



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 2, 2026 – 03:53 AM UTC

PDB ID : 6HJM / pdb_00006hjm
Title : Myxococcus xanthus MglB
Authors : Varela, P.F.; Navaza, J.; Trapani, S.; Cherfils, J.
Deposited on : 2018-09-04
Resolution : 2.39 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

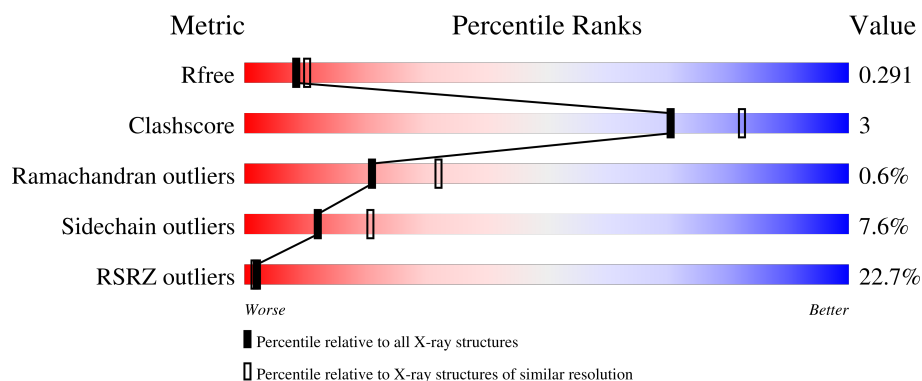
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	192	
1	B	192	
1	C	192	
1	D	192	
1	E	192	

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Mol	Chain	Length	Quality of chain
1	F	192	
1	G	192	
1	H	192	
1	I	192	
1	J	192	
1	K	192	
1	L	192	
1	M	192	
1	N	192	
1	O	192	
1	P	192	
1	Q	192	
1	R	192	
1	S	192	
1	T	192	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 19326 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 MglB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	128	Total	C	N	O	S	0	0	0
			976	616	166	190	4			
1	B	126	Total	C	N	O	S	0	0	0
			961	606	164	188	3			
1	E	123	Total	C	N	O	S	0	0	0
			933	587	161	182	3			
1	F	127	Total	C	N	O	S	0	0	0
			969	611	165	189	4			
1	C	126	Total	C	N	O	S	0	0	0
			961	605	164	188	4			
1	D	120	Total	C	N	O	S	0	0	0
			907	571	158	175	3			
1	G	126	Total	C	N	O	S	0	0	0
			961	605	164	188	4			
1	H	121	Total	C	N	O	S	0	0	0
			916	576	159	178	3			
1	I	127	Total	C	N	O	S	0	0	0
			969	611	165	189	4			
1	J	124	Total	C	N	O	S	0	0	0
			948	597	162	185	4			
1	M	127	Total	C	N	O	S	0	0	0
			969	611	165	189	4			
1	N	123	Total	C	N	O	S	0	0	0
			933	587	161	182	3			
1	Q	125	Total	C	N	O	S	0	0	0
			949	597	163	186	3			
1	R	125	Total	C	N	O	S	0	0	0
			954	600	163	187	4			
1	K	119	Total	C	N	O	S	0	0	0
			901	568	157	173	3			
1	L	125	Total	C	N	O	S	0	0	0
			954	601	163	187	3			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	O	122	Total	C	N	O	S	0	0	0
			925	581	160	181	3			
1	P	133	Total	C	N	O	S	0	0	0
			1017	642	173	198	4			
1	S	127	Total	C	N	O	S	0	0	0
			969	611	165	189	4			
1	T	126	Total	C	N	O	S	0	0	0
			961	605	164	188	4			

There are 680 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	MET	-	initiating methionine	UNP Q50883
A	-31	GLY	-	expression tag	UNP Q50883
A	-30	SER	-	expression tag	UNP Q50883
A	-29	SER	-	expression tag	UNP Q50883
A	-28	HIS	-	expression tag	UNP Q50883
A	-27	HIS	-	expression tag	UNP Q50883
A	-26	HIS	-	expression tag	UNP Q50883
A	-25	HIS	-	expression tag	UNP Q50883
A	-24	HIS	-	expression tag	UNP Q50883
A	-23	HIS	-	expression tag	UNP Q50883
A	-22	SER	-	expression tag	UNP Q50883
A	-21	SER	-	expression tag	UNP Q50883
A	-20	GLY	-	expression tag	UNP Q50883
A	-19	LEU	-	expression tag	UNP Q50883
A	-18	VAL	-	expression tag	UNP Q50883
A	-17	PRO	-	expression tag	UNP Q50883
A	-16	ARG	-	expression tag	UNP Q50883
A	-15	GLY	-	expression tag	UNP Q50883
A	-14	SER	-	expression tag	UNP Q50883
A	-13	HIS	-	expression tag	UNP Q50883
A	-12	MET	-	expression tag	UNP Q50883
A	-11	ALA	-	expression tag	UNP Q50883
A	-10	SER	-	expression tag	UNP Q50883
A	-9	MET	-	expression tag	UNP Q50883
A	-8	THR	-	expression tag	UNP Q50883
A	-7	GLY	-	expression tag	UNP Q50883
A	-6	GLY	-	expression tag	UNP Q50883
A	-5	GLN	-	expression tag	UNP Q50883
A	-4	GLN	-	expression tag	UNP Q50883
A	-3	MET	-	expression tag	UNP Q50883
A	-2	GLY	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ARG	-	expression tag	UNP Q50883
A	0	GLY	-	expression tag	UNP Q50883
A	1	SER	-	expression tag	UNP Q50883
B	-32	MET	-	initiating methionine	UNP Q50883
B	-31	GLY	-	expression tag	UNP Q50883
B	-30	SER	-	expression tag	UNP Q50883
B	-29	SER	-	expression tag	UNP Q50883
B	-28	HIS	-	expression tag	UNP Q50883
B	-27	HIS	-	expression tag	UNP Q50883
B	-26	HIS	-	expression tag	UNP Q50883
B	-25	HIS	-	expression tag	UNP Q50883
B	-24	HIS	-	expression tag	UNP Q50883
B	-23	HIS	-	expression tag	UNP Q50883
B	-22	SER	-	expression tag	UNP Q50883
B	-21	SER	-	expression tag	UNP Q50883
B	-20	GLY	-	expression tag	UNP Q50883
B	-19	LEU	-	expression tag	UNP Q50883
B	-18	VAL	-	expression tag	UNP Q50883
B	-17	PRO	-	expression tag	UNP Q50883
B	-16	ARG	-	expression tag	UNP Q50883
B	-15	GLY	-	expression tag	UNP Q50883
B	-14	SER	-	expression tag	UNP Q50883
B	-13	HIS	-	expression tag	UNP Q50883
B	-12	MET	-	expression tag	UNP Q50883
B	-11	ALA	-	expression tag	UNP Q50883
B	-10	SER	-	expression tag	UNP Q50883
B	-9	MET	-	expression tag	UNP Q50883
B	-8	THR	-	expression tag	UNP Q50883
B	-7	GLY	-	expression tag	UNP Q50883
B	-6	GLY	-	expression tag	UNP Q50883
B	-5	GLN	-	expression tag	UNP Q50883
B	-4	GLN	-	expression tag	UNP Q50883
B	-3	MET	-	expression tag	UNP Q50883
B	-2	GLY	-	expression tag	UNP Q50883
B	-1	ARG	-	expression tag	UNP Q50883
B	0	GLY	-	expression tag	UNP Q50883
B	1	SER	-	expression tag	UNP Q50883
E	-32	MET	-	initiating methionine	UNP Q50883
E	-31	GLY	-	expression tag	UNP Q50883
E	-30	SER	-	expression tag	UNP Q50883
E	-29	SER	-	expression tag	UNP Q50883
E	-28	HIS	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-27	HIS	-	expression tag	UNP Q50883
E	-26	HIS	-	expression tag	UNP Q50883
E	-25	HIS	-	expression tag	UNP Q50883
E	-24	HIS	-	expression tag	UNP Q50883
E	-23	HIS	-	expression tag	UNP Q50883
E	-22	SER	-	expression tag	UNP Q50883
E	-21	SER	-	expression tag	UNP Q50883
E	-20	GLY	-	expression tag	UNP Q50883
E	-19	LEU	-	expression tag	UNP Q50883
E	-18	VAL	-	expression tag	UNP Q50883
E	-17	PRO	-	expression tag	UNP Q50883
E	-16	ARG	-	expression tag	UNP Q50883
E	-15	GLY	-	expression tag	UNP Q50883
E	-14	SER	-	expression tag	UNP Q50883
E	-13	HIS	-	expression tag	UNP Q50883
E	-12	MET	-	expression tag	UNP Q50883
E	-11	ALA	-	expression tag	UNP Q50883
E	-10	SER	-	expression tag	UNP Q50883
E	-9	MET	-	expression tag	UNP Q50883
E	-8	THR	-	expression tag	UNP Q50883
E	-7	GLY	-	expression tag	UNP Q50883
E	-6	GLY	-	expression tag	UNP Q50883
E	-5	GLN	-	expression tag	UNP Q50883
E	-4	GLN	-	expression tag	UNP Q50883
E	-3	MET	-	expression tag	UNP Q50883
E	-2	GLY	-	expression tag	UNP Q50883
E	-1	ARG	-	expression tag	UNP Q50883
E	0	GLY	-	expression tag	UNP Q50883
E	1	SER	-	expression tag	UNP Q50883
F	-32	MET	-	initiating methionine	UNP Q50883
F	-31	GLY	-	expression tag	UNP Q50883
F	-30	SER	-	expression tag	UNP Q50883
F	-29	SER	-	expression tag	UNP Q50883
F	-28	HIS	-	expression tag	UNP Q50883
F	-27	HIS	-	expression tag	UNP Q50883
F	-26	HIS	-	expression tag	UNP Q50883
F	-25	HIS	-	expression tag	UNP Q50883
F	-24	HIS	-	expression tag	UNP Q50883
F	-23	HIS	-	expression tag	UNP Q50883
F	-22	SER	-	expression tag	UNP Q50883
F	-21	SER	-	expression tag	UNP Q50883
F	-20	GLY	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-19	LEU	-	expression tag	UNP Q50883
F	-18	VAL	-	expression tag	UNP Q50883
F	-17	PRO	-	expression tag	UNP Q50883
F	-16	ARG	-	expression tag	UNP Q50883
F	-15	GLY	-	expression tag	UNP Q50883
F	-14	SER	-	expression tag	UNP Q50883
F	-13	HIS	-	expression tag	UNP Q50883
F	-12	MET	-	expression tag	UNP Q50883
F	-11	ALA	-	expression tag	UNP Q50883
F	-10	SER	-	expression tag	UNP Q50883
F	-9	MET	-	expression tag	UNP Q50883
F	-8	THR	-	expression tag	UNP Q50883
F	-7	GLY	-	expression tag	UNP Q50883
F	-6	GLY	-	expression tag	UNP Q50883
F	-5	GLN	-	expression tag	UNP Q50883
F	-4	GLN	-	expression tag	UNP Q50883
F	-3	MET	-	expression tag	UNP Q50883
F	-2	GLY	-	expression tag	UNP Q50883
F	-1	ARG	-	expression tag	UNP Q50883
F	0	GLY	-	expression tag	UNP Q50883
F	1	SER	-	expression tag	UNP Q50883
C	-32	MET	-	initiating methionine	UNP Q50883
C	-31	GLY	-	expression tag	UNP Q50883
C	-30	SER	-	expression tag	UNP Q50883
C	-29	SER	-	expression tag	UNP Q50883
C	-28	HIS	-	expression tag	UNP Q50883
C	-27	HIS	-	expression tag	UNP Q50883
C	-26	HIS	-	expression tag	UNP Q50883
C	-25	HIS	-	expression tag	UNP Q50883
C	-24	HIS	-	expression tag	UNP Q50883
C	-23	HIS	-	expression tag	UNP Q50883
C	-22	SER	-	expression tag	UNP Q50883
C	-21	SER	-	expression tag	UNP Q50883
C	-20	GLY	-	expression tag	UNP Q50883
C	-19	LEU	-	expression tag	UNP Q50883
C	-18	VAL	-	expression tag	UNP Q50883
C	-17	PRO	-	expression tag	UNP Q50883
C	-16	ARG	-	expression tag	UNP Q50883
C	-15	GLY	-	expression tag	UNP Q50883
C	-14	SER	-	expression tag	UNP Q50883
C	-13	HIS	-	expression tag	UNP Q50883
C	-12	MET	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-11	ALA	-	expression tag	UNP Q50883
C	-10	SER	-	expression tag	UNP Q50883
C	-9	MET	-	expression tag	UNP Q50883
C	-8	THR	-	expression tag	UNP Q50883
C	-7	GLY	-	expression tag	UNP Q50883
C	-6	GLY	-	expression tag	UNP Q50883
C	-5	GLN	-	expression tag	UNP Q50883
C	-4	GLN	-	expression tag	UNP Q50883
C	-3	MET	-	expression tag	UNP Q50883
C	-2	GLY	-	expression tag	UNP Q50883
C	-1	ARG	-	expression tag	UNP Q50883
C	0	GLY	-	expression tag	UNP Q50883
C	1	SER	-	expression tag	UNP Q50883
D	-32	MET	-	initiating methionine	UNP Q50883
D	-31	GLY	-	expression tag	UNP Q50883
D	-30	SER	-	expression tag	UNP Q50883
D	-29	SER	-	expression tag	UNP Q50883
D	-28	HIS	-	expression tag	UNP Q50883
D	-27	HIS	-	expression tag	UNP Q50883
D	-26	HIS	-	expression tag	UNP Q50883
D	-25	HIS	-	expression tag	UNP Q50883
D	-24	HIS	-	expression tag	UNP Q50883
D	-23	HIS	-	expression tag	UNP Q50883
D	-22	SER	-	expression tag	UNP Q50883
D	-21	SER	-	expression tag	UNP Q50883
D	-20	GLY	-	expression tag	UNP Q50883
D	-19	LEU	-	expression tag	UNP Q50883
D	-18	VAL	-	expression tag	UNP Q50883
D	-17	PRO	-	expression tag	UNP Q50883
D	-16	ARG	-	expression tag	UNP Q50883
D	-15	GLY	-	expression tag	UNP Q50883
D	-14	SER	-	expression tag	UNP Q50883
D	-13	HIS	-	expression tag	UNP Q50883
D	-12	MET	-	expression tag	UNP Q50883
D	-11	ALA	-	expression tag	UNP Q50883
D	-10	SER	-	expression tag	UNP Q50883
D	-9	MET	-	expression tag	UNP Q50883
D	-8	THR	-	expression tag	UNP Q50883
D	-7	GLY	-	expression tag	UNP Q50883
D	-6	GLY	-	expression tag	UNP Q50883
D	-5	GLN	-	expression tag	UNP Q50883
D	-4	GLN	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	MET	-	expression tag	UNP Q50883
D	-2	GLY	-	expression tag	UNP Q50883
D	-1	ARG	-	expression tag	UNP Q50883
D	0	GLY	-	expression tag	UNP Q50883
D	1	SER	-	expression tag	UNP Q50883
G	-32	MET	-	initiating methionine	UNP Q50883
G	-31	GLY	-	expression tag	UNP Q50883
G	-30	SER	-	expression tag	UNP Q50883
G	-29	SER	-	expression tag	UNP Q50883
G	-28	HIS	-	expression tag	UNP Q50883
G	-27	HIS	-	expression tag	UNP Q50883
G	-26	HIS	-	expression tag	UNP Q50883
G	-25	HIS	-	expression tag	UNP Q50883
G	-24	HIS	-	expression tag	UNP Q50883
G	-23	HIS	-	expression tag	UNP Q50883
G	-22	SER	-	expression tag	UNP Q50883
G	-21	SER	-	expression tag	UNP Q50883
G	-20	GLY	-	expression tag	UNP Q50883
G	-19	LEU	-	expression tag	UNP Q50883
G	-18	VAL	-	expression tag	UNP Q50883
G	-17	PRO	-	expression tag	UNP Q50883
G	-16	ARG	-	expression tag	UNP Q50883
G	-15	GLY	-	expression tag	UNP Q50883
G	-14	SER	-	expression tag	UNP Q50883
G	-13	HIS	-	expression tag	UNP Q50883
G	-12	MET	-	expression tag	UNP Q50883
G	-11	ALA	-	expression tag	UNP Q50883
G	-10	SER	-	expression tag	UNP Q50883
G	-9	MET	-	expression tag	UNP Q50883
G	-8	THR	-	expression tag	UNP Q50883
G	-7	GLY	-	expression tag	UNP Q50883
G	-6	GLY	-	expression tag	UNP Q50883
G	-5	GLN	-	expression tag	UNP Q50883
G	-4	GLN	-	expression tag	UNP Q50883
G	-3	MET	-	expression tag	UNP Q50883
G	-2	GLY	-	expression tag	UNP Q50883
G	-1	ARG	-	expression tag	UNP Q50883
G	0	GLY	-	expression tag	UNP Q50883
G	1	SER	-	expression tag	UNP Q50883
H	-32	MET	-	initiating methionine	UNP Q50883
H	-31	GLY	-	expression tag	UNP Q50883
H	-30	SER	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-29	SER	-	expression tag	UNP Q50883
H	-28	HIS	-	expression tag	UNP Q50883
H	-27	HIS	-	expression tag	UNP Q50883
H	-26	HIS	-	expression tag	UNP Q50883
H	-25	HIS	-	expression tag	UNP Q50883
H	-24	HIS	-	expression tag	UNP Q50883
H	-23	HIS	-	expression tag	UNP Q50883
H	-22	SER	-	expression tag	UNP Q50883
H	-21	SER	-	expression tag	UNP Q50883
H	-20	GLY	-	expression tag	UNP Q50883
H	-19	LEU	-	expression tag	UNP Q50883
H	-18	VAL	-	expression tag	UNP Q50883
H	-17	PRO	-	expression tag	UNP Q50883
H	-16	ARG	-	expression tag	UNP Q50883
H	-15	GLY	-	expression tag	UNP Q50883
H	-14	SER	-	expression tag	UNP Q50883
H	-13	HIS	-	expression tag	UNP Q50883
H	-12	MET	-	expression tag	UNP Q50883
H	-11	ALA	-	expression tag	UNP Q50883
H	-10	SER	-	expression tag	UNP Q50883
H	-9	MET	-	expression tag	UNP Q50883
H	-8	THR	-	expression tag	UNP Q50883
H	-7	GLY	-	expression tag	UNP Q50883
H	-6	GLY	-	expression tag	UNP Q50883
H	-5	GLN	-	expression tag	UNP Q50883
H	-4	GLN	-	expression tag	UNP Q50883
H	-3	MET	-	expression tag	UNP Q50883
H	-2	GLY	-	expression tag	UNP Q50883
H	-1	ARG	-	expression tag	UNP Q50883
H	0	GLY	-	expression tag	UNP Q50883
H	1	SER	-	expression tag	UNP Q50883
I	-32	MET	-	initiating methionine	UNP Q50883
I	-31	GLY	-	expression tag	UNP Q50883
I	-30	SER	-	expression tag	UNP Q50883
I	-29	SER	-	expression tag	UNP Q50883
I	-28	HIS	-	expression tag	UNP Q50883
I	-27	HIS	-	expression tag	UNP Q50883
I	-26	HIS	-	expression tag	UNP Q50883
I	-25	HIS	-	expression tag	UNP Q50883
I	-24	HIS	-	expression tag	UNP Q50883
I	-23	HIS	-	expression tag	UNP Q50883
I	-22	SER	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-21	SER	-	expression tag	UNP Q50883
I	-20	GLY	-	expression tag	UNP Q50883
I	-19	LEU	-	expression tag	UNP Q50883
I	-18	VAL	-	expression tag	UNP Q50883
I	-17	PRO	-	expression tag	UNP Q50883
I	-16	ARG	-	expression tag	UNP Q50883
I	-15	GLY	-	expression tag	UNP Q50883
I	-14	SER	-	expression tag	UNP Q50883
I	-13	HIS	-	expression tag	UNP Q50883
I	-12	MET	-	expression tag	UNP Q50883
I	-11	ALA	-	expression tag	UNP Q50883
I	-10	SER	-	expression tag	UNP Q50883
I	-9	MET	-	expression tag	UNP Q50883
I	-8	THR	-	expression tag	UNP Q50883
I	-7	GLY	-	expression tag	UNP Q50883
I	-6	GLY	-	expression tag	UNP Q50883
I	-5	GLN	-	expression tag	UNP Q50883
I	-4	GLN	-	expression tag	UNP Q50883
I	-3	MET	-	expression tag	UNP Q50883
I	-2	GLY	-	expression tag	UNP Q50883
I	-1	ARG	-	expression tag	UNP Q50883
I	0	GLY	-	expression tag	UNP Q50883
I	1	SER	-	expression tag	UNP Q50883
J	-32	MET	-	initiating methionine	UNP Q50883
J	-31	GLY	-	expression tag	UNP Q50883
J	-30	SER	-	expression tag	UNP Q50883
J	-29	SER	-	expression tag	UNP Q50883
J	-28	HIS	-	expression tag	UNP Q50883
J	-27	HIS	-	expression tag	UNP Q50883
J	-26	HIS	-	expression tag	UNP Q50883
J	-25	HIS	-	expression tag	UNP Q50883
J	-24	HIS	-	expression tag	UNP Q50883
J	-23	HIS	-	expression tag	UNP Q50883
J	-22	SER	-	expression tag	UNP Q50883
J	-21	SER	-	expression tag	UNP Q50883
J	-20	GLY	-	expression tag	UNP Q50883
J	-19	LEU	-	expression tag	UNP Q50883
J	-18	VAL	-	expression tag	UNP Q50883
J	-17	PRO	-	expression tag	UNP Q50883
J	-16	ARG	-	expression tag	UNP Q50883
J	-15	GLY	-	expression tag	UNP Q50883
J	-14	SER	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-13	HIS	-	expression tag	UNP Q50883
J	-12	MET	-	expression tag	UNP Q50883
J	-11	ALA	-	expression tag	UNP Q50883
J	-10	SER	-	expression tag	UNP Q50883
J	-9	MET	-	expression tag	UNP Q50883
J	-8	THR	-	expression tag	UNP Q50883
J	-7	GLY	-	expression tag	UNP Q50883
J	-6	GLY	-	expression tag	UNP Q50883
J	-5	GLN	-	expression tag	UNP Q50883
J	-4	GLN	-	expression tag	UNP Q50883
J	-3	MET	-	expression tag	UNP Q50883
J	-2	GLY	-	expression tag	UNP Q50883
J	-1	ARG	-	expression tag	UNP Q50883
J	0	GLY	-	expression tag	UNP Q50883
J	1	SER	-	expression tag	UNP Q50883
M	-32	MET	-	initiating methionine	UNP Q50883
M	-31	GLY	-	expression tag	UNP Q50883
M	-30	SER	-	expression tag	UNP Q50883
M	-29	SER	-	expression tag	UNP Q50883
M	-28	HIS	-	expression tag	UNP Q50883
M	-27	HIS	-	expression tag	UNP Q50883
M	-26	HIS	-	expression tag	UNP Q50883
M	-25	HIS	-	expression tag	UNP Q50883
M	-24	HIS	-	expression tag	UNP Q50883
M	-23	HIS	-	expression tag	UNP Q50883
M	-22	SER	-	expression tag	UNP Q50883
M	-21	SER	-	expression tag	UNP Q50883
M	-20	GLY	-	expression tag	UNP Q50883
M	-19	LEU	-	expression tag	UNP Q50883
M	-18	VAL	-	expression tag	UNP Q50883
M	-17	PRO	-	expression tag	UNP Q50883
M	-16	ARG	-	expression tag	UNP Q50883
M	-15	GLY	-	expression tag	UNP Q50883
M	-14	SER	-	expression tag	UNP Q50883
M	-13	HIS	-	expression tag	UNP Q50883
M	-12	MET	-	expression tag	UNP Q50883
M	-11	ALA	-	expression tag	UNP Q50883
M	-10	SER	-	expression tag	UNP Q50883
M	-9	MET	-	expression tag	UNP Q50883
M	-8	THR	-	expression tag	UNP Q50883
M	-7	GLY	-	expression tag	UNP Q50883
M	-6	GLY	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
M	-5	GLN	-	expression tag	UNP Q50883
M	-4	GLN	-	expression tag	UNP Q50883
M	-3	MET	-	expression tag	UNP Q50883
M	-2	GLY	-	expression tag	UNP Q50883
M	-1	ARG	-	expression tag	UNP Q50883
M	0	GLY	-	expression tag	UNP Q50883
M	1	SER	-	expression tag	UNP Q50883
N	-32	MET	-	initiating methionine	UNP Q50883
N	-31	GLY	-	expression tag	UNP Q50883
N	-30	SER	-	expression tag	UNP Q50883
N	-29	SER	-	expression tag	UNP Q50883
N	-28	HIS	-	expression tag	UNP Q50883
N	-27	HIS	-	expression tag	UNP Q50883
N	-26	HIS	-	expression tag	UNP Q50883
N	-25	HIS	-	expression tag	UNP Q50883
N	-24	HIS	-	expression tag	UNP Q50883
N	-23	HIS	-	expression tag	UNP Q50883
N	-22	SER	-	expression tag	UNP Q50883
N	-21	SER	-	expression tag	UNP Q50883
N	-20	GLY	-	expression tag	UNP Q50883
N	-19	LEU	-	expression tag	UNP Q50883
N	-18	VAL	-	expression tag	UNP Q50883
N	-17	PRO	-	expression tag	UNP Q50883
N	-16	ARG	-	expression tag	UNP Q50883
N	-15	GLY	-	expression tag	UNP Q50883
N	-14	SER	-	expression tag	UNP Q50883
N	-13	HIS	-	expression tag	UNP Q50883
N	-12	MET	-	expression tag	UNP Q50883
N	-11	ALA	-	expression tag	UNP Q50883
N	-10	SER	-	expression tag	UNP Q50883
N	-9	MET	-	expression tag	UNP Q50883
N	-8	THR	-	expression tag	UNP Q50883
N	-7	GLY	-	expression tag	UNP Q50883
N	-6	GLY	-	expression tag	UNP Q50883
N	-5	GLN	-	expression tag	UNP Q50883
N	-4	GLN	-	expression tag	UNP Q50883
N	-3	MET	-	expression tag	UNP Q50883
N	-2	GLY	-	expression tag	UNP Q50883
N	-1	ARG	-	expression tag	UNP Q50883
N	0	GLY	-	expression tag	UNP Q50883
N	1	SER	-	expression tag	UNP Q50883
Q	-32	MET	-	initiating methionine	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	-31	GLY	-	expression tag	UNP Q50883
Q	-30	SER	-	expression tag	UNP Q50883
Q	-29	SER	-	expression tag	UNP Q50883
Q	-28	HIS	-	expression tag	UNP Q50883
Q	-27	HIS	-	expression tag	UNP Q50883
Q	-26	HIS	-	expression tag	UNP Q50883
Q	-25	HIS	-	expression tag	UNP Q50883
Q	-24	HIS	-	expression tag	UNP Q50883
Q	-23	HIS	-	expression tag	UNP Q50883
Q	-22	SER	-	expression tag	UNP Q50883
Q	-21	SER	-	expression tag	UNP Q50883
Q	-20	GLY	-	expression tag	UNP Q50883
Q	-19	LEU	-	expression tag	UNP Q50883
Q	-18	VAL	-	expression tag	UNP Q50883
Q	-17	PRO	-	expression tag	UNP Q50883
Q	-16	ARG	-	expression tag	UNP Q50883
Q	-15	GLY	-	expression tag	UNP Q50883
Q	-14	SER	-	expression tag	UNP Q50883
Q	-13	HIS	-	expression tag	UNP Q50883
Q	-12	MET	-	expression tag	UNP Q50883
Q	-11	ALA	-	expression tag	UNP Q50883
Q	-10	SER	-	expression tag	UNP Q50883
Q	-9	MET	-	expression tag	UNP Q50883
Q	-8	THR	-	expression tag	UNP Q50883
Q	-7	GLY	-	expression tag	UNP Q50883
Q	-6	GLY	-	expression tag	UNP Q50883
Q	-5	GLN	-	expression tag	UNP Q50883
Q	-4	GLN	-	expression tag	UNP Q50883
Q	-3	MET	-	expression tag	UNP Q50883
Q	-2	GLY	-	expression tag	UNP Q50883
Q	-1	ARG	-	expression tag	UNP Q50883
Q	0	GLY	-	expression tag	UNP Q50883
Q	1	SER	-	expression tag	UNP Q50883
R	-32	MET	-	initiating methionine	UNP Q50883
R	-31	GLY	-	expression tag	UNP Q50883
R	-30	SER	-	expression tag	UNP Q50883
R	-29	SER	-	expression tag	UNP Q50883
R	-28	HIS	-	expression tag	UNP Q50883
R	-27	HIS	-	expression tag	UNP Q50883
R	-26	HIS	-	expression tag	UNP Q50883
R	-25	HIS	-	expression tag	UNP Q50883
R	-24	HIS	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
R	-23	HIS	-	expression tag	UNP Q50883
R	-22	SER	-	expression tag	UNP Q50883
R	-21	SER	-	expression tag	UNP Q50883
R	-20	GLY	-	expression tag	UNP Q50883
R	-19	LEU	-	expression tag	UNP Q50883
R	-18	VAL	-	expression tag	UNP Q50883
R	-17	PRO	-	expression tag	UNP Q50883
R	-16	ARG	-	expression tag	UNP Q50883
R	-15	GLY	-	expression tag	UNP Q50883
R	-14	SER	-	expression tag	UNP Q50883
R	-13	HIS	-	expression tag	UNP Q50883
R	-12	MET	-	expression tag	UNP Q50883
R	-11	ALA	-	expression tag	UNP Q50883
R	-10	SER	-	expression tag	UNP Q50883
R	-9	MET	-	expression tag	UNP Q50883
R	-8	THR	-	expression tag	UNP Q50883
R	-7	GLY	-	expression tag	UNP Q50883
R	-6	GLY	-	expression tag	UNP Q50883
R	-5	GLN	-	expression tag	UNP Q50883
R	-4	GLN	-	expression tag	UNP Q50883
R	-3	MET	-	expression tag	UNP Q50883
R	-2	GLY	-	expression tag	UNP Q50883
R	-1	ARG	-	expression tag	UNP Q50883
R	0	GLY	-	expression tag	UNP Q50883
R	1	SER	-	expression tag	UNP Q50883
K	-32	MET	-	initiating methionine	UNP Q50883
K	-31	GLY	-	expression tag	UNP Q50883
K	-30	SER	-	expression tag	UNP Q50883
K	-29	SER	-	expression tag	UNP Q50883
K	-28	HIS	-	expression tag	UNP Q50883
K	-27	HIS	-	expression tag	UNP Q50883
K	-26	HIS	-	expression tag	UNP Q50883
K	-25	HIS	-	expression tag	UNP Q50883
K	-24	HIS	-	expression tag	UNP Q50883
K	-23	HIS	-	expression tag	UNP Q50883
K	-22	SER	-	expression tag	UNP Q50883
K	-21	SER	-	expression tag	UNP Q50883
K	-20	GLY	-	expression tag	UNP Q50883
K	-19	LEU	-	expression tag	UNP Q50883
K	-18	VAL	-	expression tag	UNP Q50883
K	-17	PRO	-	expression tag	UNP Q50883
K	-16	ARG	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-15	GLY	-	expression tag	UNP Q50883
K	-14	SER	-	expression tag	UNP Q50883
K	-13	HIS	-	expression tag	UNP Q50883
K	-12	MET	-	expression tag	UNP Q50883
K	-11	ALA	-	expression tag	UNP Q50883
K	-10	SER	-	expression tag	UNP Q50883
K	-9	MET	-	expression tag	UNP Q50883
K	-8	THR	-	expression tag	UNP Q50883
K	-7	GLY	-	expression tag	UNP Q50883
K	-6	GLY	-	expression tag	UNP Q50883
K	-5	GLN	-	expression tag	UNP Q50883
K	-4	GLN	-	expression tag	UNP Q50883
K	-3	MET	-	expression tag	UNP Q50883
K	-2	GLY	-	expression tag	UNP Q50883
K	-1	ARG	-	expression tag	UNP Q50883
K	0	GLY	-	expression tag	UNP Q50883
K	1	SER	-	expression tag	UNP Q50883
L	-32	MET	-	initiating methionine	UNP Q50883
L	-31	GLY	-	expression tag	UNP Q50883
L	-30	SER	-	expression tag	UNP Q50883
L	-29	SER	-	expression tag	UNP Q50883
L	-28	HIS	-	expression tag	UNP Q50883
L	-27	HIS	-	expression tag	UNP Q50883
L	-26	HIS	-	expression tag	UNP Q50883
L	-25	HIS	-	expression tag	UNP Q50883
L	-24	HIS	-	expression tag	UNP Q50883
L	-23	HIS	-	expression tag	UNP Q50883
L	-22	SER	-	expression tag	UNP Q50883
L	-21	SER	-	expression tag	UNP Q50883
L	-20	GLY	-	expression tag	UNP Q50883
L	-19	LEU	-	expression tag	UNP Q50883
L	-18	VAL	-	expression tag	UNP Q50883
L	-17	PRO	-	expression tag	UNP Q50883
L	-16	ARG	-	expression tag	UNP Q50883
L	-15	GLY	-	expression tag	UNP Q50883
L	-14	SER	-	expression tag	UNP Q50883
L	-13	HIS	-	expression tag	UNP Q50883
L	-12	MET	-	expression tag	UNP Q50883
L	-11	ALA	-	expression tag	UNP Q50883
L	-10	SER	-	expression tag	UNP Q50883
L	-9	MET	-	expression tag	UNP Q50883
L	-8	THR	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-7	GLY	-	expression tag	UNP Q50883
L	-6	GLY	-	expression tag	UNP Q50883
L	-5	GLN	-	expression tag	UNP Q50883
L	-4	GLN	-	expression tag	UNP Q50883
L	-3	MET	-	expression tag	UNP Q50883
L	-2	GLY	-	expression tag	UNP Q50883
L	-1	ARG	-	expression tag	UNP Q50883
L	0	GLY	-	expression tag	UNP Q50883
L	1	SER	-	expression tag	UNP Q50883
O	-32	MET	-	initiating methionine	UNP Q50883
O	-31	GLY	-	expression tag	UNP Q50883
O	-30	SER	-	expression tag	UNP Q50883
O	-29	SER	-	expression tag	UNP Q50883
O	-28	HIS	-	expression tag	UNP Q50883
O	-27	HIS	-	expression tag	UNP Q50883
O	-26	HIS	-	expression tag	UNP Q50883
O	-25	HIS	-	expression tag	UNP Q50883
O	-24	HIS	-	expression tag	UNP Q50883
O	-23	HIS	-	expression tag	UNP Q50883
O	-22	SER	-	expression tag	UNP Q50883
O	-21	SER	-	expression tag	UNP Q50883
O	-20	GLY	-	expression tag	UNP Q50883
O	-19	LEU	-	expression tag	UNP Q50883
O	-18	VAL	-	expression tag	UNP Q50883
O	-17	PRO	-	expression tag	UNP Q50883
O	-16	ARG	-	expression tag	UNP Q50883
O	-15	GLY	-	expression tag	UNP Q50883
O	-14	SER	-	expression tag	UNP Q50883
O	-13	HIS	-	expression tag	UNP Q50883
O	-12	MET	-	expression tag	UNP Q50883
O	-11	ALA	-	expression tag	UNP Q50883
O	-10	SER	-	expression tag	UNP Q50883
O	-9	MET	-	expression tag	UNP Q50883
O	-8	THR	-	expression tag	UNP Q50883
O	-7	GLY	-	expression tag	UNP Q50883
O	-6	GLY	-	expression tag	UNP Q50883
O	-5	GLN	-	expression tag	UNP Q50883
O	-4	GLN	-	expression tag	UNP Q50883
O	-3	MET	-	expression tag	UNP Q50883
O	-2	GLY	-	expression tag	UNP Q50883
O	-1	ARG	-	expression tag	UNP Q50883
O	0	GLY	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
O	1	SER	-	expression tag	UNP Q50883
P	-32	MET	-	initiating methionine	UNP Q50883
P	-31	GLY	-	expression tag	UNP Q50883
P	-30	SER	-	expression tag	UNP Q50883
P	-29	SER	-	expression tag	UNP Q50883
P	-28	HIS	-	expression tag	UNP Q50883
P	-27	HIS	-	expression tag	UNP Q50883
P	-26	HIS	-	expression tag	UNP Q50883
P	-25	HIS	-	expression tag	UNP Q50883
P	-24	HIS	-	expression tag	UNP Q50883
P	-23	HIS	-	expression tag	UNP Q50883
P	-22	SER	-	expression tag	UNP Q50883
P	-21	SER	-	expression tag	UNP Q50883
P	-20	GLY	-	expression tag	UNP Q50883
P	-19	LEU	-	expression tag	UNP Q50883
P	-18	VAL	-	expression tag	UNP Q50883
P	-17	PRO	-	expression tag	UNP Q50883
P	-16	ARG	-	expression tag	UNP Q50883
P	-15	GLY	-	expression tag	UNP Q50883
P	-14	SER	-	expression tag	UNP Q50883
P	-13	HIS	-	expression tag	UNP Q50883
P	-12	MET	-	expression tag	UNP Q50883
P	-11	ALA	-	expression tag	UNP Q50883
P	-10	SER	-	expression tag	UNP Q50883
P	-9	MET	-	expression tag	UNP Q50883
P	-8	THR	-	expression tag	UNP Q50883
P	-7	GLY	-	expression tag	UNP Q50883
P	-6	GLY	-	expression tag	UNP Q50883
P	-5	GLN	-	expression tag	UNP Q50883
P	-4	GLN	-	expression tag	UNP Q50883
P	-3	MET	-	expression tag	UNP Q50883
P	-2	GLY	-	expression tag	UNP Q50883
P	-1	ARG	-	expression tag	UNP Q50883
P	0	GLY	-	expression tag	UNP Q50883
P	1	SER	-	expression tag	UNP Q50883
S	-32	MET	-	initiating methionine	UNP Q50883
S	-31	GLY	-	expression tag	UNP Q50883
S	-30	SER	-	expression tag	UNP Q50883
S	-29	SER	-	expression tag	UNP Q50883
S	-28	HIS	-	expression tag	UNP Q50883
S	-27	HIS	-	expression tag	UNP Q50883
S	-26	HIS	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
S	-25	HIS	-	expression tag	UNP Q50883
S	-24	HIS	-	expression tag	UNP Q50883
S	-23	HIS	-	expression tag	UNP Q50883
S	-22	SER	-	expression tag	UNP Q50883
S	-21	SER	-	expression tag	UNP Q50883
S	-20	GLY	-	expression tag	UNP Q50883
S	-19	LEU	-	expression tag	UNP Q50883
S	-18	VAL	-	expression tag	UNP Q50883
S	-17	PRO	-	expression tag	UNP Q50883
S	-16	ARG	-	expression tag	UNP Q50883
S	-15	GLY	-	expression tag	UNP Q50883
S	-14	SER	-	expression tag	UNP Q50883
S	-13	HIS	-	expression tag	UNP Q50883
S	-12	MET	-	expression tag	UNP Q50883
S	-11	ALA	-	expression tag	UNP Q50883
S	-10	SER	-	expression tag	UNP Q50883
S	-9	MET	-	expression tag	UNP Q50883
S	-8	THR	-	expression tag	UNP Q50883
S	-7	GLY	-	expression tag	UNP Q50883
S	-6	GLY	-	expression tag	UNP Q50883
S	-5	GLN	-	expression tag	UNP Q50883
S	-4	GLN	-	expression tag	UNP Q50883
S	-3	MET	-	expression tag	UNP Q50883
S	-2	GLY	-	expression tag	UNP Q50883
S	-1	ARG	-	expression tag	UNP Q50883
S	0	GLY	-	expression tag	UNP Q50883
S	1	SER	-	expression tag	UNP Q50883
T	-32	MET	-	initiating methionine	UNP Q50883
T	-31	GLY	-	expression tag	UNP Q50883
T	-30	SER	-	expression tag	UNP Q50883
T	-29	SER	-	expression tag	UNP Q50883
T	-28	HIS	-	expression tag	UNP Q50883
T	-27	HIS	-	expression tag	UNP Q50883
T	-26	HIS	-	expression tag	UNP Q50883
T	-25	HIS	-	expression tag	UNP Q50883
T	-24	HIS	-	expression tag	UNP Q50883
T	-23	HIS	-	expression tag	UNP Q50883
T	-22	SER	-	expression tag	UNP Q50883
T	-21	SER	-	expression tag	UNP Q50883
T	-20	GLY	-	expression tag	UNP Q50883
T	-19	LEU	-	expression tag	UNP Q50883
T	-18	VAL	-	expression tag	UNP Q50883

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Chain	Residue	Modelled	Actual	Comment	Reference
T	-17	PRO	-	expression tag	UNP Q50883
T	-16	ARG	-	expression tag	UNP Q50883
T	-15	GLY	-	expression tag	UNP Q50883
T	-14	SER	-	expression tag	UNP Q50883
T	-13	HIS	-	expression tag	UNP Q50883
T	-12	MET	-	expression tag	UNP Q50883
T	-11	ALA	-	expression tag	UNP Q50883
T	-10	SER	-	expression tag	UNP Q50883
T	-9	MET	-	expression tag	UNP Q50883
T	-8	THR	-	expression tag	UNP Q50883
T	-7	GLY	-	expression tag	UNP Q50883
T	-6	GLY	-	expression tag	UNP Q50883
T	-5	GLN	-	expression tag	UNP Q50883
T	-4	GLN	-	expression tag	UNP Q50883
T	-3	MET	-	expression tag	UNP Q50883
T	-2	GLY	-	expression tag	UNP Q50883
T	-1	ARG	-	expression tag	UNP Q50883
T	0	GLY	-	expression tag	UNP Q50883
T	1	SER	-	expression tag	UNP Q50883

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	32	Total O 32 32	0	0
2	B	27	Total O 27 27	0	0
2	E	12	Total O 12 12	0	0
2	F	23	Total O 23 23	0	0
2	C	13	Total O 13 13	0	0
2	D	7	Total O 7 7	0	0
2	G	9	Total O 9 9	0	0
2	H	12	Total O 12 12	0	0
2	I	18	Total O 18 18	0	0
2	J	12	Total O 12 12	0	0

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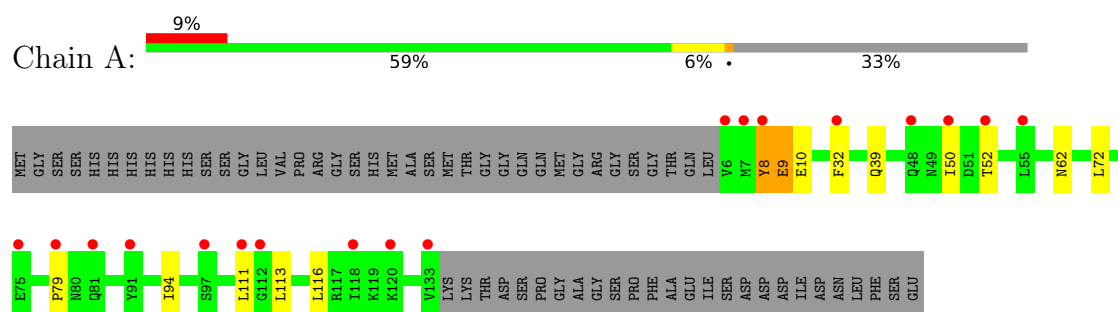
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	M	9	Total 9	O 9	0	0
2	N	13	Total 13	O 13	0	0
2	Q	19	Total 19	O 19	0	0
2	R	18	Total 18	O 18	0	0
2	K	7	Total 7	O 7	0	0
2	L	13	Total 13	O 13	0	0
2	O	6	Total 6	O 6	0	0
2	P	17	Total 17	O 17	0	0
2	S	12	Total 12	O 12	0	0
2	T	14	Total 14	O 14	0	0

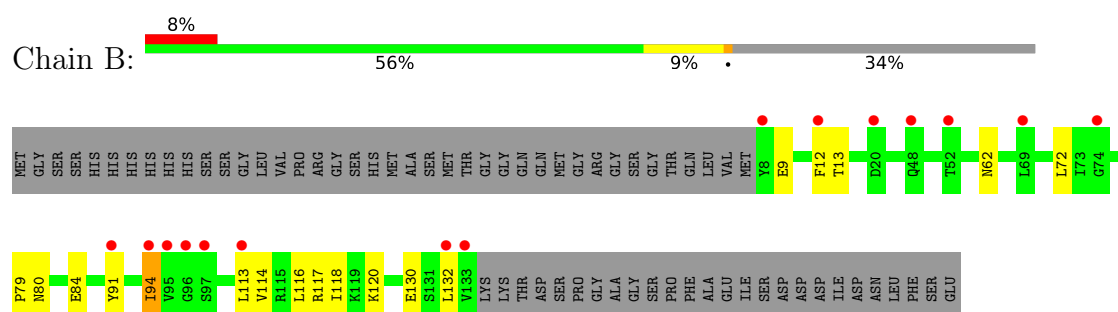
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

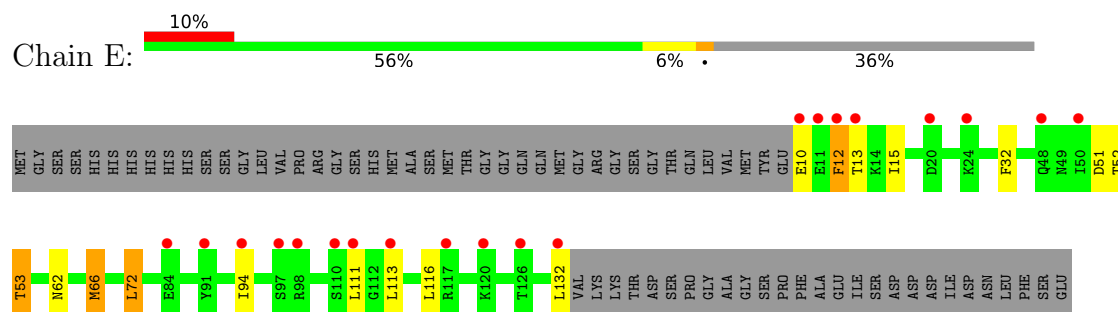
• Molecule 1: MglB



• Molecule 1: MglB

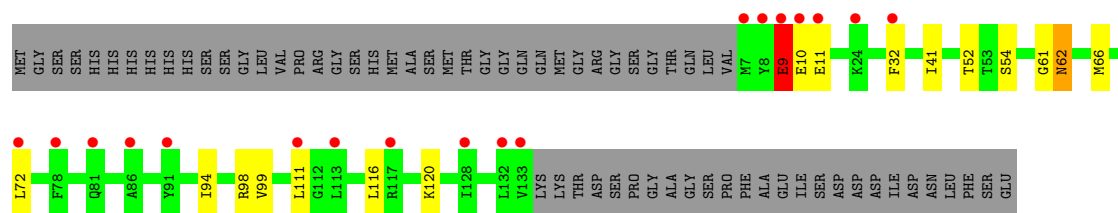


• Molecule 1: MglB

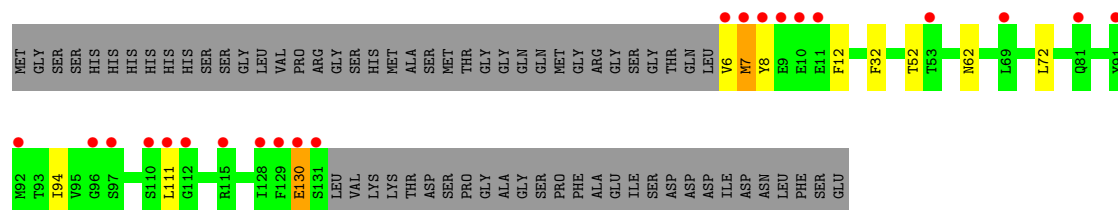


• Molecule 1: MglB

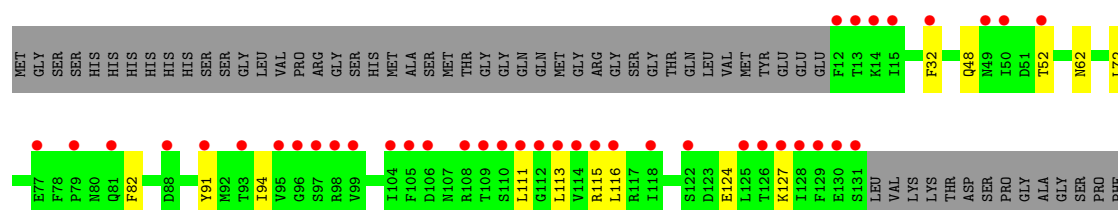




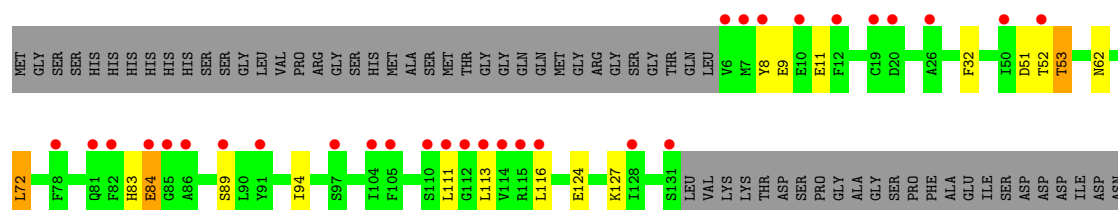
● Molecule 1: MglB



● Molecule 1: MglB

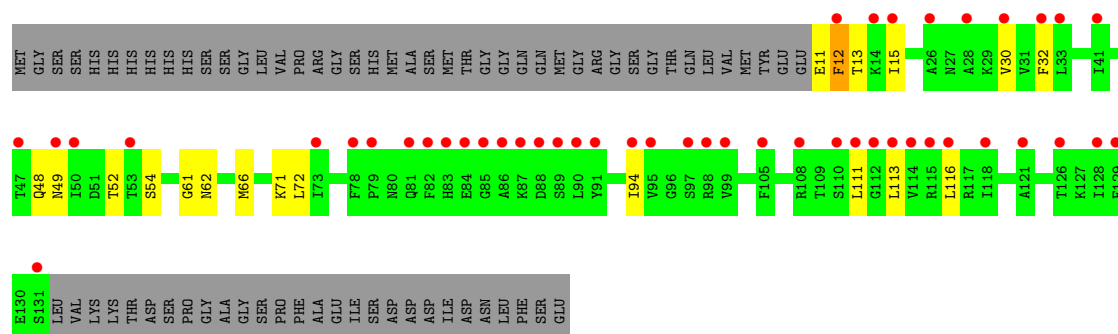


● Molecule 1: MglB

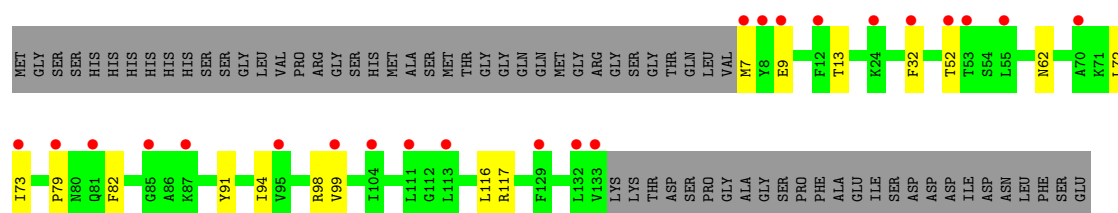


● Molecule 1: MglB

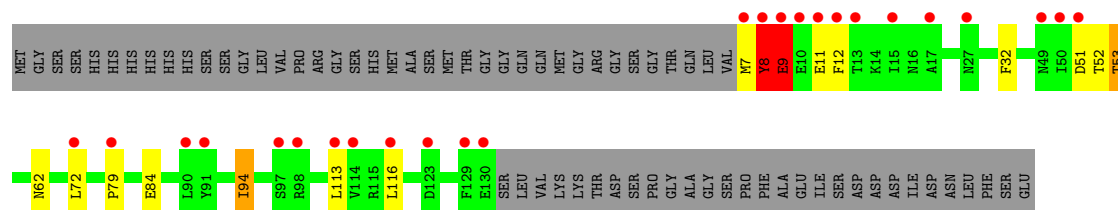




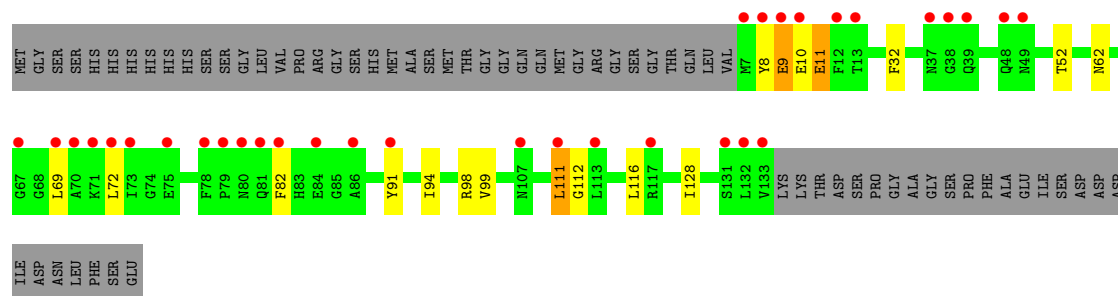
- Molecule 1: MglB



- Molecule 1: MglB

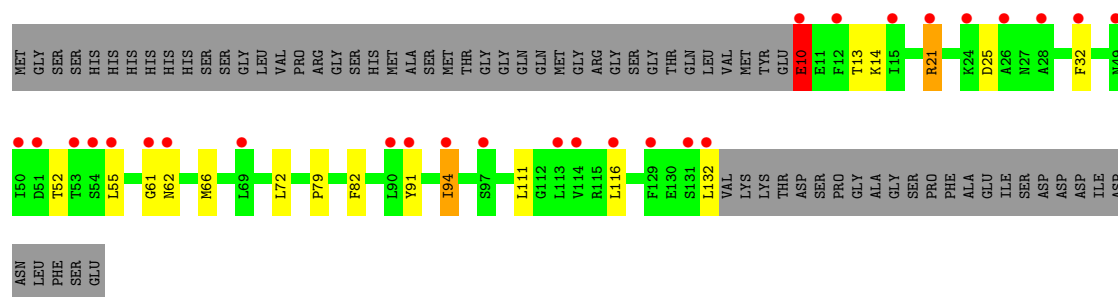


- Molecule 1: MglB

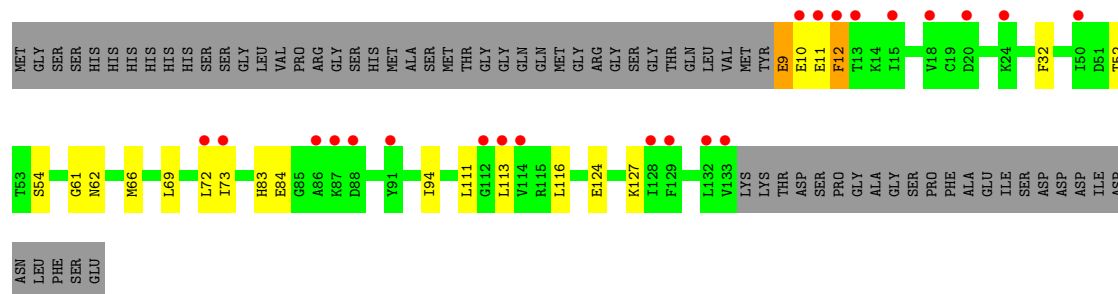


- Molecule 1: MglB

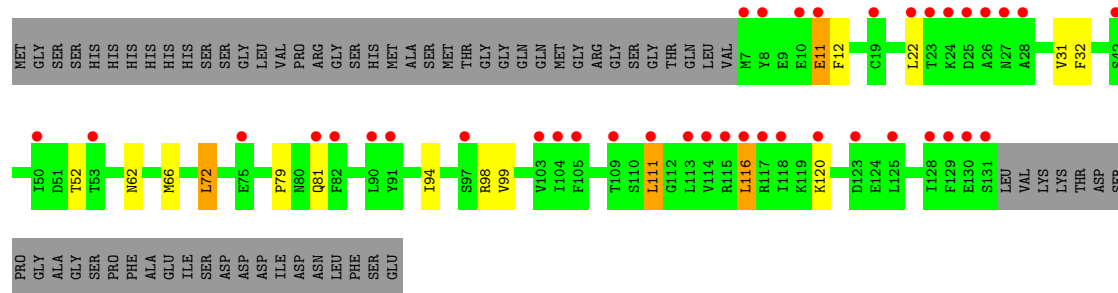




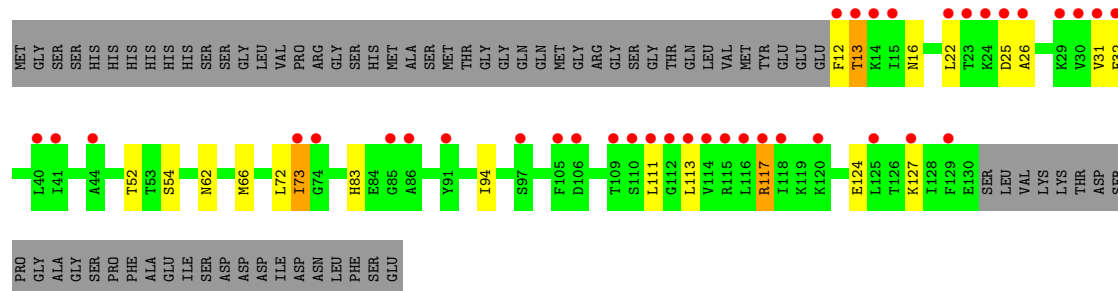
• Molecule 1: MgIB



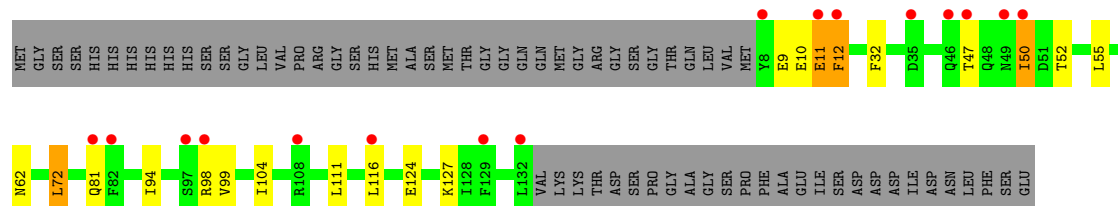
• Molecule 1: MgIB



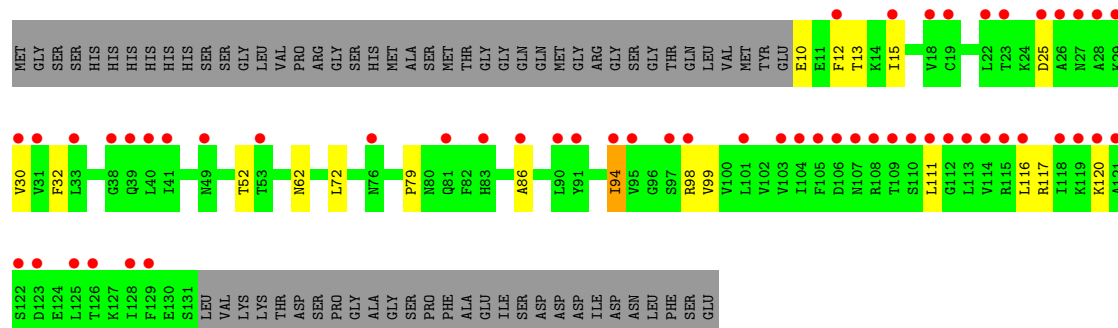
• Molecule 1: MgIB



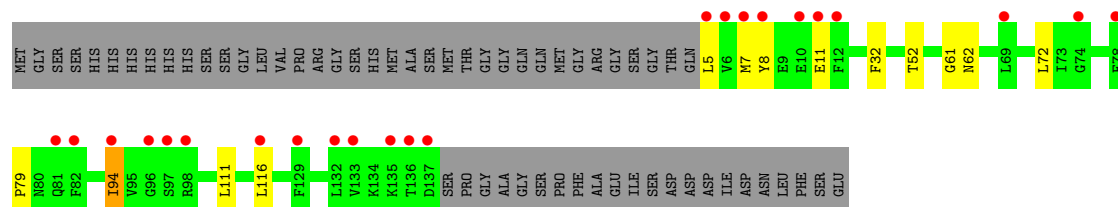
- Molecule 1: MglB



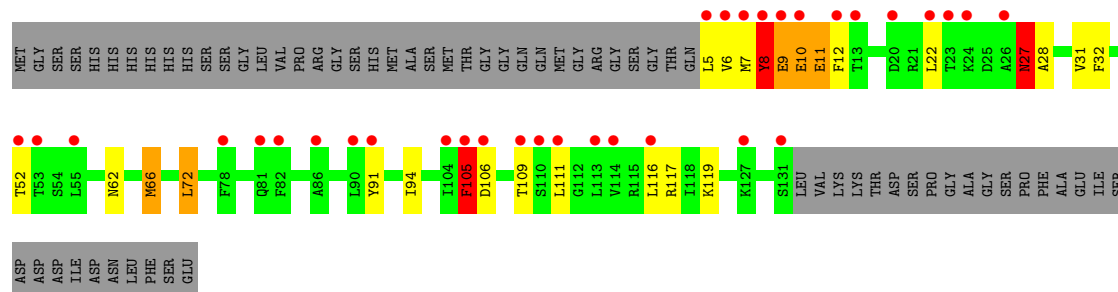
- Molecule 1: MglB



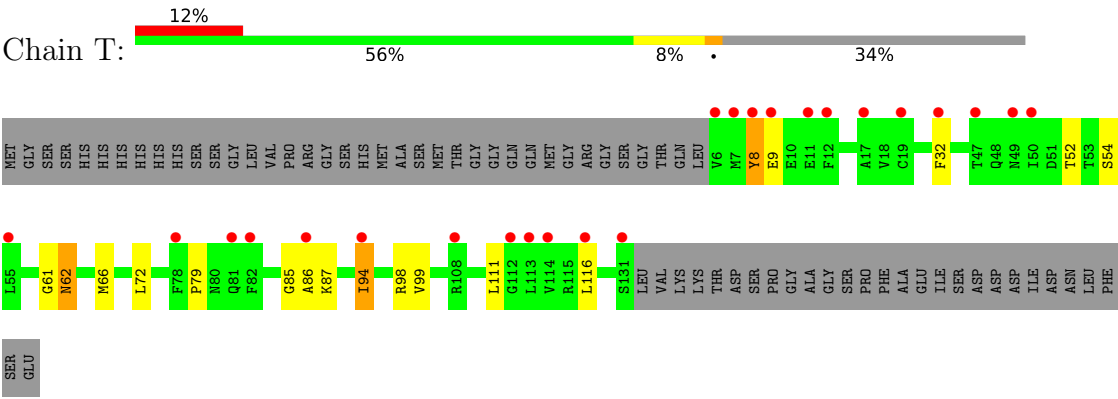
- Molecule 1: MglB



- Molecule 1: MglB



- Molecule 1: MglB



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	119.78Å 139.60Å 179.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.41 – 2.39 45.41 – 2.39	Depositor EDS
% Data completeness (in resolution range)	72.6 (45.41-2.39) 73.0 (45.41-2.39)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.30 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.249 , 0.267 0.268 , 0.291	Depositor DCC
R_{free} test set	4276 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	52.5	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	19326	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.74	0/985	1.37	2/1328 (0.2%)
1	B	0.71	0/970	1.31	0/1308
1	C	0.71	0/970	1.33	1/1307 (0.1%)
1	D	0.72	0/915	1.38	2/1233 (0.2%)
1	E	0.76	1/941 (0.1%)	1.37	4/1268 (0.3%)
1	F	0.77	1/978 (0.1%)	1.36	3/1318 (0.2%)
1	G	0.71	0/970	1.37	2/1307 (0.2%)
1	H	0.70	0/924	1.35	1/1245 (0.1%)
1	I	0.73	0/978	1.33	0/1318
1	J	0.72	0/957	1.34	4/1289 (0.3%)
1	K	0.76	1/909 (0.1%)	1.38	6/1225 (0.5%)
1	L	0.74	0/963	1.37	4/1298 (0.3%)
1	M	0.75	0/978	1.36	3/1318 (0.2%)
1	N	0.74	1/941 (0.1%)	1.34	2/1268 (0.2%)
1	O	0.70	0/933	1.37	1/1257 (0.1%)
1	P	0.73	0/1026	1.32	0/1382
1	Q	0.78	1/957 (0.1%)	1.34	2/1290 (0.2%)
1	R	0.76	1/963 (0.1%)	1.35	2/1297 (0.2%)
1	S	0.79	1/978 (0.1%)	1.48	7/1318 (0.5%)
1	T	0.74	1/970 (0.1%)	1.38	5/1307 (0.4%)
All	All	0.74	8/19206 (0.0%)	1.36	51/25881 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	S	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	66	MET	SD-CE	-8.40	1.58	1.79
1	E	66	MET	SD-CE	-7.32	1.61	1.79
1	F	66	MET	SD-CE	-6.77	1.62	1.79
1	S	66	MET	SD-CE	-6.57	1.63	1.79
1	N	66	MET	SD-CE	-6.38	1.63	1.79
1	R	66	MET	SD-CE	-6.35	1.63	1.79
1	T	66	MET	SD-CE	-6.12	1.64	1.79
1	K	66	MET	SD-CE	-6.01	1.64	1.79

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	105	PHE	CA-CB-CG	-16.25	97.55	113.80
1	O	86	ALA	N-CA-C	-10.56	93.53	110.32
1	S	10	GLU	CA-C-N	10.01	139.72	121.70
1	S	10	GLU	C-N-CA	10.01	139.72	121.70
1	T	85	GLY	N-CA-C	9.65	136.05	113.18
1	C	130	GLU	CB-CG-CD	8.59	127.20	112.60
1	L	11	GLU	CA-C-N	8.54	137.08	121.70
1	L	11	GLU	C-N-CA	8.54	137.08	121.70
1	G	8	TYR	CA-C-N	8.30	136.63	121.70
1	G	8	TYR	C-N-CA	8.30	136.63	121.70
1	D	48	GLN	CA-C-N	7.68	132.89	120.60
1	D	48	GLN	C-N-CA	7.68	132.89	120.60
1	H	49	ASN	CA-CB-CG	7.49	120.09	112.60
1	R	11	GLU	CA-C-N	7.40	135.67	121.54
1	R	11	GLU	C-N-CA	7.40	135.67	121.54
1	A	8	TYR	CA-C-N	7.29	134.83	121.70
1	A	8	TYR	C-N-CA	7.29	134.83	121.70
1	T	86	ALA	CA-C-N	7.29	135.46	121.54
1	T	86	ALA	C-N-CA	7.29	135.46	121.54
1	T	8	TYR	CA-C-N	7.08	134.44	121.70
1	T	8	TYR	C-N-CA	7.08	134.44	121.70
1	F	9	GLU	CA-C-N	6.91	134.14	121.70
1	F	9	GLU	C-N-CA	6.91	134.14	121.70
1	M	9	GLU	CA-C-N	6.83	133.99	121.70
1	M	9	GLU	C-N-CA	6.83	133.99	121.70
1	K	12	PHE	CA-C-N	6.25	133.47	121.54
1	K	12	PHE	C-N-CA	6.25	133.47	121.54
1	F	11	GLU	N-CA-C	-6.23	105.17	112.89
1	Q	9	GLU	CA-C-N	6.15	132.77	121.70
1	Q	9	GLU	C-N-CA	6.15	132.77	121.70
1	K	117	ARG	CB-CG-CD	6.13	125.41	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	13	THR	CA-C-N	5.92	128.21	120.28
1	K	13	THR	C-N-CA	5.92	128.21	120.28
1	S	27	ASN	CA-C-N	5.89	129.48	120.82
1	S	27	ASN	C-N-CA	5.89	129.48	120.82
1	N	10	GLU	CA-C-N	5.88	132.77	121.54
1	N	10	GLU	C-N-CA	5.88	132.77	121.54
1	K	16	ASN	CA-CB-CG	5.87	118.47	112.60
1	M	11	GLU	N-CA-C	-5.80	105.70	112.89
1	E	12	PHE	CA-C-O	5.55	128.75	122.37
1	E	12	PHE	CA-CB-CG	-5.53	108.27	113.80
1	J	7	MET	CA-C-N	5.28	131.62	121.54
1	J	7	MET	C-N-CA	5.28	131.62	121.54
1	S	8	TYR	CA-C-N	5.22	131.51	121.54
1	S	8	TYR	C-N-CA	5.22	131.51	121.54
1	J	8	TYR	CA-C-N	5.21	131.49	121.54
1	J	8	TYR	C-N-CA	5.21	131.49	121.54
1	E	10	GLU	CA-C-N	5.16	130.26	122.68
1	E	10	GLU	C-N-CA	5.16	130.26	122.68
1	L	10	GLU	CA-C-N	5.09	130.87	121.70
1	L	10	GLU	C-N-CA	5.09	130.87	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	S	27	ASN	Mainchain

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	976	0	1004	6	0
1	B	961	0	986	6	0
1	C	961	0	984	3	0
1	D	907	0	939	3	0
1	E	933	0	962	5	0
1	F	969	0	995	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	961	0	984	6	0
1	H	916	0	945	6	0
1	I	969	0	995	5	0
1	J	948	0	970	5	0
1	K	901	0	934	14	0
1	L	954	0	977	10	0
1	M	969	0	995	9	0
1	N	933	0	962	10	0
1	O	925	0	951	7	0
1	P	1017	0	1052	4	0
1	Q	949	0	977	12	0
1	R	954	0	975	11	0
1	S	969	0	995	22	0
1	T	961	0	984	8	0
2	A	32	0	0	0	0
2	B	27	0	0	0	0
2	C	13	0	0	0	0
2	D	7	0	0	0	0
2	E	12	0	0	0	0
2	F	23	0	0	1	0
2	G	9	0	0	0	0
2	H	12	0	0	0	0
2	I	18	0	0	0	0
2	J	12	0	0	0	0
2	K	7	0	0	0	0
2	L	13	0	0	0	0
2	M	9	0	0	0	0
2	N	13	0	0	0	0
2	O	6	0	0	0	0
2	P	17	0	0	0	0
2	Q	19	0	0	0	0
2	R	18	0	0	0	0
2	S	12	0	0	0	0
2	T	14	0	0	0	0
All	All	19326	0	19566	130	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 3.

All (130) 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:S:10:GLU:HA	1:S:12:PHE:H	1.14	1.10
1:S:10:GLU:HA	1:S:12:PHE:N	1.89	0.87
1:O:12:PHE:O	1:O:15:ILE:HG12	1.75	0.85
1:H:12:PHE:O	1:H:15:ILE:HG12	1.75	0.85
1:F:9:GLU:HA	1:F:10:GLU:HB2	1.60	0.82
1:M:9:GLU:HA	1:M:10:GLU:HB2	1.59	0.82
1:K:26:ALA:HA	1:K:117:ARG:HD3	1.66	0.78
1:B:130:GLU:HG2	1:R:116:LEU:HD11	1.65	0.77
1:S:105:PHE:CD1	1:S:106:ASP:N	2.52	0.76
1:C:8:TYR:HB3	1:C:12:PHE:HB2	1.70	0.73
1:O:25:ASP:HB3	1:O:117:ARG:CZ	2.19	0.72
1:S:105:PHE:CE2	1:S:109:THR:OG1	2.43	0.70
1:M:11:GLU:HG3	1:M:128:ILE:HG23	1.73	0.70
1:N:10:GLU:HB2	1:N:14:LYS:HE2	1.75	0.67
1:S:22:LEU:HD12	1:S:31:VAL:HG21	1.76	0.66
1:S:22:LEU:HD22	1:S:117:ARG:HG3	1.80	0.64
1:S:28:ALA:HA	1:S:105:PHE:CG	2.33	0.62
1:K:113:LEU:HD21	1:K:117:ARG:NH1	2.15	0.61
1:Q:61:GLY:HA2	1:T:61:GLY:HA2	1.83	0.60
1:F:32:PHE:HE2	1:F:52:THR:HG22	1.67	0.60
1:N:61:GLY:HA2	1:P:61:GLY:HA2	1.82	0.59
1:G:84:GLU:O	1:G:89:SER:HA	2.01	0.59
1:Q:9:GLU:N	1:Q:10:GLU:HA	2.17	0.59
1:K:22:LEU:HD12	1:K:31:VAL:HG21	1.85	0.58
1:M:82:PHE:HB2	1:M:91:TYR:CE1	2.38	0.58
1:L:124:GLU:O	1:L:127:LYS:HG2	2.04	0.58
1:S:27:ASN:O	1:S:105:PHE:CZ	2.56	0.58
1:A:39:GLN:HG2	1:F:10:GLU:HG2	1.86	0.58
1:K:124:GLU:O	1:K:127:LYS:HG2	2.04	0.57
1:A:8:TYR:HA	1:A:10:GLU:H	1.69	0.57
1:Q:124:GLU:O	1:Q:127:LYS:HG2	2.05	0.57
1:G:124:GLU:O	1:G:127:LYS:HG2	2.04	0.57
1:D:82:PHE:HB2	1:D:91:TYR:CE1	2.39	0.56
1:K:113:LEU:HD11	1:K:117:ARG:NH1	2.20	0.56
1:S:22:LEU:CD2	1:S:117:ARG:HG3	2.36	0.56
1:I:82:PHE:HB2	1:I:91:TYR:CE1	2.40	0.56
1:D:124:GLU:O	1:D:127:LYS:HG2	2.05	0.56
1:H:32:PHE:HE2	1:H:52:THR:HG22	1.71	0.55
1:Q:69:LEU:O	1:Q:73:ILE:HD12	2.06	0.55
1:L:98:ARG:HG3	1:L:99:VAL:HG23	1.89	0.54
1:N:111:LEU:HD13	1:S:8:TYR:HB3	1.88	0.54
1:O:25:ASP:HB3	1:O:117:ARG:NH1	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:98:ARG:HG3	1:T:99:VAL:HG23	1.90	0.54
1:Q:83:HIS:HD2	1:R:81:GLN:HG2	1.72	0.54
1:K:73:ILE:HD13	1:K:73:ILE:O	2.07	0.54
1:M:98:ARG:HG3	1:M:99:VAL:HG23	1.91	0.53
1:N:82:PHE:HB2	1:N:91:TYR:CE1	2.43	0.53
1:L:11:GLU:HA	1:L:12:PHE:CB	2.39	0.52
1:I:98:ARG:HG3	1:I:99:VAL:HG23	1.91	0.52
1:L:11:GLU:HA	1:L:12:PHE:HB3	1.92	0.52
1:L:32:PHE:CZ	1:L:50:ILE:HD12	2.45	0.52
1:O:32:PHE:HE2	1:O:52:THR:HG22	1.73	0.52
1:K:26:ALA:CA	1:K:117:ARG:HD3	2.40	0.51
1:O:79:PRO:HA	1:O:94:ILE:HG13	1.92	0.51
1:Q:54:SER:HB2	1:R:72:LEU:HD11	1.93	0.51
1:M:69:LEU:HD11	1:N:55:LEU:HG	1.93	0.50
1:R:98:ARG:HG3	1:R:99:VAL:HG23	1.91	0.50
1:A:32:PHE:HE1	1:A:52:THR:HG22	1.75	0.50
1:R:22:LEU:HD22	1:R:31:VAL:HG21	1.93	0.50
1:A:8:TYR:HD1	1:A:10:GLU:HB3	1.76	0.50
1:K:73:ILE:HG13	1:L:104:ILE:HG21	1.92	0.50
1:O:98:ARG:HG3	1:O:99:VAL:HG23	1.94	0.50
1:P:79:PRO:HA	1:P:94:ILE:HG13	1.94	0.50
1:C:7:MET:HB2	1:R:111:LEU:HB3	1.94	0.50
1:S:72:LEU:HD11	1:T:54:SER:HB2	1.94	0.50
1:D:32:PHE:HE1	1:D:52:THR:HG22	1.77	0.49
1:F:98:ARG:HG3	1:F:99:VAL:HG23	1.96	0.48
1:T:79:PRO:HA	1:T:94:ILE:HG13	1.95	0.48
1:I:32:PHE:HE1	1:I:52:THR:HG22	1.78	0.48
1:K:25:ASP:O	1:K:117:ARG:NH1	2.46	0.48
1:L:50:ILE:HD11	1:L:55:LEU:HD13	1.95	0.48
2:F:216:HOH:O	1:H:71:LYS:HE2	2.14	0.47
1:J:79:PRO:HA	1:J:94:ILE:HG13	1.96	0.47
1:A:9:GLU:HG2	1:F:41:ILE:HG12	1.97	0.47
1:N:79:PRO:HA	1:N:94:ILE:HG13	1.96	0.47
1:B:80:ASN:HB3	1:B:91:TYR:HE1	1.80	0.47
1:N:21:ARG:HG2	1:N:25:ASP:OD2	2.15	0.47
1:P:32:PHE:HE1	1:P:52:THR:HG22	1.80	0.46
1:M:32:PHE:HE1	1:M:52:THR:HG22	1.81	0.46
1:M:111:LEU:HB3	1:S:7:MET:HB2	1.98	0.46
1:K:83:HIS:HD2	1:L:81:GLN:HG2	1.81	0.46
1:L:32:PHE:HE1	1:L:52:THR:HG22	1.81	0.46
1:T:32:PHE:HE1	1:T:52:THR:HG22	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:PRO:HA	1:B:94:ILE:HG13	1.99	0.45
1:E:12:PHE:CB	1:E:15:ILE:HD12	2.47	0.45
1:Q:83:HIS:CD2	1:R:81:GLN:HG2	2.50	0.45
1:R:32:PHE:HE1	1:R:52:THR:HG22	1.81	0.45
1:E:66:MET:HE3	1:F:62:ASN:CG	2.42	0.45
1:T:8:TYR:HA	1:T:9:GLU:HB3	1.98	0.45
1:G:51:ASP:OD1	1:G:53:THR:HG23	2.17	0.45
1:M:112:GLY:HA2	1:S:12:PHE:CZ	2.51	0.44
1:O:79:PRO:HA	1:O:94:ILE:CG1	2.47	0.44
1:E:72:LEU:HD11	1:F:54:SER:HB2	1.99	0.44
1:F:61:GLY:HA2	1:H:61:GLY:HA2	1.98	0.44
1:S:32:PHE:HE1	1:S:52:THR:HG22	1.81	0.44
1:J:8:TYR:O	1:J:9:GLU:HB2	2.17	0.44
1:K:32:PHE:HE1	1:K:52:THR:HG22	1.82	0.44
1:G:32:PHE:HE1	1:G:52:THR:HG22	1.83	0.44
1:N:111:LEU:CD1	1:S:8:TYR:HB3	2.48	0.44
1:Q:84:GLU:O	1:R:79:PRO:HD2	2.18	0.44
1:S:27:ASN:C	1:S:105:PHE:CE2	2.96	0.44
1:S:66:MET:HE3	1:T:62:ASN:CG	2.43	0.44
1:C:32:PHE:HE1	1:C:52:THR:HG22	1.83	0.43
1:G:72:LEU:HD11	1:H:54:SER:HB2	1.99	0.43
1:K:113:LEU:HD21	1:K:117:ARG:HH11	1.82	0.43
1:I:79:PRO:HD2	1:J:84:GLU:O	2.18	0.43
1:T:79:PRO:HA	1:T:94:ILE:CG1	2.48	0.43
1:J:51:ASP:OD1	1:J:53:THR:HG23	2.19	0.43
1:K:54:SER:HB2	1:L:72:LEU:HD11	2.00	0.43
1:Q:83:HIS:HD2	1:R:81:GLN:CG	2.32	0.43
1:S:22:LEU:HD12	1:S:31:VAL:CG2	2.45	0.43
1:S:105:PHE:CG	1:S:106:ASP:N	2.87	0.42
1:R:22:LEU:O	1:R:22:LEU:HD23	2.20	0.42
1:N:32:PHE:HE1	1:N:52:THR:HG22	1.84	0.42
1:Q:32:PHE:HE1	1:Q:52:THR:HG22	1.84	0.42
1:E:32:PHE:HE1	1:E:52:THR:HG22	1.85	0.42
1:K:113:LEU:CG	1:K:117:ARG:NH1	2.82	0.42
1:P:79:PRO:HA	1:P:94:ILE:CG1	2.49	0.42
1:S:105:PHE:HD1	1:S:105:PHE:HA	1.25	0.42
1:I:9:GLU:HB2	1:Q:12:PHE:CZ	2.55	0.41
1:E:51:ASP:OD1	1:E:53:THR:HG23	2.19	0.41
1:M:112:GLY:O	1:S:12:PHE:HZ	2.04	0.41
1:B:80:ASN:HB3	1:B:91:TYR:CE1	2.56	0.41
1:Q:11:GLU:HB3	1:Q:12:PHE:HD2	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:VAL:HG12	1:B:118:ILE:CD1	2.51	0.41
1:J:32:PHE:HE1	1:J:52:THR:HG22	1.85	0.40
1:N:79:PRO:HA	1:N:94:ILE:CG1	2.51	0.40
1:A:79:PRO:HD2	1:B:84:GLU:O	2.22	0.40
1:G:83:HIS:CG	1:H:66:MET:HE2	2.56	0.40
1:S:27:ASN:HB3	1:S:105:PHE:HE2	1.86	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	126/192 (66%)	123 (98%)	3 (2%)	0	100	100
1	B	124/192 (65%)	119 (96%)	4 (3%)	1 (1%)	16	25
1	C	124/192 (65%)	122 (98%)	2 (2%)	0	100	100
1	D	118/192 (62%)	117 (99%)	1 (1%)	0	100	100
1	E	121/192 (63%)	120 (99%)	1 (1%)	0	100	100
1	F	125/192 (65%)	121 (97%)	3 (2%)	1 (1%)	16	25
1	G	124/192 (65%)	121 (98%)	2 (2%)	1 (1%)	16	25
1	H	119/192 (62%)	118 (99%)	1 (1%)	0	100	100
1	I	125/192 (65%)	122 (98%)	3 (2%)	0	100	100
1	J	122/192 (64%)	116 (95%)	4 (3%)	2 (2%)	7	11
1	K	117/192 (61%)	114 (97%)	2 (2%)	1 (1%)	14	22
1	L	123/192 (64%)	120 (98%)	2 (2%)	1 (1%)	16	25
1	M	125/192 (65%)	123 (98%)	2 (2%)	0	100	100
1	N	121/192 (63%)	117 (97%)	4 (3%)	0	100	100
1	O	120/192 (62%)	117 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	P	131/192 (68%)	125 (95%)	4 (3%)	2 (2%)	8	12
1	Q	123/192 (64%)	120 (98%)	2 (2%)	1 (1%)	16	25
1	R	123/192 (64%)	120 (98%)	2 (2%)	1 (1%)	16	25
1	S	125/192 (65%)	121 (97%)	2 (2%)	2 (2%)	7	11
1	T	124/192 (65%)	119 (96%)	4 (3%)	1 (1%)	16	25
All	All	2460/3840 (64%)	2395 (97%)	51 (2%)	14 (1%)	21	32

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	84	GLU
1	J	9	GLU
1	R	12	PHE
1	K	13	THR
1	S	9	GLU
1	T	87	LYS
1	L	12	PHE
1	P	11	GLU
1	S	11	GLU
1	P	7	MET
1	B	9	GLU
1	F	9	GLU
1	J	8	TYR
1	Q	12	PHE

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	108/159 (68%)	100 (93%)	8 (7%)	13	22
1	B	106/159 (67%)	96 (91%)	10 (9%)	8	13
1	C	106/159 (67%)	99 (93%)	7 (7%)	15	26
1	D	100/159 (63%)	93 (93%)	7 (7%)	14	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	103/159 (65%)	94 (91%)	9 (9%)	9	16
1	F	107/159 (67%)	101 (94%)	6 (6%)	19	33
1	G	106/159 (67%)	97 (92%)	9 (8%)	10	16
1	H	101/159 (64%)	90 (89%)	11 (11%)	6	9
1	I	107/159 (67%)	99 (92%)	8 (8%)	12	21
1	J	104/159 (65%)	94 (90%)	10 (10%)	8	12
1	K	99/159 (62%)	94 (95%)	5 (5%)	21	37
1	L	105/159 (66%)	97 (92%)	8 (8%)	12	21
1	M	107/159 (67%)	101 (94%)	6 (6%)	19	33
1	N	103/159 (65%)	95 (92%)	8 (8%)	11	20
1	O	102/159 (64%)	93 (91%)	9 (9%)	9	15
1	P	113/159 (71%)	106 (94%)	7 (6%)	16	29
1	Q	105/159 (66%)	99 (94%)	6 (6%)	18	33
1	R	105/159 (66%)	98 (93%)	7 (7%)	15	26
1	S	107/159 (67%)	94 (88%)	13 (12%)	5	7
1	T	106/159 (67%)	101 (95%)	5 (5%)	23	41
All	All	2100/3180 (66%)	1941 (92%)	159 (8%)	12	21

All (159) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	GLU
1	A	50	ILE
1	A	62	ASN
1	A	72	LEU
1	A	94	ILE
1	A	111	LEU
1	A	113	LEU
1	A	116	LEU
1	B	12	PHE
1	B	13	THR
1	B	62	ASN
1	B	72	LEU
1	B	94	ILE
1	B	113	LEU
1	B	116	LEU

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Mol	Chain	Res	Type
1	B	117	ARG
1	B	120	LYS
1	B	132	LEU
1	E	13	THR
1	E	53	THR
1	E	62	ASN
1	E	72	LEU
1	E	94	ILE
1	E	111	LEU
1	E	113	LEU
1	E	116	LEU
1	E	132	LEU
1	F	62	ASN
1	F	72	LEU
1	F	94	ILE
1	F	111	LEU
1	F	116	LEU
1	F	120	LYS
1	C	6	VAL
1	C	7	MET
1	C	62	ASN
1	C	72	LEU
1	C	94	ILE
1	C	111	LEU
1	C	130	GLU
1	D	62	ASN
1	D	72	LEU
1	D	94	ILE
1	D	111	LEU
1	D	113	LEU
1	D	115	ARG
1	D	116	LEU
1	G	9	GLU
1	G	11	GLU
1	G	53	THR
1	G	62	ASN
1	G	72	LEU
1	G	94	ILE
1	G	111	LEU
1	G	113	LEU
1	G	116	LEU
1	H	11	GLU

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Mol	Chain	Res	Type
1	H	12	PHE
1	H	13	THR
1	H	30	VAL
1	H	48	GLN
1	H	62	ASN
1	H	72	LEU
1	H	94	ILE
1	H	111	LEU
1	H	113	LEU
1	H	116	LEU
1	I	7	MET
1	I	13	THR
1	I	62	ASN
1	I	72	LEU
1	I	73	ILE
1	I	94	ILE
1	I	116	LEU
1	I	117	ARG
1	J	8	TYR
1	J	9	GLU
1	J	11	GLU
1	J	12	PHE
1	J	53	THR
1	J	62	ASN
1	J	72	LEU
1	J	94	ILE
1	J	113	LEU
1	J	116	LEU
1	M	8	TYR
1	M	62	ASN
1	M	72	LEU
1	M	94	ILE
1	M	111	LEU
1	M	116	LEU
1	N	10	GLU
1	N	13	THR
1	N	21	ARG
1	N	62	ASN
1	N	72	LEU
1	N	94	ILE
1	N	116	LEU
1	N	132	LEU

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Mol	Chain	Res	Type
1	Q	62	ASN
1	Q	72	LEU
1	Q	94	ILE
1	Q	111	LEU
1	Q	113	LEU
1	Q	116	LEU
1	R	11	GLU
1	R	62	ASN
1	R	72	LEU
1	R	94	ILE
1	R	111	LEU
1	R	116	LEU
1	R	120	LYS
1	K	62	ASN
1	K	72	LEU
1	K	73	ILE
1	K	94	ILE
1	K	111	LEU
1	L	9	GLU
1	L	47	THR
1	L	50	ILE
1	L	62	ASN
1	L	72	LEU
1	L	94	ILE
1	L	111	LEU
1	L	116	LEU
1	O	10	GLU
1	O	13	THR
1	O	30	VAL
1	O	62	ASN
1	O	72	LEU
1	O	94	ILE
1	O	111	LEU
1	O	116	LEU
1	O	120	LYS
1	P	5	LEU
1	P	8	TYR
1	P	62	ASN
1	P	72	LEU
1	P	94	ILE
1	P	111	LEU
1	P	116	LEU

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Mol	Chain	Res	Type
1	S	5	LEU
1	S	6	VAL
1	S	8	TYR
1	S	9	GLU
1	S	11	GLU
1	S	62	ASN
1	S	72	LEU
1	S	91	TYR
1	S	94	ILE
1	S	105	PHE
1	S	111	LEU
1	S	116	LEU
1	S	119	LYS
1	T	62	ASN
1	T	72	LEU
1	T	94	ILE
1	T	111	LEU
1	T	116	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	81	GLN
1	A	83	HIS
1	B	83	HIS
1	E	81	GLN
1	E	83	HIS
1	F	16	ASN
1	F	39	GLN
1	F	80	ASN
1	F	81	GLN
1	F	83	HIS
1	C	49	ASN
1	C	81	GLN
1	C	83	HIS
1	D	62	ASN
1	D	81	GLN
1	D	83	HIS
1	G	83	HIS
1	H	62	ASN
1	H	81	GLN

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Mol	Chain	Res	Type
1	H	83	HIS
1	I	62	ASN
1	J	83	HIS
1	M	16	ASN
1	M	62	ASN
1	M	81	GLN
1	M	83	HIS
1	N	46	GLN
1	N	83	HIS
1	Q	16	ASN
1	Q	81	GLN
1	Q	83	HIS
1	R	62	ASN
1	R	81	GLN
1	R	83	HIS
1	K	46	GLN
1	K	62	ASN
1	K	81	GLN
1	K	83	HIS
1	L	16	ASN
1	L	49	ASN
1	L	81	GLN
1	L	83	HIS
1	O	62	ASN
1	O	81	GLN
1	O	83	HIS
1	P	83	HIS
1	S	81	GLN
1	T	16	ASN
1	T	83	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	128/192 (66%)	1.05	18 (14%) 6 5	30, 50, 80, 116	0
1	B	126/192 (65%)	1.00	15 (11%) 9 6	32, 48, 90, 130	0
1	C	126/192 (65%)	1.05	21 (16%) 4 3	31, 55, 98, 133	0
1	D	120/192 (62%)	1.60	40 (33%) 1 1	32, 68, 112, 148	0
1	E	123/192 (64%)	1.24	20 (16%) 4 4	38, 60, 98, 128	0
1	F	127/192 (66%)	1.20	18 (14%) 6 5	34, 63, 102, 123	0
1	G	126/192 (65%)	1.51	30 (23%) 2 1	38, 72, 110, 139	0
1	H	121/192 (63%)	1.90	47 (38%) 1 0	40, 82, 118, 148	0
1	I	127/192 (66%)	1.37	23 (18%) 3 3	38, 62, 99, 130	0
1	J	124/192 (64%)	1.31	25 (20%) 3 2	43, 68, 104, 142	0
1	K	119/192 (61%)	1.77	38 (31%) 1 1	44, 78, 126, 153	0
1	L	125/192 (65%)	1.11	16 (12%) 7 6	38, 58, 92, 130	0
1	M	127/192 (66%)	1.44	33 (25%) 1 1	39, 64, 103, 124	0
1	N	123/192 (64%)	1.43	27 (21%) 2 2	42, 76, 112, 137	0
1	O	122/192 (63%)	2.03	55 (45%) 0 0	48, 98, 145, 175	0
1	P	133/192 (69%)	1.16	23 (17%) 4 3	39, 58, 94, 106	0
1	Q	125/192 (65%)	1.24	22 (17%) 4 3	35, 63, 102, 145	0
1	R	125/192 (65%)	1.59	39 (31%) 1 1	34, 58, 95, 138	0
1	S	127/192 (66%)	1.58	33 (25%) 1 1	37, 69, 100, 123	0
1	T	126/192 (65%)	1.31	24 (19%) 3 2	37, 64, 96, 120	0
All	All	2500/3840 (65%)	1.39	567 (22%) 2 2	30, 65, 113, 175	0

All (567) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	8	TYR	8.6
1	O	113	LEU	7.2
1	K	114	VAL	7.1
1	H	129	PHE	6.8
1	F	7	MET	6.7
1	Q	133	VAL	6.6
1	F	133	VAL	6.6
1	D	129	PHE	6.5
1	K	26	ALA	6.5
1	A	133	VAL	6.4
1	C	8	TYR	6.3
1	G	111	LEU	6.3
1	K	113	LEU	6.3
1	I	32	PHE	6.3
1	P	6	VAL	6.2
1	M	7	MET	6.0
1	A	32	PHE	5.8
1	M	133	VAL	5.7
1	C	6	VAL	5.7
1	R	114	VAL	5.6
1	L	132	LEU	5.6
1	N	91	TYR	5.5
1	H	97	SER	5.4
1	R	26	ALA	5.3
1	K	15	ILE	5.3
1	O	129	PHE	5.2
1	R	105	PHE	5.2
1	S	81	GLN	5.1
1	N	132	LEU	5.1
1	D	81	GLN	5.1
1	M	81	GLN	5.1
1	E	12	PHE	5.1
1	M	111	LEU	5.0
1	H	49	ASN	5.0
1	O	114	VAL	4.9
1	O	111	LEU	4.9
1	J	97	SER	4.9
1	S	105	PHE	4.9
1	A	8	TYR	4.8
1	H	12	PHE	4.8
1	K	111	LEU	4.8
1	O	116	LEU	4.8
1	J	7	MET	4.8

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Mol	Chain	Res	Type	RSRZ
1	H	82	PHE	4.8
1	I	111	LEU	4.7
1	O	91	TYR	4.7
1	B	133	VAL	4.7
1	O	105	PHE	4.7
1	D	15	ILE	4.6
1	I	52	THR	4.6
1	H	111	LEU	4.6
1	R	22	LEU	4.6
1	S	7	MET	4.6
1	S	26	ALA	4.6
1	O	112	GLY	4.5
1	R	7	MET	4.5
1	N	97	SER	4.5
1	G	8	TYR	4.4
1	I	73	ILE	4.4
1	P	11	GLU	4.4
1	O	81	GLN	4.4
1	B	132	LEU	4.4
1	S	5	LEU	4.4
1	F	10	GLU	4.4
1	N	55	LEU	4.4
1	R	129	PHE	4.4
1	D	126	THR	4.4
1	P	136	THR	4.4
1	O	15	ILE	4.4
1	I	132	LEU	4.3
1	G	131	SER	4.3
1	E	20	ASP	4.3
1	K	12	PHE	4.3
1	H	131	SER	4.2
1	T	12	PHE	4.2
1	R	128	ILE	4.2
1	G	6	VAL	4.2
1	H	28	ALA	4.2
1	I	8	TYR	4.2
1	R	81	GLN	4.1
1	D	12	PHE	4.1
1	J	12	PHE	4.1
1	S	111	LEU	4.1
1	L	116	LEU	4.1
1	L	8	TYR	4.1

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Mol	Chain	Res	Type	RSRZ
1	D	114	VAL	4.1
1	S	6	VAL	4.1
1	P	5	LEU	4.0
1	H	32	PHE	4.0
1	R	10	GLU	4.0
1	B	8	TYR	4.0
1	K	129	PHE	4.0
1	R	91	TYR	4.0
1	S	91	TYR	4.0
1	I	133	VAL	4.0
1	E	132	LEU	4.0
1	Q	11	GLU	4.0
1	L	97	SER	4.0
1	A	6	VAL	3.9
1	T	6	VAL	3.9
1	N	32	PHE	3.9
1	D	111	LEU	3.9
1	K	112	GLY	3.8
1	E	11	GLU	3.8
1	O	104	ILE	3.8
1	K	30	VAL	3.8
1	I	53	THR	3.8
1	M	70	ALA	3.8
1	M	10	GLU	3.8
1	O	110	SER	3.8
1	S	131	SER	3.8
1	O	22	LEU	3.8
1	E	91	TYR	3.7
1	L	35	ASP	3.7
1	I	9	GLU	3.7
1	T	7	MET	3.7
1	D	32	PHE	3.7
1	G	113	LEU	3.7
1	B	97	SER	3.7
1	A	81	GLN	3.7
1	B	91	TYR	3.7
1	B	94	ILE	3.7
1	A	111	LEU	3.7
1	N	90	LEU	3.7
1	H	98	ARG	3.7
1	R	113	LEU	3.6
1	M	39	GLN	3.6

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Mol	Chain	Res	Type	RSRZ
1	P	12	PHE	3.6
1	P	8	TYR	3.6
1	N	12	PHE	3.6
1	O	109	THR	3.6
1	D	125	LEU	3.6
1	H	126	THR	3.6
1	D	122	SER	3.5
1	R	97	SER	3.5
1	L	98	ARG	3.5
1	F	8	TYR	3.5
1	G	112	GLY	3.5
1	N	53	THR	3.5
1	Q	113	LEU	3.5
1	H	95	VAL	3.5
1	K	23	THR	3.5
1	K	109	THR	3.5
1	O	118	ILE	3.5
1	S	8	TYR	3.5
1	F	111	LEU	3.5
1	J	51	ASP	3.5
1	B	52	THR	3.4
1	S	23	THR	3.4
1	S	104	ILE	3.4
1	C	91	TYR	3.4
1	M	8	TYR	3.4
1	T	8	TYR	3.4
1	H	114	VAL	3.4
1	G	116	LEU	3.4
1	K	105	PHE	3.4
1	S	12	PHE	3.4
1	T	32	PHE	3.4
1	R	131	SER	3.4
1	I	81	GLN	3.4
1	S	114	VAL	3.4
1	F	132	LEU	3.3
1	H	113	LEU	3.3
1	N	113	LEU	3.3
1	L	12	PHE	3.3
1	O	115	ARG	3.3
1	P	96	GLY	3.3
1	D	95	VAL	3.3
1	C	112	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	I	7	MET	3.2
1	H	33	LEU	3.2
1	M	69	LEU	3.2
1	M	9	GLU	3.2
1	F	81	GLN	3.2
1	S	109	THR	3.2
1	N	129	PHE	3.2
1	N	54	SER	3.2
1	K	25	ASP	3.2
1	R	111	LEU	3.2
1	H	78	PHE	3.2
1	H	86	ALA	3.2
1	Q	132	LEU	3.2
1	K	116	LEU	3.2
1	O	101	LEU	3.2
1	S	13	THR	3.2
1	S	53	THR	3.2
1	D	97	SER	3.1
1	H	81	GLN	3.1
1	R	23	THR	3.1
1	R	90	LEU	3.1
1	O	125	LEU	3.1
1	D	50	ILE	3.1
1	D	104	ILE	3.1
1	R	104	ILE	3.1
1	T	11	GLU	3.1
1	M	72	LEU	3.1
1	C	9	GLU	3.1
1	O	95	VAL	3.1
1	C	131	SER	3.0
1	G	97	SER	3.0
1	T	131	SER	3.0
1	B	20	ASP	3.0
1	M	12	PHE	3.0
1	K	74	GLY	3.0
1	H	116	LEU	3.0
1	R	42	SER	3.0
1	D	49	ASN	3.0
1	P	116	LEU	3.0
1	I	70	ALA	3.0
1	K	22	LEU	3.0
1	G	81	GLN	3.0

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Mol	Chain	Res	Type	RSRZ
1	S	52	THR	3.0
1	F	78	PHE	2.9
1	O	103	VAL	2.9
1	P	133	VAL	2.9
1	H	47	THR	2.9
1	H	53	THR	2.9
1	O	23	THR	2.9
1	D	91	TYR	2.9
1	H	91	TYR	2.9
1	P	97	SER	2.9
1	T	82	PHE	2.9
1	K	125	LEU	2.9
1	E	117	ARG	2.9
1	A	50	ILE	2.9
1	N	50	ILE	2.9
1	Q	91	TYR	2.9
1	I	79	PRO	2.9
1	G	86	ALA	2.9
1	M	132	LEU	2.9
1	O	86	ALA	2.9
1	M	48	GLN	2.9
1	G	114	VAL	2.9
1	S	110	SER	2.9
1	F	72	LEU	2.9
1	C	129	PHE	2.9
1	R	125	LEU	2.9
1	D	109	THR	2.9
1	M	38	GLY	2.8
1	K	14	LYS	2.8
1	K	115	ARG	2.8
1	C	111	LEU	2.8
1	J	113	LEU	2.8
1	R	109	THR	2.8
1	O	41	ILE	2.8
1	K	120	LYS	2.8
1	P	135	LYS	2.8
1	O	25	ASP	2.8
1	A	112	GLY	2.8
1	O	97	SER	2.8
1	M	91	TYR	2.8
1	R	116	LEU	2.8
1	P	132	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	F	32	PHE	2.8
1	J	129	PHE	2.8
1	Q	12	PHE	2.8
1	O	12	PHE	2.8
1	O	28	ALA	2.8
1	R	24	LYS	2.8
1	D	131	SER	2.8
1	G	91	TYR	2.8
1	K	91	TYR	2.8
1	L	11	GLU	2.8
1	C	7	MET	2.8
1	S	82	PHE	2.8
1	J	50	ILE	2.8
1	R	118	ILE	2.8
1	J	10	GLU	2.8
1	A	91	TYR	2.8
1	B	12	PHE	2.8
1	G	12	PHE	2.8
1	H	128	ILE	2.7
1	R	53	THR	2.7
1	B	96	GLY	2.7
1	P	74	GLY	2.7
1	J	91	TYR	2.7
1	E	94	ILE	2.7
1	O	27	ASN	2.7
1	E	84	GLU	2.7
1	Q	24	LYS	2.7
1	K	40	LEU	2.7
1	N	28	ALA	2.7
1	D	105	PHE	2.7
1	K	106	ASP	2.7
1	D	96	GLY	2.7
1	G	50	ILE	2.7
1	K	73	ILE	2.7
1	L	50	ILE	2.7
1	E	97	SER	2.7
1	J	79	PRO	2.7
1	K	110	SER	2.7
1	E	111	LEU	2.7
1	N	116	LEU	2.7
1	H	105	PHE	2.7
1	I	12	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	H	30	VAL	2.7
1	A	52	THR	2.7
1	H	84	GLU	2.7
1	P	10	GLU	2.7
1	Q	15	ILE	2.7
1	N	131	SER	2.7
1	I	55	LEU	2.7
1	J	116	LEU	2.7
1	R	28	ALA	2.6
1	E	24	LYS	2.6
1	R	8	TYR	2.6
1	C	10	GLU	2.6
1	Q	88	ASP	2.6
1	D	13	THR	2.6
1	O	53	THR	2.6
1	N	94	ILE	2.6
1	E	110	SER	2.6
1	B	113	LEU	2.6
1	D	116	LEU	2.6
1	H	83	HIS	2.6
1	K	86	ALA	2.6
1	F	9	GLU	2.6
1	M	107	ASN	2.6
1	R	117	ARG	2.6
1	T	108	ARG	2.6
1	C	97	SER	2.6
1	D	110	SER	2.6
1	P	94	ILE	2.6
1	A	55	LEU	2.6
1	E	48	GLN	2.6
1	S	116	LEU	2.6
1	S	10	GLU	2.6
1	N	26	ALA	2.6
1	S	106	ASP	2.6
1	P	78	PHE	2.6
1	D	99	VAL	2.6
1	K	13	THR	2.6
1	O	38	GLY	2.6
1	D	118	ILE	2.6
1	H	15	ILE	2.6
1	S	127	LYS	2.6
1	J	130	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	M	75	GLU	2.6
1	D	98	ARG	2.6
1	E	13	THR	2.6
1	I	129	PHE	2.6
1	O	94	ILE	2.6
1	A	75	GLU	2.5
1	M	113	LEU	2.5
1	G	115	ARG	2.5
1	O	76	ASN	2.5
1	M	79	PRO	2.5
1	S	78	PHE	2.5
1	C	110	SER	2.5
1	O	30	VAL	2.5
1	H	118	ILE	2.5
1	M	84	GLU	2.5
1	J	72	LEU	2.5
1	F	86	ALA	2.5
1	O	19	CYS	2.5
1	H	85	GLY	2.5
1	H	112	GLY	2.5
1	M	67	GLY	2.5
1	N	24	LYS	2.5
1	T	112	GLY	2.5
1	O	126	THR	2.5
1	L	81	GLN	2.5
1	O	122	SER	2.5
1	H	50	ILE	2.5
1	K	41	ILE	2.5
1	K	118	ILE	2.5
1	H	115	ARG	2.5
1	M	37	ASN	2.5
1	R	120	LYS	2.5
1	G	105	PHE	2.5
1	L	82	PHE	2.5
1	N	15	ILE	2.5
1	Q	114	VAL	2.5
1	J	49	ASN	2.5
1	O	107	ASN	2.5
1	O	26	ALA	2.5
1	C	81	GLN	2.5
1	K	117	ARG	2.4
1	C	128	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	H	94	ILE	2.4
1	H	99	VAL	2.4
1	K	24	LYS	2.4
1	J	27	ASN	2.4
1	Q	20	ASP	2.4
1	R	25	ASP	2.4
1	L	49	ASN	2.4
1	G	84	GLU	2.4
1	G	52	THR	2.4
1	A	118	ILE	2.4
1	D	128	ILE	2.4
1	T	50	ILE	2.4
1	H	87	LYS	2.4
1	D	113	LEU	2.4
1	D	108	ARG	2.4
1	S	20	ASP	2.4
1	N	61	GLY	2.4
1	D	52	THR	2.4
1	H	14	LYS	2.4
1	O	128	ILE	2.4
1	T	94	ILE	2.4
1	O	40	LEU	2.4
1	D	115	ARG	2.4
1	T	49	ASN	2.4
1	K	29	LYS	2.4
1	H	110	SER	2.4
1	Q	73	ILE	2.4
1	T	116	LEU	2.4
1	P	81	GLN	2.4
1	D	79	PRO	2.3
1	H	79	PRO	2.3
1	D	14	LYS	2.3
1	G	85	GLY	2.3
1	K	127	LYS	2.3
1	J	15	ILE	2.3
1	M	73	ILE	2.3
1	L	46	GLN	2.3
1	T	9	GLU	2.3
1	P	137	ASP	2.3
1	C	96	GLY	2.3
1	I	85	GLY	2.3
1	S	86	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	L	47	THR	2.3
1	P	7	MET	2.3
1	T	47	THR	2.3
1	E	10	GLU	2.3
1	T	78	PHE	2.3
1	R	19	CYS	2.3
1	M	71	LYS	2.3
1	S	24	LYS	2.3
1	H	26	ALA	2.3
1	T	17	ALA	2.3
1	S	9	GLU	2.3
1	T	81	GLN	2.3
1	R	50	ILE	2.3
1	Q	129	PHE	2.3
1	O	31	VAL	2.3
1	O	90	LEU	2.3
1	O	119	LYS	2.3
1	P	69	LEU	2.3
1	S	55	LEU	2.3
1	N	21	ARG	2.3
1	Q	86	ALA	2.3
1	G	110	SER	2.3
1	D	130	GLU	2.3
1	R	11	GLU	2.3
1	Q	128	ILE	2.3
1	O	120	LYS	2.3
1	C	69	LEU	2.2
1	I	113	LEU	2.2
1	M	82	PHE	2.2
1	Q	18	VAL	2.3
1	P	82	PHE	2.2
1	G	7	MET	2.2
1	O	98	ARG	2.2
1	F	11	GLU	2.2
1	D	77	GLU	2.2
1	D	93	THR	2.2
1	A	97	SER	2.2
1	F	24	LYS	2.2
1	I	24	LYS	2.2
1	H	41	ILE	2.2
1	B	95	VAL	2.2
1	J	90	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	J	114	VAL	2.2
1	N	69	LEU	2.2
1	M	49	ASN	2.2
1	O	106	ASP	2.2
1	E	98	ARG	2.2
1	J	9	GLU	2.2
1	O	39	GLN	2.2
1	M	13	THR	2.2
1	G	128	ILE	2.2
1	H	73	ILE	2.2
1	T	113	LEU	2.2
1	N	114	VAL	2.2
1	L	129	PHE	2.2
1	P	129	PHE	2.2
1	J	98	ARG	2.2
1	M	117	ARG	2.2
1	R	123	ASP	2.2
1	O	49	ASN	2.2
1	A	7	MET	2.2
1	D	112	GLY	2.2
1	D	127	LYS	2.2
1	O	29	LYS	2.2
1	E	126	THR	2.2
1	Q	13	THR	2.2
1	H	108	ARG	2.2
1	L	108	ARG	2.2
1	R	103	VAL	2.2
1	G	78	PHE	2.2
1	G	82	PHE	2.2
1	B	74	GLY	2.2
1	H	121	ALA	2.2
1	I	104	ILE	2.1
1	Q	72	LEU	2.1
1	D	88	ASP	2.1
1	D	106	ASP	2.1
1	I	95	VAL	2.1
1	T	114	VAL	2.1
1	Q	10	GLU	2.1
1	Q	87	LYS	2.1
1	K	32	PHE	2.1
1	K	85	GLY	2.1
1	C	53	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	26	ALA	2.1
1	H	89	SER	2.1
1	K	97	SER	2.1
1	F	117	ARG	2.1
1	Q	50	ILE	2.1
1	O	33	LEU	2.1
1	C	11	GLU	2.1
1	H	88	ASP	2.1
1	M	80	ASN	2.1
1	R	27	ASN	2.1
1	R	130	GLU	2.1
1	O	108	ARG	2.1
1	T	86	ALA	2.1
1	E	120	LYS	2.1
1	E	113	LEU	2.1
1	F	113	LEU	2.1
1	F	128	ILE	2.1
1	S	22	LEU	2.1
1	S	90	LEU	2.1
1	J	123	ASP	2.1
1	N	51	ASP	2.1
1	A	79	PRO	2.1
1	K	31	VAL	2.1
1	O	18	VAL	2.1
1	Q	112	GLY	2.1
1	G	19	CYS	2.1
1	J	13	THR	2.1
1	M	131	SER	2.1
1	K	44	ALA	2.1
1	C	92	MET	2.1
1	R	75	GLU	2.1
1	A	48	GLN	2.1
1	H	90	LEU	2.1
1	T	55	LEU	2.1
1	G	104	ILE	2.1
1	N	62	ASN	2.1
1	F	91	TYR	2.1
1	I	99	VAL	2.1
1	R	82	PHE	2.1
1	R	115	ARG	2.1
1	G	89	SER	2.0
1	G	10	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	J	11	GLU	2.0
1	J	17	ALA	2.0
1	M	86	ALA	2.0
1	N	10	GLU	2.0
1	B	48	GLN	2.0
1	N	49	ASN	2.0
1	O	123	ASP	2.0
1	E	50	ILE	2.0
1	P	98	ARG	2.0
1	M	78	PHE	2.0
1	I	87	LYS	2.0
1	C	130	GLU	2.0
1	O	121	ALA	2.0
1	O	83	HIS	2.0
1	T	19	CYS	2.0
1	B	69	LEU	2.0
1	G	20	ASP	2.0
1	S	113	LEU	2.0
1	C	115	ARG	2.0
1	A	120	LYS	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.