:B:217:LEU:HD23	2.35	0.47
1:A:19:VAL:HG23	1:A:19:VAL:O	2.15	0.47
1:B:26:GLU:O	1:B:29:LEU:O	2.33	0.47
1:B:193:ILE:HA	1:B:197:GLU:HG2	1.97	0.46
1:B:254:VAL:HG13	1:B:258:ILE:CD1	2.46	0.46
1:D:100:HIS:O	1:D:103:GLU:HB3	2.16	0.46
1:B:107:VAL:O	1:B:108:MET:HB2	2.15	0.46
1:A:231:LEU:O	1:A:238:VAL:HG22	2.15	0.46
1:B:153:ILE:HG21	5:B:295:L2P:H243	1.97	0.46
1:A:65:LYS:O	1:A:69:VAL:HG23	2.16	0.46
1:A:131:THR:N	1:A:132:PRO:CD	2.79	0.46
1:B:131:THR:N	1:B:132:PRO:CD	2.79	0.46
1:D:45:ALA:O	1:D:49:ILE:HG13	2.16	0.46
1:B:157:ILE:HG21	5:B:296:L2P:H241	1.97	0.45
2:B:292:RET:H181	2:B:292:RET:H7	1.81	0.45
1:D:258:ILE:O	1:D:262:LEU:HG	2.17	0.45
1:A:45:ALA:CB	1:A:79:ILE:HG23	2.40	0.45
1:D:239:LEU:HB3	1:D:244:THR:HG23	1.98	0.45
1:D:41:ASN:HA	1:D:41:ASN:HD22	1.54	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:219:VAL:O	1:D:223:LEU:HG	2.16	0.45
1:B:65:LYS:HD3	3:B:300:22B:H253	1.99	0.45
1:D:136:LEU:HD21	5:D:293:L2P:H191	1.99	0.45
1:B:188:ILE:HG13	1:B:189:VAL:N	2.31	0.45
1:A:33:LEU:HD22	1:A:246:TRP:CD1	2.51	0.45
1:B:20:THR:CG2	1:B:22:ARG:H	2.31	0.44
1:B:144:SER:HB2	1:B:198:TRP:NE1	2.32	0.44
1:D:107:VAL:HG13	1:D:108:MET:N	2.32	0.44
1:B:28:VAL:C	1:B:29:LEU:O	2.53	0.44
4:A:293:L1P:H571	4:A:293:L1P:H543	1.99	0.44
1:D:267:LEU:CD1	1:D:274:VAL:HG21	2.48	0.44
1:D:225:TYR:N	1:D:226:PRO:HD2	2.33	0.44
1:B:154:THR:HG22	5:B:296:L2P:H202	2.00	0.44
1:A:59:LEU:HB3	1:A:65:LYS:HG2	1.98	0.44
1:D:224:GLY:O	1:D:228:VAL:HG23	2.18	0.44
1:D:61:ASP:OD1	1:D:277:SER:HB2	2.17	0.44
1:D:145:ASN:C	1:D:145:ASN:ND2	2.70	0.44
1:D:93:VAL:HA	1:D:117:VAL:O	2.18	0.44
1:D:28:VAL:HG13	1:D:34:LEU:CD1	2.48	0.44
4:B:294:L1P:H543	4:B:294:L1P:H571	1.98	0.44
1:A:267:LEU:CD1	1:A:274:VAL:HG21	2.48	0.44
1:D:37:SER:HB3	1:D:246:TRP:CD1	2.53	0.44
1:D:267:LEU:HD11	1:D:274:VAL:HG21	2.00	0.43
1:B:193:ILE:HA	1:B:197:GLU:CG	2.47	0.43
1:D:193:ILE:C	1:D:193:ILE:HD12	2.39	0.43
1:D:94:LEU:HD11	1:D:168:LEU:HD13	2.00	0.43
1:B:176:ARG:HH22	1:B:234:GLU:HG3	1.82	0.43
1:A:27:PHE:HB2	1:A:109:LEU:HD12	1.99	0.43
1:D:100:HIS:CD2	1:D:102:ALA:HB3	2.54	0.43
1:D:145:ASN:HD21	1:D:148:LYS:HG3	1.84	0.43
1:B:119:THR:HG23	1:B:234:GLU:OE1	2.19	0.43
4:B:293:L1P:H18	4:B:293:L1P:H451	2.01	0.43
1:A:232:GLY:HA2	1:A:239:LEU:HB2	2.01	0.42
1:B:128:ALA:O	1:B:132:PRO:HG2	2.19	0.42
1:B:144:SER:HG	1:B:149:LEU:HD22	1.84	0.42
4:B:293:L1P:H521	4:B:293:L1P:H23	2.01	0.42
1:D:209:ASP:CG	1:D:210:ILE:H	2.22	0.42
1:A:179:TRP:CH2	1:B:84:GLY:HA2	2.50	0.42
1:A:154:THR:HG22	5:A:294:L2P:H202	2.01	0.42
1:A:33:LEU:HD23	6:A:333:L3P:H152	2.01	0.42
1:B:71:THR:HG23	8:B:521:HOH:O	2.18	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:121:TRP:HA	1:B:124:TYR:CD2	2.54	0.42
1:D:252:ASP:O	1:D:256:LYS:HB2	2.20	0.42
1:D:249:SER:O	1:D:253:ILE:HG13	2.19	0.42
1:D:63:ARG:NH1	1:D:63:ARG:HG2	2.35	0.42
1:A:61:ASP:O	1:A:65:LYS:HG3	2.20	0.42
1:D:75:PRO:O	1:D:79:ILE:HG12	2.19	0.42
1:A:79:ILE:H	1:A:79:ILE:HG13	1.58	0.41
1:B:109:LEU:O	1:B:112:GLU:HG2	2.20	0.41
1:D:137:ALA:HB1	1:D:263:LEU:HD21	2.02	0.41
1:B:252:ASP:O	1:B:256:LYS:HB2	2.20	0.41
1:D:248:TYR:HA	1:D:251:LEU:HD12	2.01	0.41
1:A:42:ILE:HG13	1:A:82:TYR:HB3	2.02	0.41
1:D:231:LEU:HA	1:D:236:VAL:HG12	2.01	0.41
1:B:20:THR:HG23	1:B:22:ARG:H	1.86	0.41
1:B:193:ILE:C	1:B:193:ILE:HD12	2.41	0.41
1:B:259:PHE:C	1:B:259:PHE:CD1	2.93	0.41
1:B:41:ASN:HD22	1:B:41:ASN:HA	1.63	0.41
1:D:96:MET:HG3	1:D:100:HIS:CD2	2.56	0.41
1:A:220:VAL:HG12	1:A:221:MET:CE	2.51	0.41
1:B:20:THR:HG22	1:B:22:ARG:N	2.36	0.41
1:A:148:LYS:HD3	1:A:197:GLU:HB3	2.02	0.41
1:A:68:ALA:O	1:A:72:ILE:HG13	2.21	0.41
1:A:106:SER:HB3	1:A:113:GLU:CG	2.51	0.41
1:D:72:ILE:O	1:D:76:VAL:HG23	2.21	0.40
1:B:270:ASN:HB3	1:B:273:VAL:HG11	2.03	0.40
1:A:253:ILE:HA	1:A:257:TYR:CD2	2.56	0.40
1:A:133:MET:CE	5:A:295:L2P:H271	2.51	0.40
1:B:71:THR:O	1:B:75:PRO:HD2	2.20	0.40
1:B:105:SER:HB3	8:B:525:HOH:O	2.20	0.40
5:B:295:L2P:H242	5:B:296:L2P:H143	2.03	0.40
1:B:236:VAL:HG22	1:B:236:VAL:O	2.22	0.40
1:A:90:THR:HG21	4:A:293:L1P:H242	2.03	0.40
1:B:161:VAL:HG11	4:B:294:L1P:H292	2.03	0.40
1:B:24:LEU:HD12	1:B:24:LEU:HA	1.82	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)
8:A:600:HOH:O	8:A:600:HOH:O 2_656	1.13	1.07

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	257/291 (88%)	247 (96%)	9 (4%)	1 (0%)	39	33
1	B	256/291 (88%)	249 (97%)	7 (3%)	0	100	100
1	D	257/291 (88%)	245 (95%)	10 (4%)	2 (1%)	24	15
All	All	770/873 (88%)	741 (96%)	26 (3%)	3 (0%)	39	33

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	275	SER
1	A	276	GLY
1	D	108	MET

### 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	208/233 (89%)	194 (93%)	14 (7%)	20	14
1	B	207/233 (89%)	195 (94%)	12 (6%)	25	19
1	D	208/233 (89%)	200 (96%)	8 (4%)	40	36
All	All	623/699 (89%)	589 (94%)	34 (6%)	27	21

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LEU
1	A	38	LEU
1	A	59	LEU
1	A	66	LEU
1	A	79	ILE
1	A	108	MET
1	A	135	LEU
1	A	136	LEU
1	A	149	LEU
1	A	168	LEU
1	A	179	TRP
1	A	216	LEU
1	A	258	ILE
1	A	264	LEU
1	B	20	THR
1	B	24	LEU
1	B	38	LEU
1	B	66	LEU
1	B	108	MET
1	B	135	LEU
1	B	149	LEU
1	B	174	LEU
1	B	179	TRP
1	B	234	GLU
1	B	259	PHE
1	B	264	LEU
1	D	38	LEU
1	D	41	ASN
1	D	66	LEU
1	D	79	ILE
1	D	136	LEU
1	D	145	ASN
1	D	179	TRP
1	D	264	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	B	41	ASN
1	B	265	ASN
1	D	41	ASN
1	D	100	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	D	145	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 ⓘ

Of 30 ligands modelled in this entry, 6 are monoatomic - leaving 24 for Mogul analysis.

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	292	1	19,20,21	2.06	4 (21%)	27,27,28	1.60	6 (22%)
4	L1P	A	293	-	45,45,49	1.76	15 (33%)	50,53,60	1.53	6 (12%)
5	L2P	A	294	-	19,19,45	1.80	7 (36%)	22,22,53	0.97	1 (4%)
5	L2P	A	295	-	19,19,45	1.84	7 (36%)	22,22,53	0.84	1 (4%)
6	L3P	A	296	-	19,19,58	1.85	7 (36%)	22,22,73	1.20	3 (13%)
6	L3P	A	297	-	19,19,58	1.92	7 (36%)	22,22,73	1.26	3 (13%)
6	L3P	A	298	-	19,19,58	1.85	7 (36%)	22,22,73	1.19	3 (13%)
6	L3P	A	299	-	19,19,58	1.88	7 (36%)	22,22,73	1.31	3 (13%)
3	22B	A	300	-	51,53,53	3.07	17 (33%)	58,72,72	1.93	17 (29%)
6	L3P	A	301	-	19,19,58	1.86	7 (36%)	22,22,73	1.21	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	L3P	A	331	-	19,19,58	1.89	7 (36%)	22,22,73	1.22	3 (13%)
6	L3P	A	333	-	19,19,58	1.84	7 (36%)	22,22,73	1.17	3 (13%)
2	RET	B	292	1	19,20,21	2.00	4 (21%)	27,27,28	1.67	6 (22%)
4	L1P	B	293	-	45,45,49	1.74	14 (31%)	50,53,60	1.58	6 (12%)
4	L1P	B	294	-	45,45,49	1.76	15 (33%)	50,53,60	1.54	6 (12%)
5	L2P	B	295	-	19,19,45	1.77	7 (36%)	22,22,53	0.84	1 (4%)
5	L2P	B	296	-	19,19,45	1.81	7 (36%)	22,22,53	0.96	1 (4%)
3	22B	B	300	-	51,53,53	3.17	19 (37%)	58,72,72	1.79	16 (27%)
6	L3P	B	331	-	19,19,58	1.86	7 (36%)	22,22,73	1.23	3 (13%)
2	RET	D	292	1	19,20,21	2.08	4 (21%)	27,27,28	1.81	9 (33%)
5	L2P	D	293	-	19,19,45	1.83	7 (36%)	22,22,53	0.88	0
5	L2P	D	294	-	19,19,45	1.83	7 (36%)	22,22,53	0.89	0
3	22B	D	300	-	51,53,53	2.95	20 (39%)	58,72,72	1.96	18 (31%)
6	L3P	D	330	-	19,19,58	1.86	7 (36%)	22,22,73	1.16	2 (9%)

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	292	1	-	0/13/30/31	0/1/1/1
4	L1P	A	293	-	-	0/51/51/55	0/0/0/0
5	L2P	A	294	-	-	0/20/20/51	0/0/0/0
5	L2P	A	295	-	-	0/20/20/51	0/0/0/0
6	L3P	A	296	-	-	0/20/20/67	0/0/0/0
6	L3P	A	297	-	-	0/20/20/67	0/0/0/0
6	L3P	A	298	-	-	0/20/20/67	0/0/0/0
6	L3P	A	299	-	-	0/20/20/67	0/0/0/0
3	22B	A	300	-	-	0/65/65/65	0/0/0/0
6	L3P	A	301	-	-	0/20/20/67	0/0/0/0
6	L3P	A	331	-	-	0/20/20/67	0/0/0/0
6	L3P	A	333	-	-	0/20/20/67	0/0/0/0
2	RET	B	292	1	-	0/13/30/31	0/1/1/1
4	L1P	B	293	-	-	0/51/51/55	0/0/0/0
4	L1P	B	294	-	-	0/51/51/55	0/0/0/0
5	L2P	B	295	-	-	0/20/20/51	0/0/0/0
5	L2P	B	296	-	-	0/20/20/51	0/0/0/0
3	22B	B	300	-	-	0/65/65/65	0/0/0/0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	L3P	B	331	-	-	0/20/20/67	0/0/0/0
2	RET	D	292	1	-	0/13/30/31	0/1/1/1
5	L2P	D	293	-	-	0/20/20/51	0/0/0/0
5	L2P	D	294	-	-	0/20/20/51	0/0/0/0
3	22B	D	300	-	-	0/65/65/65	0/0/0/0
6	L3P	D	330	-	-	0/20/20/67	0/0/0/0

All (217) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	292	RET	C2-C3	-2.48	1.45	1.52
2	B	292	RET	C2-C3	-2.34	1.46	1.52
2	D	292	RET	C2-C3	-2.30	1.46	1.52
3	D	300	22B	O1-C36	-2.01	1.39	1.44
3	D	300	22B	C38-C39	2.02	1.50	1.45
5	B	296	L2P	C19-C18	2.03	1.59	1.52
3	D	300	22B	C35-C34	2.04	1.57	1.53
4	B	294	L1P	O2-C41	2.05	1.48	1.42
5	A	294	L2P	C26-C25	2.09	1.61	1.52
5	A	294	L2P	C19-C18	2.14	1.60	1.52
5	B	295	L2P	C26-C25	2.14	1.62	1.52
5	B	295	L2P	C19-C18	2.15	1.60	1.52
5	D	293	L2P	C26-C25	2.15	1.62	1.52
4	B	293	L1P	C1-C2	2.15	1.56	1.50
6	A	296	L3P	C26-C25	2.17	1.62	1.52
5	B	296	L2P	C26-C25	2.17	1.62	1.52
6	B	331	L3P	C26-C25	2.17	1.62	1.52
4	A	293	L1P	C1-C2	2.18	1.56	1.50
4	A	293	L1P	O2-C41	2.18	1.49	1.42
3	B	300	22B	C38-C39	2.19	1.50	1.45
4	B	294	L1P	C1-C2	2.19	1.56	1.50
3	B	300	22B	C18-C5	2.20	1.55	1.50
6	A	298	L3P	C26-C25	2.20	1.62	1.52
5	D	294	L2P	C19-C18	2.22	1.60	1.52
6	A	301	L3P	C26-C25	2.22	1.62	1.52
5	A	295	L2P	C19-C18	2.23	1.60	1.52
5	D	293	L2P	C19-C18	2.23	1.60	1.52
4	A	293	L1P	C26-C25	2.24	1.62	1.52
6	A	333	L3P	C26-C25	2.24	1.62	1.52
6	D	330	L3P	C26-C25	2.25	1.62	1.52
5	D	293	L2P	C26-C27	2.25	1.62	1.52
6	A	331	L3P	C26-C25	2.26	1.62	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	300	22B	C28-C29	2.27	1.38	1.35
6	A	299	L3P	C19-C18	2.27	1.60	1.52
5	A	295	L2P	C26-C25	2.27	1.62	1.52
5	A	294	L2P	C26-C27	2.27	1.62	1.52
5	B	295	L2P	C26-C27	2.27	1.62	1.52
6	A	297	L3P	C26-C25	2.29	1.62	1.52
6	A	297	L3P	C14-C13	2.32	1.60	1.52
4	B	293	L1P	C26-C25	2.32	1.62	1.52
6	A	296	L3P	C19-C18	2.32	1.60	1.52
5	B	295	L2P	C17-C18	2.33	1.64	1.52
6	B	331	L3P	C14-C13	2.33	1.60	1.52
6	A	299	L3P	C26-C25	2.33	1.62	1.52
5	B	295	L2P	C25-C23	2.33	1.64	1.52
4	B	293	L1P	C54-C53	2.33	1.60	1.52
6	A	333	L3P	C14-C13	2.34	1.60	1.52
6	A	298	L3P	C19-C18	2.35	1.60	1.52
5	A	295	L2P	C17-C18	2.35	1.64	1.52
4	B	294	L1P	C26-C25	2.35	1.63	1.52
4	A	293	L1P	C19-C18	2.35	1.60	1.52
4	B	294	L1P	C19-C18	2.36	1.60	1.52
4	A	293	L1P	C26-C27	2.36	1.63	1.52
5	D	294	L2P	C26-C25	2.36	1.63	1.52
4	A	293	L1P	C14-C13	2.37	1.60	1.52
4	B	293	L1P	C19-C18	2.37	1.60	1.52
4	B	293	L1P	C26-C27	2.37	1.63	1.52
6	A	299	L3P	C17-C18	2.37	1.65	1.52
5	A	294	L2P	C17-C18	2.37	1.65	1.52
6	D	330	L3P	C19-C18	2.37	1.60	1.52
5	B	296	L2P	C26-C27	2.38	1.63	1.52
5	D	294	L2P	C17-C18	2.38	1.65	1.52
5	D	293	L2P	C17-C18	2.39	1.65	1.52
6	A	298	L3P	C14-C13	2.40	1.61	1.52
6	A	333	L3P	C19-C18	2.40	1.61	1.52
2	A	292	RET	C7-C6	2.40	1.54	1.45
6	A	296	L3P	C26-C27	2.40	1.63	1.52
6	D	330	L3P	C14-C13	2.40	1.61	1.52
6	B	331	L3P	C19-C18	2.41	1.61	1.52
4	B	294	L1P	C26-C27	2.41	1.63	1.52
6	A	301	L3P	C19-C18	2.42	1.61	1.52
6	A	301	L3P	C14-C13	2.42	1.61	1.52
4	B	293	L1P	C14-C13	2.42	1.61	1.52
6	A	331	L3P	C19-C18	2.42	1.61	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	299	L3P	C14-C13	2.43	1.61	1.52
4	B	294	L1P	C17-C18	2.43	1.65	1.52
4	B	294	L1P	C14-C13	2.43	1.61	1.52
6	A	298	L3P	C17-C18	2.44	1.65	1.52
6	A	296	L3P	C14-C13	2.44	1.61	1.52
5	D	294	L2P	C26-C27	2.44	1.63	1.52
6	A	301	L3P	C17-C18	2.44	1.65	1.52
4	B	293	L1P	C17-C18	2.45	1.65	1.52
5	B	296	L2P	C17-C18	2.45	1.65	1.52
4	A	293	L1P	C17-C18	2.45	1.65	1.52
6	A	298	L3P	C26-C27	2.45	1.63	1.52
6	A	331	L3P	C14-C13	2.45	1.61	1.52
6	B	331	L3P	C26-C27	2.46	1.63	1.52
6	D	330	L3P	C26-C27	2.47	1.63	1.52
3	A	300	22B	C18-C5	2.47	1.56	1.50
6	A	331	L3P	C26-C27	2.47	1.63	1.52
6	A	301	L3P	C26-C27	2.48	1.63	1.52
5	A	294	L2P	C25-C23	2.48	1.65	1.52
4	A	293	L1P	O1-C11	2.49	1.52	1.42
6	A	333	L3P	C26-C27	2.50	1.63	1.52
6	D	330	L3P	C17-C18	2.50	1.65	1.52
5	B	296	L2P	C25-C23	2.51	1.65	1.52
4	A	293	L1P	C54-C53	2.52	1.61	1.52
5	A	295	L2P	C25-C23	2.52	1.65	1.52
6	A	296	L3P	C17-C18	2.52	1.65	1.52
4	B	293	L1P	C56-C55	2.53	1.63	1.52
5	D	293	L2P	C25-C23	2.53	1.65	1.52
6	A	297	L3P	C19-C18	2.55	1.61	1.52
3	A	300	22B	C50-C43	2.55	1.56	1.50
4	B	293	L1P	O1-C11	2.55	1.52	1.42
5	B	295	L2P	C14-C13	2.55	1.61	1.52
5	B	296	L2P	C14-C13	2.55	1.61	1.52
5	D	294	L2P	C25-C23	2.56	1.66	1.52
6	A	297	L3P	C17-C18	2.56	1.66	1.52
4	B	294	L1P	O1-C11	2.56	1.52	1.42
6	A	331	L3P	C17-C18	2.57	1.66	1.52
3	B	300	22B	C35-C34	2.57	1.58	1.53
6	B	331	L3P	C17-C18	2.57	1.66	1.52
6	A	333	L3P	C17-C18	2.58	1.66	1.52
5	D	294	L2P	C14-C13	2.58	1.61	1.52
6	A	299	L3P	C26-C27	2.59	1.64	1.52
3	D	300	22B	C18-C5	2.59	1.56	1.50

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	294	L1P	C54-C53	2.59	1.61	1.52
6	A	296	L3P	C25-C23	2.59	1.66	1.52
3	D	300	22B	C50-C43	2.59	1.56	1.50
5	A	295	L2P	C14-C13	2.59	1.61	1.52
3	B	300	22B	C50-C43	2.60	1.56	1.50
6	A	333	L3P	C25-C23	2.61	1.66	1.52
2	D	292	RET	C7-C6	2.61	1.55	1.45
4	B	294	L1P	C15-C13	2.61	1.66	1.52
6	B	331	L3P	C25-C23	2.61	1.66	1.52
6	A	298	L3P	C25-C23	2.62	1.66	1.52
4	B	294	L1P	C56-C55	2.62	1.64	1.52
6	A	331	L3P	C25-C23	2.62	1.66	1.52
5	A	295	L2P	C26-C27	2.64	1.64	1.52
5	A	294	L2P	C14-C13	2.64	1.61	1.52
6	A	301	L3P	C25-C23	2.64	1.66	1.52
5	D	293	L2P	C14-C13	2.64	1.61	1.52
6	D	330	L3P	C25-C23	2.65	1.66	1.52
4	A	293	L1P	C25-C23	2.65	1.66	1.52
4	A	293	L1P	C15-C13	2.67	1.66	1.52
4	A	293	L1P	C56-C55	2.68	1.64	1.52
4	B	293	L1P	C15-C13	2.68	1.66	1.52
6	A	297	L3P	C25-C23	2.70	1.66	1.52
3	A	300	22B	C35-C34	2.71	1.59	1.53
3	D	300	22B	C20-C13	2.73	1.56	1.50
6	A	297	L3P	C26-C27	2.75	1.64	1.52
4	B	293	L1P	C55-C53	2.76	1.67	1.52
2	B	292	RET	C7-C6	2.77	1.55	1.45
6	A	299	L3P	C25-C23	2.78	1.67	1.52
4	B	294	L1P	C25-C23	2.78	1.67	1.52
4	B	293	L1P	C25-C23	2.78	1.67	1.52
3	B	300	22B	C28-C29	2.79	1.39	1.35
3	A	300	22B	C20-C13	2.79	1.56	1.50
3	B	300	22B	C20-C13	2.81	1.56	1.50
5	A	294	L2P	C15-C13	2.82	1.67	1.52
3	D	300	22B	C26-C39	2.83	1.57	1.50
4	A	293	L1P	C55-C53	2.86	1.67	1.52
6	A	333	L3P	C15-C13	2.86	1.67	1.52
4	B	294	L1P	C55-C53	2.86	1.67	1.52
5	B	296	L2P	C15-C13	2.89	1.67	1.52
4	A	293	L1P	C12-C11	2.90	1.61	1.50
6	A	298	L3P	C15-C13	2.90	1.67	1.52
6	A	296	L3P	C15-C13	2.92	1.67	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	330	L3P	C15-C13	2.92	1.67	1.52
5	D	294	L2P	C15-C13	2.92	1.67	1.52
3	A	300	22B	C26-C39	2.93	1.57	1.50
6	A	297	L3P	C15-C13	2.93	1.68	1.52
6	A	301	L3P	C15-C13	2.93	1.68	1.52
6	A	299	L3P	C15-C13	2.94	1.68	1.52
3	B	300	22B	C17-C1	2.95	1.57	1.52
5	A	295	L2P	C15-C13	2.95	1.68	1.52
4	B	294	L1P	C12-C11	2.96	1.61	1.50
6	B	331	L3P	C15-C13	2.97	1.68	1.52
3	B	300	22B	C26-C39	2.97	1.57	1.50
6	A	331	L3P	C15-C13	2.98	1.68	1.52
4	B	293	L1P	C12-C11	2.98	1.61	1.50
5	B	295	L2P	C15-C13	2.98	1.68	1.52
3	D	300	22B	C30-C29	3.00	1.57	1.50
3	D	300	22B	C17-C1	3.03	1.57	1.52
5	D	293	L2P	C15-C13	3.04	1.68	1.52
3	B	300	22B	C30-C29	3.07	1.57	1.50
3	A	300	22B	C30-C29	3.10	1.57	1.50
3	A	300	22B	C17-C1	3.12	1.57	1.52
3	D	300	22B	C48-C47	3.38	1.58	1.52
3	A	300	22B	C48-C47	3.41	1.58	1.52
3	B	300	22B	C48-C47	3.44	1.58	1.52
3	D	300	22B	C19-C9	3.47	1.58	1.50
3	A	300	22B	C19-C9	3.48	1.58	1.50
3	B	300	22B	O27-C23	3.52	1.54	1.44
3	B	300	22B	C19-C9	3.53	1.58	1.50
3	D	300	22B	O27-C23	3.54	1.54	1.44
3	A	300	22B	O27-C23	3.58	1.54	1.44
4	B	293	L1P	C3-C2	3.61	1.60	1.50
3	B	300	22B	C22-C21	3.63	1.61	1.53
3	D	300	22B	C22-C21	3.63	1.61	1.53
4	B	294	L1P	C3-C2	3.71	1.60	1.50
4	A	293	L1P	C3-C2	3.72	1.60	1.50
3	D	300	22B	C16-C1	3.72	1.58	1.52
3	A	300	22B	C22-C21	3.75	1.61	1.53
3	A	300	22B	C16-C1	3.89	1.59	1.52
3	B	300	22B	C21-C2	3.90	1.59	1.54
3	B	300	22B	C16-C1	3.97	1.59	1.52
3	D	300	22B	C21-C2	4.22	1.59	1.54
2	B	292	RET	C5-C6	4.22	1.41	1.34
3	A	300	22B	C49-C47	4.22	1.59	1.52

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	300	22B	C21-C2	4.28	1.59	1.54
3	D	300	22B	C49-C47	4.30	1.59	1.52
3	B	300	22B	C49-C47	4.31	1.59	1.52
3	D	300	22B	C34-C33	4.62	1.60	1.54
2	A	292	RET	C5-C6	4.69	1.41	1.34
2	D	292	RET	C5-C6	4.72	1.41	1.34
2	B	292	RET	C1-C6	5.61	1.61	1.53
2	A	292	RET	C1-C6	5.65	1.61	1.53
2	D	292	RET	C1-C6	5.88	1.62	1.53
3	A	300	22B	C34-C33	6.63	1.63	1.54
3	B	300	22B	C34-C33	6.82	1.63	1.54
3	D	300	22B	C33-C32	8.93	1.59	1.50
3	A	300	22B	C33-C32	9.23	1.60	1.50
3	B	300	22B	C33-C32	10.36	1.61	1.50
3	D	300	22B	C2-C3	12.03	1.63	1.50
3	B	300	22B	C2-C3	12.23	1.63	1.50
3	A	300	22B	C2-C3	12.26	1.63	1.50

All (120) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	300	22B	C12-C13-C14	-5.20	110.60	118.98
3	A	300	22B	C12-C13-C14	-4.89	111.11	118.98
3	B	300	22B	C12-C13-C14	-4.05	112.46	118.98
3	A	300	22B	C42-C43-C44	-3.99	112.56	118.98
3	D	300	22B	C42-C43-C44	-3.97	112.58	118.98
3	D	300	22B	C4-C5-C6	-3.35	113.58	118.98
3	B	300	22B	C4-C5-C6	-3.33	113.62	118.98
3	A	300	22B	C4-C5-C6	-3.31	113.65	118.98
3	D	300	22B	C17-C1-C16	-3.24	105.63	110.51
3	B	300	22B	C42-C43-C44	-3.20	113.83	118.98
3	A	300	22B	C17-C1-C16	-3.09	105.86	110.51
3	B	300	22B	C17-C1-C16	-3.06	105.90	110.51
2	B	292	RET	C1-C6-C5	-3.05	118.17	122.66
3	A	300	22B	C31-C29-C28	-3.01	114.14	118.98
2	D	292	RET	C1-C6-C5	-2.90	118.39	122.66
3	D	300	22B	C31-C29-C28	-2.87	114.36	118.98
2	A	292	RET	C8-C9-C10	-2.83	114.43	118.98
2	A	292	RET	C1-C6-C5	-2.83	118.51	122.66
3	A	300	22B	C49-C47-C48	-2.80	106.29	110.51
3	B	300	22B	C31-C29-C28	-2.69	114.65	118.98
3	B	300	22B	C49-C47-C48	-2.68	106.47	110.51

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	292	RET	C7-C6-C5	-2.47	115.73	121.37
4	B	293	L1P	C47-C46-C45	-2.38	101.19	112.99
3	D	300	22B	C49-C47-C48	-2.38	106.93	110.51
2	B	292	RET	C8-C9-C10	-2.37	115.16	118.98
4	B	294	L1P	C47-C46-C45	-2.33	101.44	112.99
3	D	300	22B	C38-C39-C40	-2.24	115.37	118.98
3	A	300	22B	C38-C39-C40	-2.22	115.41	118.98
3	D	300	22B	C8-C9-C10	-2.19	115.46	118.98
2	D	292	RET	C8-C9-C10	-2.18	115.46	118.98
4	A	293	L1P	C47-C46-C45	-2.18	102.16	112.99
2	B	292	RET	C7-C6-C5	-2.05	116.67	121.37
3	B	300	22B	C8-C9-C10	-2.02	115.72	118.98
6	A	333	L3P	C16-C17-C18	2.01	122.16	115.49
4	A	293	L1P	O1-C11-C12	2.02	115.39	109.52
6	A	333	L3P	C21-C20-C18	2.03	122.23	115.49
5	B	295	L2P	C17-C16-C15	2.04	123.08	112.99
6	A	298	L3P	C16-C17-C18	2.09	122.42	115.49
6	A	298	L3P	C21-C20-C18	2.11	122.48	115.49
6	D	330	L3P	C16-C17-C18	2.11	122.49	115.49
6	A	331	L3P	C21-C20-C18	2.12	122.51	115.49
2	D	292	RET	C20-C13-C12	2.13	121.64	118.10
4	B	293	L1P	O1-C11-C12	2.14	115.74	109.52
3	B	300	22B	C30-C29-C31	2.14	121.66	118.10
6	A	301	L3P	C21-C20-C18	2.15	122.60	115.49
2	D	292	RET	C17-C1-C6	2.16	113.69	110.30
3	D	300	22B	C25-C23-C22	2.17	118.02	111.59
3	D	300	22B	C30-C29-C31	2.17	121.70	118.10
4	B	294	L1P	O1-C11-C12	2.19	115.90	109.52
6	A	301	L3P	C16-C17-C18	2.22	122.84	115.49
6	A	296	L3P	C21-C20-C18	2.22	122.86	115.49
6	B	331	L3P	C16-C17-C18	2.22	122.86	115.49
6	A	296	L3P	C16-C17-C18	2.23	122.88	115.49
4	B	294	L1P	C56-C55-C53	2.23	122.88	115.49
5	A	295	L2P	C17-C16-C15	2.23	124.05	112.99
3	B	300	22B	C25-C23-C22	2.24	118.24	111.59
6	B	331	L3P	C21-C20-C18	2.25	122.96	115.49
3	A	300	22B	C25-C23-C22	2.26	118.31	111.59
2	A	292	RET	C17-C1-C6	2.27	113.87	110.30
3	A	300	22B	C30-C29-C31	2.28	121.89	118.10
6	A	299	L3P	C16-C17-C18	2.31	123.16	115.49
6	A	297	L3P	C21-C20-C18	2.32	123.17	115.49
4	A	293	L1P	C56-C55-C53	2.33	123.20	115.49

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	331	L3P	C16-C17-C18	2.36	123.32	115.49
6	A	297	L3P	C16-C17-C18	2.44	123.59	115.49
2	B	292	RET	C19-C9-C8	2.45	122.17	118.10
2	D	292	RET	C2-C1-C6	2.45	114.24	110.36
5	B	296	L2P	C21-C20-C18	2.46	123.66	115.49
3	B	300	22B	C26-C39-C38	2.47	122.21	118.10
2	A	292	RET	C19-C9-C8	2.55	122.34	118.10
2	D	292	RET	C16-C1-C6	2.56	114.31	110.30
2	D	292	RET	C19-C9-C8	2.56	122.36	118.10
2	A	292	RET	C2-C1-C6	2.62	114.50	110.36
6	A	299	L3P	C21-C20-C18	2.64	124.24	115.49
4	B	293	L1P	C16-C17-C18	2.65	124.27	115.49
3	A	300	22B	C45-C44-C43	2.68	131.07	127.20
3	A	300	22B	C26-C39-C38	2.70	122.58	118.10
5	A	294	L2P	C21-C20-C18	2.71	124.46	115.49
3	D	300	22B	C45-C44-C43	2.73	131.14	127.20
3	B	300	22B	C50-C43-C42	2.75	122.67	118.10
3	D	300	22B	C26-C39-C38	2.77	122.71	118.10
4	B	294	L1P	C16-C17-C18	2.84	124.91	115.49
3	B	300	22B	C18-C5-C4	2.88	122.89	118.10
2	B	292	RET	C2-C1-C6	2.91	114.97	110.36
4	A	293	L1P	C16-C17-C18	2.95	125.28	115.49
2	A	292	RET	C1-C6-C7	3.01	124.26	115.82
3	A	300	22B	C18-C5-C4	3.05	123.18	118.10
3	D	300	22B	C50-C43-C42	3.08	123.22	118.10
4	B	293	L1P	C56-C55-C53	3.09	125.72	115.49
3	D	300	22B	C16-C1-C2	3.13	116.31	111.59
3	D	300	22B	C18-C5-C4	3.13	123.31	118.10
3	A	300	22B	C50-C43-C42	3.15	123.34	118.10
3	A	300	22B	C16-C1-C2	3.18	116.39	111.59
4	B	293	L1P	C21-C20-C18	3.27	126.34	115.49
2	B	292	RET	C1-C6-C7	3.33	125.16	115.82
4	B	294	L1P	C21-C20-C18	3.34	126.58	115.49
3	D	300	22B	C21-C22-C23	3.38	123.15	116.36
4	A	293	L1P	C21-C20-C18	3.44	126.90	115.49
6	A	296	L3P	C26-C25-C23	3.45	126.93	115.49
6	D	330	L3P	C26-C25-C23	3.48	127.02	115.49
3	B	300	22B	C20-C13-C12	3.50	123.93	118.10
6	A	331	L3P	C26-C25-C23	3.57	127.33	115.49
6	A	298	L3P	C26-C25-C23	3.57	127.33	115.49
2	D	292	RET	C1-C6-C7	3.59	125.88	115.82
6	A	301	L3P	C26-C25-C23	3.64	127.57	115.49

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	331	L3P	C26-C25-C23	3.70	127.76	115.49
6	A	333	L3P	C26-C25-C23	3.70	127.77	115.49
3	B	300	22B	C15-C14-C13	3.73	132.58	127.20
3	A	300	22B	C21-C22-C23	3.83	124.05	116.36
6	A	297	L3P	C26-C25-C23	3.84	128.24	115.49
3	B	300	22B	C16-C1-C2	3.89	117.47	111.59
6	A	299	L3P	C26-C25-C23	3.91	128.46	115.49
3	D	300	22B	C20-C13-C12	3.98	124.72	118.10
3	B	300	22B	C21-C22-C23	4.00	124.38	116.36
3	A	300	22B	C20-C13-C12	4.03	124.80	118.10
3	A	300	22B	C15-C14-C13	4.33	133.46	127.20
3	D	300	22B	C15-C14-C13	5.18	134.68	127.20
4	B	293	L1P	O1-C1-C2	7.66	121.64	108.71
4	A	293	L1P	O1-C1-C2	7.71	121.71	108.71
4	B	294	L1P	O1-C1-C2	7.76	121.80	108.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

13 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	293	L1P	3	0
5	A	294	L2P	4	0
5	A	295	L2P	4	0
6	A	298	L3P	1	0
6	A	333	L3P	1	0
2	B	292	RET	1	0
4	B	293	L1P	2	0
4	B	294	L1P	2	0
5	B	295	L2P	5	0
5	B	296	L2P	3	0
3	B	300	22B	2	0
5	D	293	L2P	2	0
5	D	294	L2P	3	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	259/291 (89%)	0.28	20 (7%) 16 17	23, 34, 66, 85	0
1	B	258/291 (88%)	0.14	8 (3%) 52 53	26, 39, 55, 67	0
1	D	259/291 (89%)	1.17	46 (17%) 2 2	33, 54, 79, 96	0
All	All	776/873 (88%)	0.53	74 (9%) 10 11	23, 42, 72, 96	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	109	LEU	9.2
1	D	276	GLY	8.6
1	D	277	SER	8.0
1	A	110	GLY	7.7
1	D	111	GLY	7.5
1	D	112	GLU	6.8
1	D	32	PRO	6.5
1	A	107	VAL	5.9
1	D	243	TYR	5.8
1	A	104	GLY	5.7
1	B	276	GLY	5.5
1	D	110	GLY	5.5
1	D	113	GLU	5.2
1	D	275	SER	4.9
1	A	111	GLY	4.8
1	D	269	SER	4.8
1	B	104	GLY	4.5
1	D	261	PHE	4.4
1	A	109	LEU	4.3
1	D	108	MET	4.2
1	D	249	SER	4.2
1	D	29	LEU	4.1
1	D	240	PRO	4.0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	D	107	VAL	3.8
1	A	30	ASN	3.6
1	A	276	GLY	3.4
1	D	209	ASP	3.4
1	A	54	PHE	3.4
1	D	241	VAL	3.3
1	D	273	VAL	3.3
1	D	54	PHE	3.3
1	B	98	ALA	3.3
1	D	270	ASN	3.3
1	D	211	PHE	3.3
1	A	112	GLU	3.2
1	A	108	MET	3.1
1	D	205	ALA	3.0
1	D	101	PHE	3.0
1	A	99	GLY	2.9
1	D	30	ASN	2.9
1	D	248	TYR	2.8
1	D	193	ILE	2.8
1	D	33	LEU	2.8
1	A	277	SER	2.8
1	B	107	VAL	2.7
1	A	113	GLU	2.7
1	A	57	ARG	2.7
1	D	265	ASN	2.7
1	D	34	LEU	2.7
1	D	267	LEU	2.6
1	D	268	THR	2.6
1	B	200	GLN	2.5
1	A	101	PHE	2.5
1	D	57	ARG	2.5
1	B	243	TYR	2.4
1	D	258	ILE	2.4
1	A	129	LEU	2.4
1	D	104	GLY	2.3
1	B	203	LYS	2.3
1	D	31	ASP	2.3
1	A	179	TRP	2.2
1	D	61	ASP	2.2
1	A	22	ARG	2.1
1	D	231	LEU	2.1
1	A	233	VAL	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	D	157	ILE	2.1
1	D	208	ALA	2.1
1	D	59	LEU	2.1
1	D	266	TYR	2.1
1	A	59	LEU	2.0
1	D	125	LEU	2.0
1	D	260	ALA	2.0
1	B	112	GLU	2.0
1	D	105	SER	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(Å <sup>2</sup> )	Q<0.9
5	L2P	B	296	20/46	0.64	0.69	16.51	85,90,93,93	0
5	L2P	A	294	20/46	0.70	0.65	14.90	79,89,96,96	0
5	L2P	D	294	20/46	0.50	0.67	14.63	88,90,96,97	0
5	L2P	D	293	20/46	0.47	0.61	13.75	94,96,98,99	0
4	L1P	B	293	46/50	0.40	0.69	13.30	92,103,105,105	0
4	L1P	B	294	46/50	0.44	0.67	13.13	94,101,105,105	0
6	L3P	A	296	20/59	0.38	0.49	12.23	102,103,104,104	0
5	L2P	B	295	20/46	0.52	0.61	12.03	94,96,97,97	0
4	L1P	A	293	46/50	0.53	0.63	12.00	70,96,99,100	0
5	L2P	A	295	20/46	0.34	0.79	11.83	114,115,118,118	0
6	L3P	A	333	20/59	0.56	0.42	11.37	60,73,75,77	0
6	L3P	A	297	20/59	0.44	0.57	11.06	110,112,114,114	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
6	L3P	A	301	20/59	0.45	0.45	10.70	90,91,92,92	0
6	L3P	A	331	20/59	0.29	0.40	6.63	80,82,83,83	0
6	L3P	B	331	20/59	0.46	0.46	6.52	94,97,99,99	0
6	L3P	D	330	20/59	0.44	0.33	6.45	96,97,98,98	0
3	22B	D	300	54/54	0.46	0.46	5.76	111,114,120,120	0
3	22B	A	300	54/54	0.59	0.36	4.24	71,82,110,111	0
3	22B	B	300	54/54	0.82	0.21	3.71	36,57,91,91	0
7	CL	D	402	1/1	0.84	0.24	3.51	65,65,65,65	0
2	RET	A	292	20/21	0.96	0.13	1.14	19,25,29,29	0
2	RET	B	292	20/21	0.96	0.12	0.70	24,30,35,35	0
7	CL	D	401	1/1	0.96	0.15	0.55	51,51,51,51	0
2	RET	D	292	20/21	0.83	0.15	0.34	42,44,45,47	0
7	CL	B	401	1/1	0.99	0.09	-0.99	28,28,28,28	0
7	CL	A	401	1/1	1.00	0.11	-1.41	26,26,26,26	0
6	L3P	A	298	20/59	0.31	0.69	-	111,112,113,113	0
7	CL	B	402	1/1	0.95	0.20	-	62,62,62,62	0
7	CL	A	402	1/1	0.97	0.05	-	42,42,42,42	0
6	L3P	A	299	20/59	0.49	0.92	-	115,116,118,118	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.