



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:51 PM GMT

PDB ID : 1HA7
Title : STRUCTURE OF A LIGHT-HARVESTING PHYCOBILIPROTEIN, C-PHYCOCYANIN FROM SPIRULINA PLATENSIS AT 2.2Å RESOLUTION
Authors : Padyana, A.K.; Rajashankar, K.R.; Ramakumar, S.
Deposited on : 2001-03-29
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (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

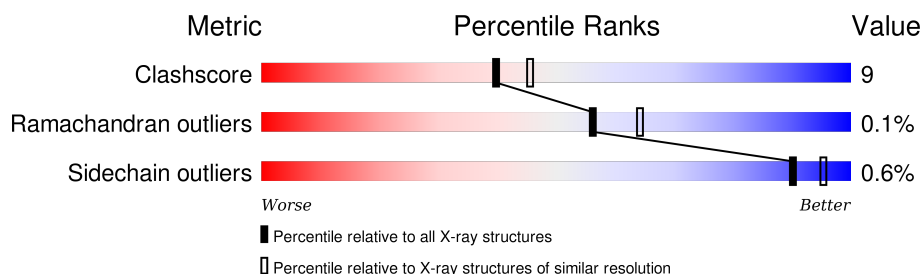
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)









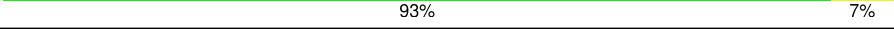


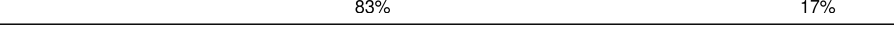





The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	162	
1	C	162	
1	E	162	
1	G	162	
1	I	162	
1	K	162	
1	M	162	

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Mol	Chain	Length	Quality of chain
1	O	162	 88% 12%
1	Q	162	 85% 15%
1	S	162	 83% 17%
1	U	162	 83% 17%
1	W	162	 81% 19%
2	B	172	 82% 18%
2	D	172	 88% 10% •
2	F	172	 85% 15%
2	H	172	 93% 7%
2	J	172	 87% 13%
2	L	172	 90% 9% •
2	N	172	 83% 17%
2	P	172	 88% 12%
2	R	172	 84% 16%
2	T	172	 80% 20%
2	V	172	 88% 11% •
2	X	172	 88% 12% •

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	CYC	E	184	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 33855 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 C-PHYCOCYANIN ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	C	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	E	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	G	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	I	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	K	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	M	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	O	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	Q	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	S	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	U	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			
1	W	162	Total	C	N	O	S	0	0	0
			1238	781	208	243	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	LEU	ARG	CONFLICT	UNP P72509
A	160	THR	GLY	CONFLICT	UNP P72509
C	51	LEU	ARG	CONFLICT	UNP P72509
C	160	THR	GLY	CONFLICT	UNP P72509
E	51	LEU	ARG	CONFLICT	UNP P72509

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Chain	Residue	Modelled	Actual	Comment	Reference
E	160	THR	GLY	CONFLICT	UNP P72509
G	51	LEU	ARG	CONFLICT	UNP P72509
G	160	THR	GLY	CONFLICT	UNP P72509
I	51	LEU	ARG	CONFLICT	UNP P72509
I	160	THR	GLY	CONFLICT	UNP P72509
K	51	LEU	ARG	CONFLICT	UNP P72509
K	160	THR	GLY	CONFLICT	UNP P72509
M	51	LEU	ARG	CONFLICT	UNP P72509
M	160	THR	GLY	CONFLICT	UNP P72509
O	51	LEU	ARG	CONFLICT	UNP P72509
O	160	THR	GLY	CONFLICT	UNP P72509
Q	51	LEU	ARG	CONFLICT	UNP P72509
Q	160	THR	GLY	CONFLICT	UNP P72509
S	51	LEU	ARG	CONFLICT	UNP P72509
S	160	THR	GLY	CONFLICT	UNP P72509
U	51	LEU	ARG	CONFLICT	UNP P72509
U	160	THR	GLY	CONFLICT	UNP P72509
W	51	LEU	ARG	CONFLICT	UNP P72509
W	160	THR	GLY	CONFLICT	UNP P72509

- Molecule 2 is a protein called C-PHYCOCYANIN BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	D	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	F	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	H	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	J	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	L	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	N	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	P	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	R	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	T	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			

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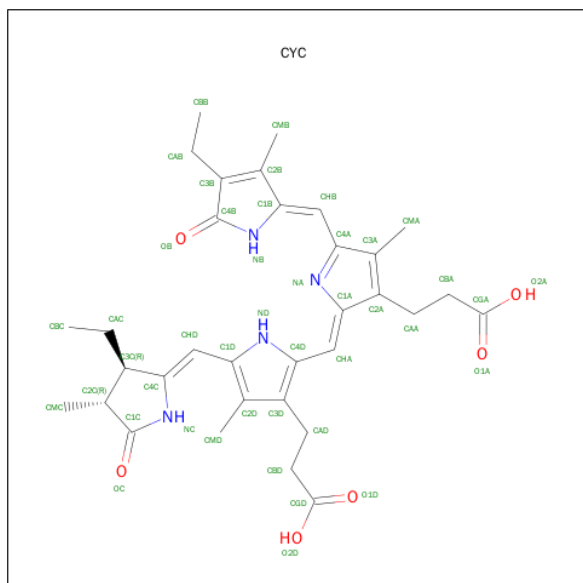
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	V	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			
2	X	172	Total	C	N	O	S	0	0	0
			1264	781	221	252	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	78	SER	ASN	CONFLICT	UNP P72508
D	78	SER	ASN	CONFLICT	UNP P72508
F	78	SER	ASN	CONFLICT	UNP P72508
H	78	SER	ASN	CONFLICT	UNP P72508
J	78	SER	ASN	CONFLICT	UNP P72508
L	78	SER	ASN	CONFLICT	UNP P72508
N	78	SER	ASN	CONFLICT	UNP P72508
P	78	SER	ASN	CONFLICT	UNP P72508
R	78	SER	ASN	CONFLICT	UNP P72508
T	78	SER	ASN	CONFLICT	UNP P72508
V	78	SER	ASN	CONFLICT	UNP P72508
X	78	SER	ASN	CONFLICT	UNP P72508

- Molecule 3 is PHYCOCYANOBILIN (three-letter code: CYC) (formula: $C_{33}H_{40}N_4O_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			43	33	4	6		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total 43	C 33	N 4	O 6	0	0
3	B	1	Total 43	C 33	N 4	O 6	0	0
3	C	1	Total 43	C 33	N 4	O 6	0	0
3	D	1	Total 43	C 33	N 4	O 6	0	0
3	D	1	Total 43	C 33	N 4	O 6	0	0
3	E	1	Total 43	C 33	N 4	O 6	0	0
3	F	1	Total 43	C 33	N 4	O 6	0	0
3	F	1	Total 43	C 33	N 4	O 6	0	0
3	G	1	Total 43	C 33	N 4	O 6	0	0
3	H	1	Total 43	C 33	N 4	O 6	0	0
3	H	1	Total 43	C 33	N 4	O 6	0	0
3	I	1	Total 43	C 33	N 4	O 6	0	0
3	J	1	Total 43	C 33	N 4	O 6	0	0
3	J	1	Total 43	C 33	N 4	O 6	0	0
3	K	1	Total 43	C 33	N 4	O 6	0	0
3	L	1	Total 43	C 33	N 4	O 6	0	0
3	L	1	Total 43	C 33	N 4	O 6	0	0
3	M	1	Total 43	C 33	N 4	O 6	0	0
3	N	1	Total 43	C 33	N 4	O 6	0	0
3	N	1	Total 43	C 33	N 4	O 6	0	0
3	O	1	Total 43	C 33	N 4	O 6	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	P	1	Total 43	C 33	N 4	O 6	0	0
3	P	1	Total 43	C 33	N 4	O 6	0	0
3	Q	1	Total 43	C 33	N 4	O 6	0	0
3	R	1	Total 43	C 33	N 4	O 6	0	0
3	R	1	Total 43	C 33	N 4	O 6	0	0
3	S	1	Total 43	C 33	N 4	O 6	0	0
3	T	1	Total 43	C 33	N 4	O 6	0	0
3	T	1	Total 43	C 33	N 4	O 6	0	0
3	U	1	Total 43	C 33	N 4	O 6	0	0
3	V	1	Total 43	C 33	N 4	O 6	0	0
3	V	1	Total 43	C 33	N 4	O 6	0	0
3	W	1	Total 43	C 33	N 4	O 6	0	0
3	X	1	Total 43	C 33	N 4	O 6	0	0
3	X	1	Total 43	C 33	N 4	O 6	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	120	Total 120	O 120	0	0
4	B	102	Total 102	O 102	0	0
4	C	77	Total 77	O 77	0	0
4	D	95	Total 95	O 95	0	0
4	E	111	Total 111	O 111	0	0

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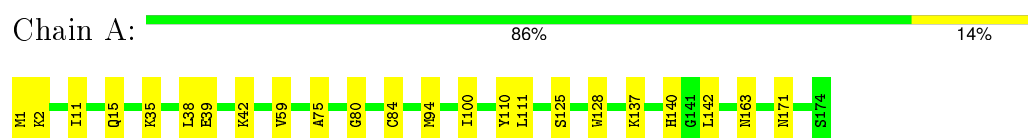
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	115	Total 115	O 115	0	0
4	G	79	Total 79	O 79	0	0
4	H	113	Total 113	O 113	0	0
4	I	120	Total 120	O 120	0	0
4	J	102	Total 102	O 102	0	0
4	K	98	Total 98	O 98	0	0
4	L	107	Total 107	O 107	0	0
4	M	73	Total 73	O 73	0	0
4	N	94	Total 94	O 94	0	0
4	O	102	Total 102	O 102	0	0
4	P	83	Total 83	O 83	0	0
4	Q	93	Total 93	O 93	0	0
4	R	72	Total 72	O 72	0	0
4	S	104	Total 104	O 104	0	0
4	T	58	Total 58	O 58	0	0
4	U	62	Total 62	O 62	0	0
4	V	90	Total 90	O 90	0	0
4	W	111	Total 111	O 111	0	0
4	X	102	Total 102	O 102	0	0

3 Residue-property plots [i](#)

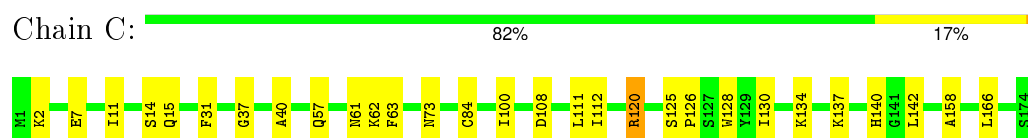
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

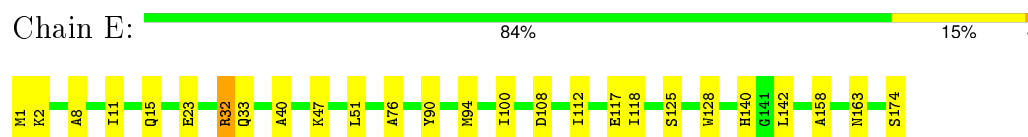
- Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



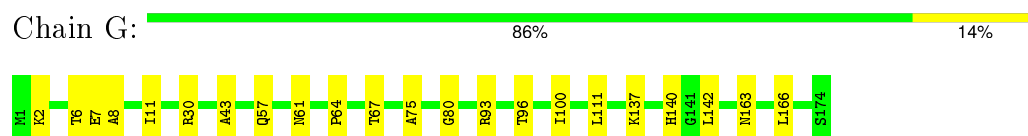
- Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



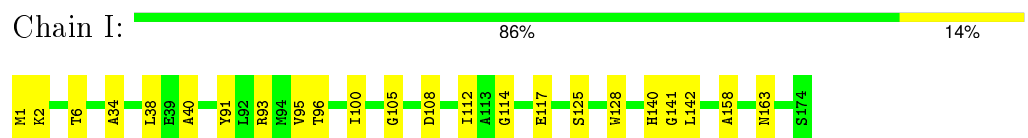
- Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



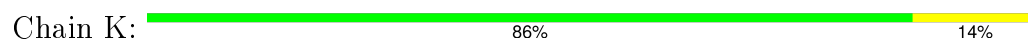
- Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



- Molecule 1: C-PHYCOCYANIN ALPHA CHAIN

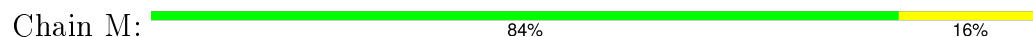


- Molecule 1: C-PHYCOCYANIN ALPHA CHAIN

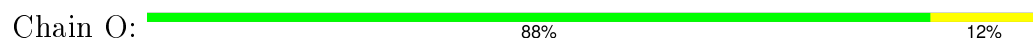




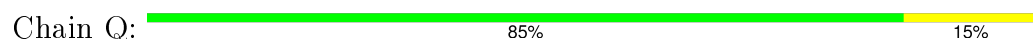
• Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



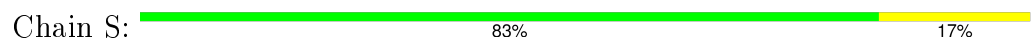
• Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



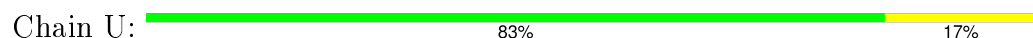
• Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



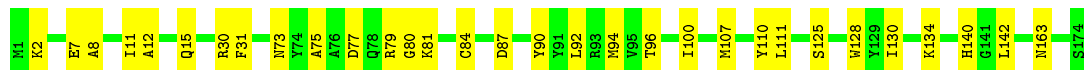
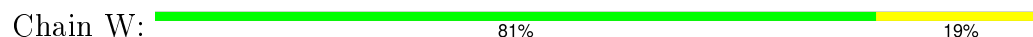
• Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



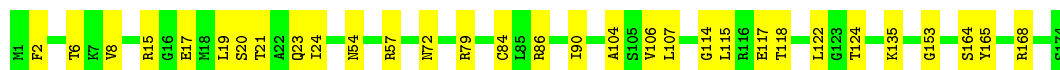
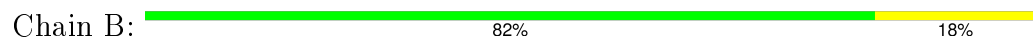
• Molecule 1: C-PHYCOCYANIN ALPHA CHAIN




• Molecule 1: C-PHYCOCYANIN ALPHA CHAIN



• Molecule 2: C-PHYCOCYANIN BETA CHAIN




- Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain D:  88% 10%



- Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain F:  85% 15%




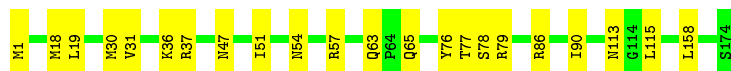
- Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain H:  93% 7%




- Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain J:  87% 13%




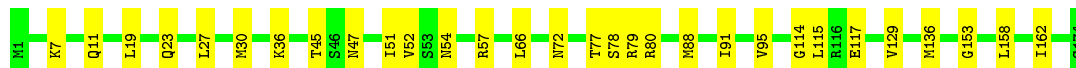
- Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain L:  90% 9%




- Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain N:  83% 17%




- Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain P:  88% 12%



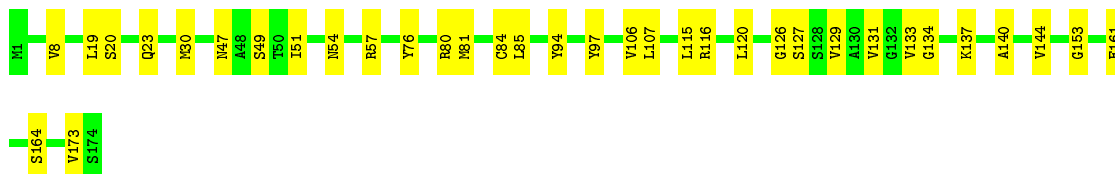
- Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain R:  84% 16%



• Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain T: 80% 20%



• Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain V: 88% 11%



• Molecule 2: C-PHYCOCYANIN BETA CHAIN

Chain X: 88% 12%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	107.20Å 115.40Å 183.04Å 90.00° 90.21° 90.00°	Depositor
Resolution (Å)	22.90 – 2.20	Depositor
% Data completeness (in resolution range)	92.4 (22.90-2.20)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.192 , 0.238	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	33855	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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: CYC, MEN

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	0.34	0/1261	0.54	0/1704
1	C	0.33	0/1261	0.53	0/1704
1	E	0.34	0/1261	0.54	0/1704
1	G	0.32	0/1261	0.52	0/1704
1	I	0.34	0/1261	0.55	0/1704
1	K	0.33	0/1261	0.54	0/1704
1	M	0.32	0/1261	0.52	0/1704
1	O	0.35	0/1261	0.53	0/1704
1	Q	0.32	0/1261	0.53	0/1704
1	S	0.34	0/1261	0.54	0/1704
1	U	0.31	0/1261	0.52	0/1704
1	W	0.34	0/1261	0.53	0/1704
2	B	0.31	0/1268	0.55	0/1715
2	D	0.32	0/1268	0.54	0/1715
2	F	0.33	0/1268	0.54	0/1715
2	H	0.34	0/1268	0.56	0/1715
2	J	0.32	0/1268	0.55	0/1715
2	L	0.31	0/1268	0.54	0/1715
2	N	0.32	0/1268	0.54	0/1715
2	P	0.30	0/1268	0.53	0/1715
2	R	0.31	0/1268	0.54	0/1715
2	T	0.31	0/1268	0.54	0/1715
2	V	0.32	0/1268	0.55	0/1715
2	X	0.33	0/1268	0.55	0/1715
All	All	0.32	0/30348	0.54	0/41028

There are no bond length outliers.

There are no bond angle outliers.

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	1238	0	1216	23	0
1	C	1238	0	1216	29	0
1	E	1238	0	1216	21	0
1	G	1238	0	1216	21	0
1	I	1238	0	1216	18	0
1	K	1238	0	1216	24	0
1	M	1238	0	1216	27	0
1	O	1238	0	1216	20	0
1	Q	1238	0	1216	26	0
1	S	1238	0	1216	29	0
1	U	1238	0	1216	30	0
1	W	1238	0	1216	31	0
2	B	1264	0	1263	31	0
2	D	1264	0	1263	21	0
2	F	1264	0	1263	20	0
2	H	1264	0	1263	13	0
2	J	1264	0	1263	20	0
2	L	1264	0	1263	15	0
2	N	1264	0	1263	30	0
2	P	1264	0	1263	15	0
2	R	1264	0	1263	19	0
2	T	1264	0	1263	33	0
2	V	1264	0	1263	21	0
2	X	1264	0	1263	19	0
3	A	43	0	36	4	0
3	B	86	0	72	9	0
3	C	43	0	36	4	0
3	D	86	0	72	6	0
3	E	43	0	36	2	0
3	F	86	0	72	8	0
3	G	43	0	35	1	0
3	H	86	0	72	8	0
3	I	43	0	36	1	0
3	J	86	0	72	5	0
3	K	43	0	36	2	0
3	L	86	0	72	9	0
3	M	43	0	36	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	N	86	0	72	11	0
3	O	43	0	36	4	0
3	P	86	0	72	8	0
3	Q	43	0	36	3	0
3	R	86	0	72	7	0
3	S	43	0	36	5	0
3	T	86	0	72	7	0
3	U	43	0	36	5	0
3	V	86	0	72	5	0
3	W	43	0	36	3	0
3	X	86	0	72	6	0
4	A	120	0	0	2	0
4	B	102	0	0	3	0
4	C	77	0	0	4	0
4	D	95	0	0	1	0
4	E	111	0	0	1	0
4	F	115	0	0	2	0
4	G	79	0	0	3	0
4	H	113	0	0	1	0
4	I	120	0	0	1	0
4	J	102	0	0	1	0
4	K	98	0	0	1	0
4	L	107	0	0	0	0
4	M	73	0	0	3	0
4	N	94	0	0	1	0
4	O	102	0	0	2	0
4	P	83	0	0	1	0
4	Q	93	0	0	3	0
4	R	72	0	0	2	0
4	S	104	0	0	3	0
4	T	58	0	0	1	0
4	U	62	0	0	3	0
4	V	90	0	0	1	0
4	W	111	0	0	1	0
4	X	102	0	0	3	0
All	All	33855	0	31043	553	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 9.

The worst 5 of 553 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)
2:D:20:SER:H	2:D:23:GLN:HE21	1.09	0.97
1:Q:11:ILE:HD11	1:U:11:ILE:HD11	1.50	0.94
1:O:140:HIS:HD2	1:O:142:LEU:H	1.12	0.93
1:K:42:LYS:HE3	2:L:21:THR:HG23	1.51	0.93
1:K:73:ASN:H	1:K:73:ASN:HD22	1.10	0.92

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	160/162 (99%)	155 (97%)	5 (3%)	0	100	100
1	C	160/162 (99%)	153 (96%)	7 (4%)	0	100	100
1	E	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
1	G	160/162 (99%)	155 (97%)	5 (3%)	0	100	100
1	I	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
1	K	160/162 (99%)	154 (96%)	6 (4%)	0	100	100
1	M	160/162 (99%)	153 (96%)	7 (4%)	0	100	100
1	O	160/162 (99%)	155 (97%)	5 (3%)	0	100	100
1	Q	160/162 (99%)	156 (98%)	4 (2%)	0	100	100
1	S	160/162 (99%)	154 (96%)	5 (3%)	1 (1%)	30	29
1	U	160/162 (99%)	151 (94%)	8 (5%)	1 (1%)	30	29
1	W	160/162 (99%)	154 (96%)	6 (4%)	0	100	100
2	B	169/172 (98%)	164 (97%)	5 (3%)	0	100	100
2	D	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	F	169/172 (98%)	165 (98%)	3 (2%)	1 (1%)	30	29
2	H	169/172 (98%)	167 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	J	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	L	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
2	N	169/172 (98%)	166 (98%)	2 (1%)	1 (1%)	30	29
2	P	169/172 (98%)	166 (98%)	3 (2%)	0	100	100
2	R	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	T	169/172 (98%)	165 (98%)	4 (2%)	0	100	100
2	V	169/172 (98%)	166 (98%)	2 (1%)	1 (1%)	30	29
2	X	169/172 (98%)	167 (99%)	2 (1%)	0	100	100
All	All	3948/4008 (98%)	3842 (97%)	101 (3%)	5 (0%)	56	64

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	S	2	LYS
1	U	71	GLY
2	N	77	THR
2	F	77	THR
2	V	77	THR

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	125/125 (100%)	125 (100%)	0	100	100
1	C	125/125 (100%)	124 (99%)	1 (1%)	86	93
1	E	125/125 (100%)	124 (99%)	1 (1%)	86	93
1	G	125/125 (100%)	125 (100%)	0	100	100
1	I	125/125 (100%)	125 (100%)	0	100	100
1	K	125/125 (100%)	124 (99%)	1 (1%)	86	93
1	M	125/125 (100%)	124 (99%)	1 (1%)	86	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	125/125 (100%)	125 (100%)	0	100	100
1	Q	125/125 (100%)	124 (99%)	1 (1%)	86	93
1	S	125/125 (100%)	125 (100%)	0	100	100
1	U	125/125 (100%)	125 (100%)	0	100	100
1	W	125/125 (100%)	125 (100%)	0	100	100
2	B	131/131 (100%)	131 (100%)	0	100	100
2	D	131/131 (100%)	129 (98%)	2 (2%)	72	84
2	F	131/131 (100%)	131 (100%)	0	100	100
2	H	131/131 (100%)	131 (100%)	0	100	100
2	J	131/131 (100%)	130 (99%)	1 (1%)	86	93
2	L	131/131 (100%)	130 (99%)	1 (1%)	86	93
2	N	131/131 (100%)	131 (100%)	0	100	100
2	P	131/131 (100%)	130 (99%)	1 (1%)	86	93
2	R	131/131 (100%)	129 (98%)	2 (2%)	72	84
2	T	131/131 (100%)	130 (99%)	1 (1%)	86	93
2	V	131/131 (100%)	129 (98%)	2 (2%)	72	84
2	X	131/131 (100%)	129 (98%)	2 (2%)	72	84
All	All	3072/3072 (100%)	3055 (99%)	17 (1%)	90	95

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	69	MET
2	P	113	ASN
2	V	65	GLN
2	L	30	MET
2	V	168	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 112 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	47	ASN
1	O	61	ASN
2	V	65	GLN
2	L	113	ASN

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Mol	Chain	Res	Type
1	M	171	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 non-standard protein/DNA/RNA residues 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	MEN	B	72	2	7,8,9	0.44	0	5,9,11	0.88	0
2	MEN	D	72	2	7,8,9	0.42	0	5,9,11	0.97	1 (20%)
2	MEN	F	72	2	7,8,9	0.44	0	5,9,11	1.01	1 (20%)
2	MEN	H	72	2	7,8,9	0.51	0	5,9,11	0.94	1 (20%)
2	MEN	J	72	2	7,8,9	0.43	0	5,9,11	0.90	0
2	MEN	L	72	2	7,8,9	0.45	0	5,9,11	0.92	1 (20%)
2	MEN	N	72	2	7,8,9	0.47	0	5,9,11	0.97	1 (20%)
2	MEN	P	72	2	7,8,9	0.44	0	5,9,11	0.95	1 (20%)
2	MEN	R	72	2	7,8,9	0.48	0	5,9,11	0.96	1 (20%)
2	MEN	T	72	2	7,8,9	0.48	0	5,9,11	0.92	1 (20%)
2	MEN	V	72	2	7,8,9	0.48	0	5,9,11	0.89	0
2	MEN	X	72	2	7,8,9	0.41	0	5,9,11	0.94	1 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MEN	B	72	2	-	0/6/8/10	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MEN	D	72	2	-	0/6/8/10	0/0/0/0
2	MEN	F	72	2	-	0/6/8/10	0/0/0/0
2	MEN	H	72	2	-	0/6/8/10	0/0/0/0
2	MEN	J	72	2	-	0/6/8/10	0/0/0/0
2	MEN	L	72	2	-	0/6/8/10	0/0/0/0
2	MEN	N	72	2	-	0/6/8/10	0/0/0/0
2	MEN	P	72	2	-	0/6/8/10	0/0/0/0
2	MEN	R	72	2	-	0/6/8/10	0/0/0/0
2	MEN	T	72	2	-	0/6/8/10	0/0/0/0
2	MEN	V	72	2	-	0/6/8/10	0/0/0/0
2	MEN	X	72	2	-	0/6/8/10	0/0/0/0

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	72	MEN	O-C-CA	-2.22	119.71	125.49
2	D	72	MEN	O-C-CA	-2.15	119.89	125.49
2	R	72	MEN	O-C-CA	-2.15	119.90	125.49
2	N	72	MEN	O-C-CA	-2.14	119.90	125.49
2	P	72	MEN	O-C-CA	-2.12	119.96	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	72	MEN	2	0
2	H	72	MEN	1	0
2	N	72	MEN	2	0
2	P	72	MEN	1	0
2	V	72	MEN	1	0
2	X	72	MEN	1	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

36 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$
3	CYC	A	184	1	35,46,46	1.94	11 (31%)	47,67,67	3.01	16 (34%)
3	CYC	B	184	2	35,46,46	2.01	8 (22%)	47,67,67	2.97	15 (31%)
3	CYC	B	255	2	35,46,46	1.97	10 (28%)	47,67,67	2.95	16 (34%)
3	CYC	C	184	1	35,46,46	1.96	9 (25%)	47,67,67	3.05	14 (29%)
3	CYC	D	184	2	35,46,46	1.93	10 (28%)	47,67,67	3.03	13 (27%)
3	CYC	D	255	2	35,46,46	2.04	8 (22%)	47,67,67	2.87	13 (27%)
3	CYC	E	184	1	35,46,46	1.83	9 (25%)	47,67,67	3.04	16 (34%)
3	CYC	F	184	2	35,46,46	1.98	9 (25%)	47,67,67	3.06	14 (29%)
3	CYC	F	255	2	35,46,46	2.02	8 (22%)	47,67,67	2.92	14 (29%)
3	CYC	G	184	1	35,46,46	1.87	9 (25%)	47,67,67	3.01	17 (36%)
3	CYC	H	184	2	35,46,46	1.94	10 (28%)	47,67,67	2.96	14 (29%)
3	CYC	H	255	2	35,46,46	2.17	8 (22%)	47,67,67	2.92	13 (27%)
3	CYC	I	184	1	35,46,46	1.92	10 (28%)	47,67,67	3.05	14 (29%)
3	CYC	J	184	2	35,46,46	2.15	8 (22%)	47,67,67	2.94	15 (31%)
3	CYC	J	255	2	35,46,46	1.94	8 (22%)	47,67,67	3.02	15 (31%)
3	CYC	K	184	1	35,46,46	1.99	10 (28%)	47,67,67	3.10	17 (36%)
3	CYC	L	184	2	35,46,46	1.97	10 (28%)	47,67,67	3.04	14 (29%)
3	CYC	L	255	2	35,46,46	2.03	8 (22%)	47,67,67	2.91	14 (29%)
3	CYC	M	184	1	35,46,46	1.89	11 (31%)	47,67,67	3.03	14 (29%)
3	CYC	N	184	2	35,46,46	1.96	8 (22%)	47,67,67	2.94	14 (29%)
3	CYC	N	255	2	35,46,46	2.13	9 (25%)	47,67,67	2.93	13 (27%)
3	CYC	O	184	1	35,46,46	1.91	10 (28%)	47,67,67	2.95	15 (31%)
3	CYC	P	184	2	35,46,46	1.99	9 (25%)	47,67,67	3.00	14 (29%)
3	CYC	P	255	2	35,46,46	2.05	8 (22%)	47,67,67	2.92	14 (29%)
3	CYC	Q	184	1	35,46,46	1.89	10 (28%)	47,67,67	3.07	15 (31%)
3	CYC	R	184	2	35,46,46	2.02	10 (28%)	47,67,67	3.10	16 (34%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	CYC	R	255	2	35,46,46	1.98	10 (28%)	47,67,67	2.98	15 (31%)
3	CYC	S	184	1	35,46,46	1.88	10 (28%)	47,67,67	3.02	16 (34%)
3	CYC	T	184	2	35,46,46	1.98	12 (34%)	47,67,67	3.01	14 (29%)
3	CYC	T	255	2	35,46,46	2.04	10 (28%)	47,67,67	2.94	16 (34%)
3	CYC	U	184	1	35,46,46	2.02	10 (28%)	47,67,67	3.05	16 (34%)
3	CYC	V	184	2	35,46,46	1.96	9 (25%)	47,67,67	3.01	15 (31%)
3	CYC	V	255	2	35,46,46	2.00	9 (25%)	47,67,67	2.91	14 (29%)
3	CYC	W	184	1	35,46,46	1.85	11 (31%)	47,67,67	3.05	15 (31%)
3	CYC	X	184	2	35,46,46	1.96	10 (28%)	47,67,67	3.00	13 (27%)
3	CYC	X	255	2	35,46,46	2.00	10 (28%)	47,67,67	2.90	15 (31%)

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
3	CYC	A	184	1	-	2/21/74/74	0/4/4/4
3	CYC	B	184	2	-	2/21/74/74	0/4/4/4
3	CYC	B	255	2	-	2/21/74/74	0/4/4/4
3	CYC	C	184	1	-	2/21/74/74	0/4/4/4
3	CYC	D	184	2	-	2/21/74/74	0/4/4/4
3	CYC	D	255	2	-	2/21/74/74	0/4/4/4
3	CYC	E	184	1	1/1/14/19	2/21/74/74	0/4/4/4
3	CYC	F	184	2	-	2/21/74/74	0/4/4/4
3	CYC	F	255	2	-	2/21/74/74	0/4/4/4
3	CYC	G	184	1	-	2/21/74/74	0/4/4/4
3	CYC	H	184	2	-	2/21/74/74	0/4/4/4
3	CYC	H	255	2	-	2/21/74/74	0/4/4/4
3	CYC	I	184	1	-	2/21/74/74	0/4/4/4
3	CYC	J	184	2	-	2/21/74/74	0/4/4/4
3	CYC	J	255	2	-	2/21/74/74	0/4/4/4
3	CYC	K	184	1	-	2/21/74/74	0/4/4/4
3	CYC	L	184	2	-	2/21/74/74	0/4/4/4
3	CYC	L	255	2	-	2/21/74/74	0/4/4/4
3	CYC	M	184	1	-	2/21/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CYC	N	184	2	-	2/21/74/74	0/4/4/4
3	CYC	N	255	2	-	2/21/74/74	0/4/4/4
3	CYC	O	184	1	-	2/21/74/74	0/4/4/4
3	CYC	P	184	2	-	2/21/74/74	0/4/4/4
3	CYC	P	255	2	-	2/21/74/74	0/4/4/4
3	CYC	Q	184	1	-	2/21/74/74	0/4/4/4
3	CYC	R	184	2	-	2/21/74/74	0/4/4/4
3	CYC	R	255	2	-	2/21/74/74	0/4/4/4
3	CYC	S	184	1	-	2/21/74/74	0/4/4/4
3	CYC	T	184	2	-	2/21/74/74	0/4/4/4
3	CYC	T	255	2	-	2/21/74/74	0/4/4/4
3	CYC	U	184	1	-	2/21/74/74	0/4/4/4
3	CYC	V	184	2	-	2/21/74/74	0/4/4/4
3	CYC	V	255	2	-	2/21/74/74	0/4/4/4
3	CYC	W	184	1	-	2/21/74/74	0/4/4/4
3	CYC	X	184	2	-	2/21/74/74	0/4/4/4
3	CYC	X	255	2	-	2/21/74/74	0/4/4/4

The worst 5 of 339 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	255	CYC	C1C-NC	-5.09	1.31	1.37
3	V	255	CYC	C1C-NC	-4.88	1.31	1.37
3	F	255	CYC	C1C-NC	-4.69	1.31	1.37
3	P	255	CYC	C1C-NC	-4.68	1.31	1.37
3	H	255	CYC	C1C-NC	-4.58	1.31	1.37

The worst 5 of 528 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	R	184	CYC	C4B-C3B-C2B	-7.56	103.73	108.05
3	F	184	CYC	C4B-C3B-C2B	-7.54	103.74	108.05
3	L	184	CYC	C4B-C3B-C2B	-7.40	103.82	108.05
3	T	184	CYC	C4B-C3B-C2B	-7.34	103.86	108.05
3	D	184	CYC	C4B-C3B-C2B	-7.33	103.86	108.05

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	E	184	CYC	C2C

5 of 72 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	X	184	CYC	C1B-CHB-C4A-C3A
3	L	184	CYC	C1B-CHB-C4A-C3A
3	H	184	CYC	C1B-CHB-C4A-C3A
3	J	184	CYC	C1B-CHB-C4A-C3A
3	B	184	CYC	C1B-CHB-C4A-C3A

There are no ring outliers.

36 monomers are involved in 126 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	184	CYC	4	0
3	B	184	CYC	5	0
3	B	255	CYC	4	0
3	C	184	CYC	4	0
3	D	184	CYC	3	0
3	D	255	CYC	3	0
3	E	184	CYC	2	0
3	F	184	CYC	4	0
3	F	255	CYC	4	0
3	G	184	CYC	1	0
3	H	184	CYC	4	0
3	H	255	CYC	4	0
3	I	184	CYC	1	0
3	J	184	CYC	2	0
3	J	255	CYC	3	0
3	K	184	CYC	2	0
3	L	184	CYC	4	0
3	L	255	CYC	5	0
3	M	184	CYC	3	0
3	N	184	CYC	6	0
3	N	255	CYC	5	0
3	O	184	CYC	4	0
3	P	184	CYC	4	0
3	P	255	CYC	4	0
3	Q	184	CYC	3	0
3	R	184	CYC	4	0
3	R	255	CYC	3	0
3	S	184	CYC	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	T	184	CYC	3	0
3	T	255	CYC	4	0
3	U	184	CYC	5	0
3	V	184	CYC	2	0
3	V	255	CYC	3	0
3	W	184	CYC	3	0
3	X	184	CYC	3	0
3	X	255	CYC	3	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 ⓘ

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

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

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

6.4 Ligands ⓘ

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

6.5 Other polymers ⓘ

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