



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:55 AM UTC

PDB ID : 5L8F / pdb_00005l8f
Title : Crystal structure of Rhodospirillum rubrum Rru_A0973 mutant E32A, E62A, H65A.
Authors : He, D.; Hughes, S.; Vanden-Hehir, S.; Georgiev, A.; Altenbach, K.; Tarrant, E.; Mackay, C.L.; Waldron, K.J.; Clarke, D.J.; Marles-Wright, J.
Deposited on : 2016-06-07
Resolution : 2.25 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
Mogul : 2022.3.0, CSD as543be (2022)
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

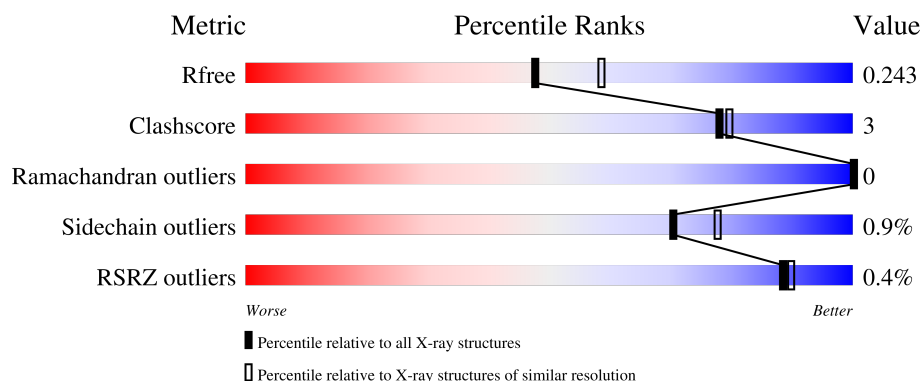
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

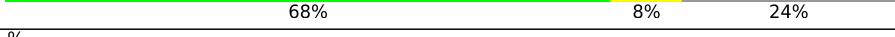
The reported resolution of this entry is 2.25 Å.

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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	116	
1	B	116	
1	C	116	
1	D	116	
1	E	116	

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Mol	Chain	Length	Quality of chain
1	F	116	 73%23%
1	G	116	 70%9%22%
1	H	116	 72%5%22%
1	I	116	 73%5%22%
1	J	116	 %71%7%22%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14566 atoms, of which 7005 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 Rru_A0973.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	89	Total	C	H	N	O	S	0	0	0
			1418	451	695	128	142	2			
1	B	91	Total	C	H	N	O	S	0	0	0
			1438	457	705	130	144	2			
1	C	89	Total	C	H	N	O	S	0	0	0
			1418	451	695	128	142	2			
1	D	88	Total	C	H	N	O	S	0	0	0
			1408	448	691	127	140	2			
1	E	90	Total	C	H	N	O	S	0	0	0
			1428	454	700	129	143	2			
1	F	89	Total	C	H	N	O	S	0	0	0
			1418	451	695	128	142	2			
1	G	91	Total	C	H	N	O	S	0	0	0
			1438	457	705	130	144	2			
1	H	90	Total	C	H	N	O	S	0	0	0
			1428	454	700	129	143	2			
1	I	91	Total	C	H	N	O	S	0	0	0
			1438	457	705	130	144	2			
1	J	90	Total	C	H	N	O	S	0	0	0
			1428	454	700	129	143	2			

There are 230 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	ALA	GLU	engineered mutation	UNP Q2RVS1
A	62	ALA	GLU	engineered mutation	UNP Q2RVS1
A	65	ALA	HIS	engineered mutation	UNP Q2RVS1
A	97	ALA	-	expression tag	UNP Q2RVS1
A	98	ASN	-	expression tag	UNP Q2RVS1
A	99	SER	-	expression tag	UNP Q2RVS1
A	100	SER	-	expression tag	UNP Q2RVS1
A	101	SER	-	expression tag	UNP Q2RVS1
A	102	VAL	-	expression tag	UNP Q2RVS1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	103	ASP	-	expression tag	UNP Q2RVS1
A	104	LYS	-	expression tag	UNP Q2RVS1
A	105	LEU	-	expression tag	UNP Q2RVS1
A	106	ALA	-	expression tag	UNP Q2RVS1
A	107	ALA	-	expression tag	UNP Q2RVS1
A	108	ALA	-	expression tag	UNP Q2RVS1
A	109	LEU	-	expression tag	UNP Q2RVS1
A	110	GLU	-	expression tag	UNP Q2RVS1
A	111	HIS	-	expression tag	UNP Q2RVS1
A	112	HIS	-	expression tag	UNP Q2RVS1
A	113	HIS	-	expression tag	UNP Q2RVS1
A	114	HIS	-	expression tag	UNP Q2RVS1
A	115	HIS	-	expression tag	UNP Q2RVS1
A	116	HIS	-	expression tag	UNP Q2RVS1
B	32	ALA	GLU	engineered mutation	UNP Q2RVS1
B	62	ALA	GLU	engineered mutation	UNP Q2RVS1
B	65	ALA	HIS	engineered mutation	UNP Q2RVS1
B	97	ALA	-	expression tag	UNP Q2RVS1
B	98	ASN	-	expression tag	UNP Q2RVS1
B	99	SER	-	expression tag	UNP Q2RVS1
B	100	SER	-	expression tag	UNP Q2RVS1
B	101	SER	-	expression tag	UNP Q2RVS1
B	102	VAL	-	expression tag	UNP Q2RVS1
B	103	ASP	-	expression tag	UNP Q2RVS1
B	104	LYS	-	expression tag	UNP Q2RVS1
B	105	LEU	-	expression tag	UNP Q2RVS1
B	106	ALA	-	expression tag	UNP Q2RVS1
B	107	ALA	-	expression tag	UNP Q2RVS1
B	108	ALA	-	expression tag	UNP Q2RVS1
B	109	LEU	-	expression tag	UNP Q2RVS1
B	110	GLU	-	expression tag	UNP Q2RVS1
B	111	HIS	-	expression tag	UNP Q2RVS1
B	112	HIS	-	expression tag	UNP Q2RVS1
B	113	HIS	-	expression tag	UNP Q2RVS1
B	114	HIS	-	expression tag	UNP Q2RVS1
B	115	HIS	-	expression tag	UNP Q2RVS1
B	116	HIS	-	expression tag	UNP Q2RVS1
C	32	ALA	GLU	engineered mutation	UNP Q2RVS1
C	62	ALA	GLU	engineered mutation	UNP Q2RVS1
C	65	ALA	HIS	engineered mutation	UNP Q2RVS1
C	97	ALA	-	expression tag	UNP Q2RVS1
C	98	ASN	-	expression tag	UNP Q2RVS1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	99	SER	-	expression tag	UNP Q2RVS1
C	100	SER	-	expression tag	UNP Q2RVS1
C	101	SER	-	expression tag	UNP Q2RVS1
C	102	VAL	-	expression tag	UNP Q2RVS1
C	103	ASP	-	expression tag	UNP Q2RVS1
C	104	LYS	-	expression tag	UNP Q2RVS1
C	105	LEU	-	expression tag	UNP Q2RVS1
C	106	ALA	-	expression tag	UNP Q2RVS1
C	107	ALA	-	expression tag	UNP Q2RVS1
C	108	ALA	-	expression tag	UNP Q2RVS1
C	109	LEU	-	expression tag	UNP Q2RVS1
C	110	GLU	-	expression tag	UNP Q2RVS1
C	111	HIS	-	expression tag	UNP Q2RVS1
C	112	HIS	-	expression tag	UNP Q2RVS1
C	113	HIS	-	expression tag	UNP Q2RVS1
C	114	HIS	-	expression tag	UNP Q2RVS1
C	115	HIS	-	expression tag	UNP Q2RVS1
C	116	HIS	-	expression tag	UNP Q2RVS1
D	32	ALA	GLU	engineered mutation	UNP Q2RVS1
D	62	ALA	GLU	engineered mutation	UNP Q2RVS1
D	65	ALA	HIS	engineered mutation	UNP Q2RVS1
D	97	ALA	-	expression tag	UNP Q2RVS1
D	98	ASN	-	expression tag	UNP Q2RVS1
D	99	SER	-	expression tag	UNP Q2RVS1
D	100	SER	-	expression tag	UNP Q2RVS1
D	101	SER	-	expression tag	UNP Q2RVS1
D	102	VAL	-	expression tag	UNP Q2RVS1
D	103	ASP	-	expression tag	UNP Q2RVS1
D	104	LYS	-	expression tag	UNP Q2RVS1
D	105	LEU	-	expression tag	UNP Q2RVS1
D	106	ALA	-	expression tag	UNP Q2RVS1
D	107	ALA	-	expression tag	UNP Q2RVS1
D	108	ALA	-	expression tag	UNP Q2RVS1
D	109	LEU	-	expression tag	UNP Q2RVS1
D	110	GLU	-	expression tag	UNP Q2RVS1
D	111	HIS	-	expression tag	UNP Q2RVS1
D	112	HIS	-	expression tag	UNP Q2RVS1
D	113	HIS	-	expression tag	UNP Q2RVS1
D	114	HIS	-	expression tag	UNP Q2RVS1
D	115	HIS	-	expression tag	UNP Q2RVS1
D	116	HIS	-	expression tag	UNP Q2RVS1
E	32	ALA	GLU	engineered mutation	UNP Q2RVS1

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Chain	Residue	Modelled	Actual	Comment	Reference
E	62	ALA	GLU	engineered mutation	UNP Q2RVS1
E	65	ALA	HIS	engineered mutation	UNP Q2RVS1
E	97	ALA	-	expression tag	UNP Q2RVS1
E	98	ASN	-	expression tag	UNP Q2RVS1
E	99	SER	-	expression tag	UNP Q2RVS1
E	100	SER	-	expression tag	UNP Q2RVS1
E	101	SER	-	expression tag	UNP Q2RVS1
E	102	VAL	-	expression tag	UNP Q2RVS1
E	103	ASP	-	expression tag	UNP Q2RVS1
E	104	LYS	-	expression tag	UNP Q2RVS1
E	105	LEU	-	expression tag	UNP Q2RVS1
E	106	ALA	-	expression tag	UNP Q2RVS1
E	107	ALA	-	expression tag	UNP Q2RVS1
E	108	ALA	-	expression tag	UNP Q2RVS1
E	109	LEU	-	expression tag	UNP Q2RVS1
E	110	GLU	-	expression tag	UNP Q2RVS1
E	111	HIS	-	expression tag	UNP Q2RVS1
E	112	HIS	-	expression tag	UNP Q2RVS1
E	113	HIS	-	expression tag	UNP Q2RVS1
E	114	HIS	-	expression tag	UNP Q2RVS1
E	115	HIS	-	expression tag	UNP Q2RVS1
E	116	HIS	-	expression tag	UNP Q2RVS1
F	32	ALA	GLU	engineered mutation	UNP Q2RVS1
F	62	ALA	GLU	engineered mutation	UNP Q2RVS1
F	65	ALA	HIS	engineered mutation	UNP Q2RVS1
F	97	ALA	-	expression tag	UNP Q2RVS1
F	98	ASN	-	expression tag	UNP Q2RVS1
F	99	SER	-	expression tag	UNP Q2RVS1
F	100	SER	-	expression tag	UNP Q2RVS1
F	101	SER	-	expression tag	UNP Q2RVS1
F	102	VAL	-	expression tag	UNP Q2RVS1
F	103	ASP	-	expression tag	UNP Q2RVS1
F	104	LYS	-	expression tag	UNP Q2RVS1
F	105	LEU	-	expression tag	UNP Q2RVS1
F	106	ALA	-	expression tag	UNP Q2RVS1
F	107	ALA	-	expression tag	UNP Q2RVS1
F	108	ALA	-	expression tag	UNP Q2RVS1
F	109	LEU	-	expression tag	UNP Q2RVS1
F	110	GLU	-	expression tag	UNP Q2RVS1
F	111	HIS	-	expression tag	UNP Q2RVS1
F	112	HIS	-	expression tag	UNP Q2RVS1
F	113	HIS	-	expression tag	UNP Q2RVS1

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Chain	Residue	Modelled	Actual	Comment	Reference
F	114	HIS	-	expression tag	UNP Q2RVS1
F	115	HIS	-	expression tag	UNP Q2RVS1
F	116	HIS	-	expression tag	UNP Q2RVS1
G	32	ALA	GLU	engineered mutation	UNP Q2RVS1
G	62	ALA	GLU	engineered mutation	UNP Q2RVS1
G	65	ALA	HIS	engineered mutation	UNP Q2RVS1
G	97	ALA	-	expression tag	UNP Q2RVS1
G	98	ASN	-	expression tag	UNP Q2RVS1
G	99	SER	-	expression tag	UNP Q2RVS1
G	100	SER	-	expression tag	UNP Q2RVS1
G	101	SER	-	expression tag	UNP Q2RVS1
G	102	VAL	-	expression tag	UNP Q2RVS1
G	103	ASP	-	expression tag	UNP Q2RVS1
G	104	LYS	-	expression tag	UNP Q2RVS1
G	105	LEU	-	expression tag	UNP Q2RVS1
G	106	ALA	-	expression tag	UNP Q2RVS1
G	107	ALA	-	expression tag	UNP Q2RVS1
G	108	ALA	-	expression tag	UNP Q2RVS1
G	109	LEU	-	expression tag	UNP Q2RVS1
G	110	GLU	-	expression tag	UNP Q2RVS1
G	111	HIS	-	expression tag	UNP Q2RVS1
G	112	HIS	-	expression tag	UNP Q2RVS1
G	113	HIS	-	expression tag	UNP Q2RVS1
G	114	HIS	-	expression tag	UNP Q2RVS1
G	115	HIS	-	expression tag	UNP Q2RVS1
G	116	HIS	-	expression tag	UNP Q2RVS1
H	32	ALA	GLU	engineered mutation	UNP Q2RVS1
H	62	ALA	GLU	engineered mutation	UNP Q2RVS1
H	65	ALA	HIS	engineered mutation	UNP Q2RVS1
H	97	ALA	-	expression tag	UNP Q2RVS1
H	98	ASN	-	expression tag	UNP Q2RVS1
H	99	SER	-	expression tag	UNP Q2RVS1
H	100	SER	-	expression tag	UNP Q2RVS1
H	101	SER	-	expression tag	UNP Q2RVS1
H	102	VAL	-	expression tag	UNP Q2RVS1
H	103	ASP	-	expression tag	UNP Q2RVS1
H	104	LYS	-	expression tag	UNP Q2RVS1
H	105	LEU	-	expression tag	UNP Q2RVS1
H	106	ALA	-	expression tag	UNP Q2RVS1
H	107	ALA	-	expression tag	UNP Q2RVS1
H	108	ALA	-	expression tag	UNP Q2RVS1
H	109	LEU	-	expression tag	UNP Q2RVS1

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Chain	Residue	Modelled	Actual	Comment	Reference
H	110	GLU	-	expression tag	UNP Q2RVS1
H	111	HIS	-	expression tag	UNP Q2RVS1
H	112	HIS	-	expression tag	UNP Q2RVS1
H	113	HIS	-	expression tag	UNP Q2RVS1
H	114	HIS	-	expression tag	UNP Q2RVS1
H	115	HIS	-	expression tag	UNP Q2RVS1
H	116	HIS	-	expression tag	UNP Q2RVS1
I	32	ALA	GLU	engineered mutation	UNP Q2RVS1
I	62	ALA	GLU	engineered mutation	UNP Q2RVS1
I	65	ALA	HIS	engineered mutation	UNP Q2RVS1
I	97	ALA	-	expression tag	UNP Q2RVS1
I	98	ASN	-	expression tag	UNP Q2RVS1
I	99	SER	-	expression tag	UNP Q2RVS1
I	100	SER	-	expression tag	UNP Q2RVS1
I	101	SER	-	expression tag	UNP Q2RVS1
I	102	VAL	-	expression tag	UNP Q2RVS1
I	103	ASP	-	expression tag	UNP Q2RVS1
I	104	LYS	-	expression tag	UNP Q2RVS1
I	105	LEU	-	expression tag	UNP Q2RVS1
I	106	ALA	-	expression tag	UNP Q2RVS1
I	107	ALA	-	expression tag	UNP Q2RVS1
I	108	ALA	-	expression tag	UNP Q2RVS1
I	109	LEU	-	expression tag	UNP Q2RVS1
I	110	GLU	-	expression tag	UNP Q2RVS1
I	111	HIS	-	expression tag	UNP Q2RVS1
I	112	HIS	-	expression tag	UNP Q2RVS1
I	113	HIS	-	expression tag	UNP Q2RVS1
I	114	HIS	-	expression tag	UNP Q2RVS1
I	115	HIS	-	expression tag	UNP Q2RVS1
I	116	HIS	-	expression tag	UNP Q2RVS1
J	32	ALA	GLU	engineered mutation	UNP Q2RVS1
J	62	ALA	GLU	engineered mutation	UNP Q2RVS1
J	65	ALA	HIS	engineered mutation	UNP Q2RVS1
J	97	ALA	-	expression tag	UNP Q2RVS1
J	98	ASN	-	expression tag	UNP Q2RVS1
J	99	SER	-	expression tag	UNP Q2RVS1
J	100	SER	-	expression tag	UNP Q2RVS1
J	101	SER	-	expression tag	UNP Q2RVS1
J	102	VAL	-	expression tag	UNP Q2RVS1
J	103	ASP	-	expression tag	UNP Q2RVS1
J	104	LYS	-	expression tag	UNP Q2RVS1
J	105	LEU	-	expression tag	UNP Q2RVS1

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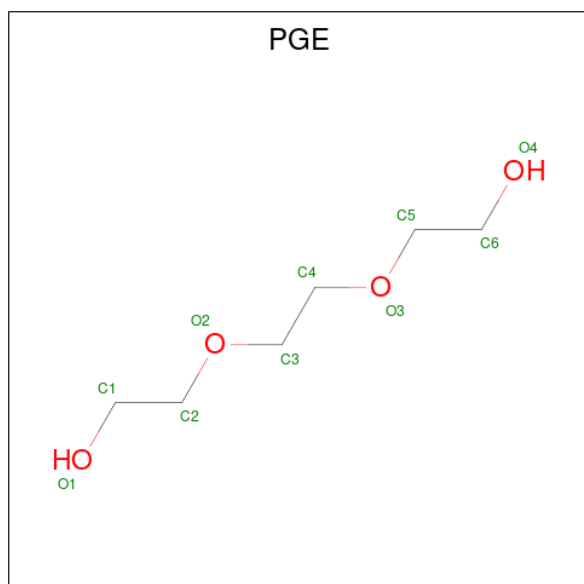
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Chain	Residue	Modelled	Actual	Comment	Reference
J	106	ALA	-	expression tag	UNP Q2RVS1
J	107	ALA	-	expression tag	UNP Q2RVS1
J	108	ALA	-	expression tag	UNP Q2RVS1
J	109	LEU	-	expression tag	UNP Q2RVS1
J	110	GLU	-	expression tag	UNP Q2RVS1
J	111	HIS	-	expression tag	UNP Q2RVS1
J	112	HIS	-	expression tag	UNP Q2RVS1
J	113	HIS	-	expression tag	UNP Q2RVS1
J	114	HIS	-	expression tag	UNP Q2RVS1
J	115	HIS	-	expression tag	UNP Q2RVS1
J	116	HIS	-	expression tag	UNP Q2RVS1

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mg 2 2	0	0
2	D	2	Total Mg 2 2	0	0
2	F	2	Total Mg 2 2	0	0
2	G	3	Total Mg 3 3	0	0
2	J	1	Total Mg 1 1	0	0

- Molecule 3 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	G	1	Total	C	H	O	0	0
			24	6	14	4		

- Molecule 4 is water.

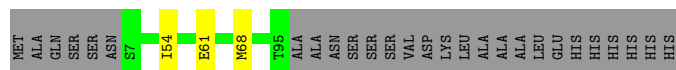
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	31	Total	O	0	0
			31	31		
4	B	22	Total	O	0	0
			22	22		
4	C	16	Total	O	0	0
			16	16		
4	D	19	Total	O	0	0
			19	19		
4	E	22	Total	O	0	0
			22	22		
4	F	24	Total	O	0	0
			24	24		
4	G	39	Total	O	0	0
			39	39		
4	H	29	Total	O	0	0
			29	29		
4	I	29	Total	O	0	0
			29	29		
4	J	41	Total	O	0	0
			41	41		

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.

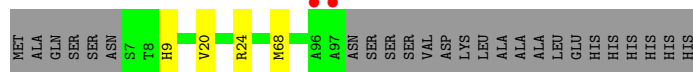
• Molecule 1: Rru_A0973

Chain A: 



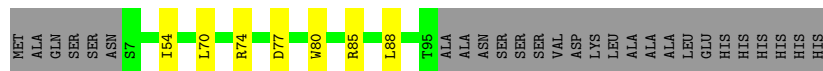
• Molecule 1: Rru_A0973

Chain B: 



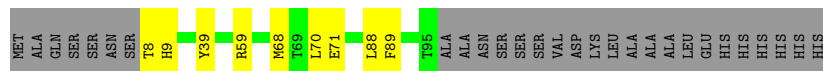
• Molecule 1: Rru_A0973

Chain C: 



• Molecule 1: Rru_A0973

Chain D: 



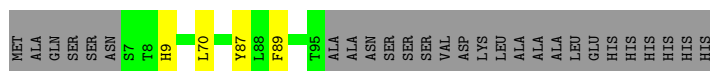
• Molecule 1: Rru_A0973

Chain E: 



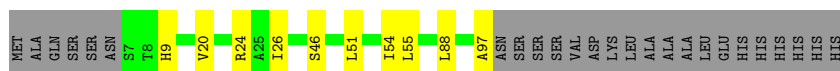
• Molecule 1: Rru_A0973

Chain F:  73% 23%



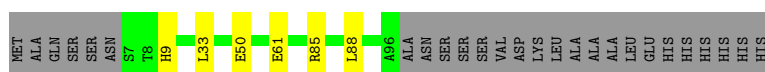
• Molecule 1: Rru_A0973

Chain G:  70% 9% 22%



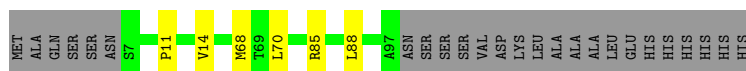
• Molecule 1: Rru_A0973

Chain H:  72% 5% 22%



• Molecule 1: Rru_A0973

Chain I:  73% 5% 22%



• Molecule 1: Rru_A0973

Chain J:  71% 7% 22%



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	92.10Å 92.10Å 217.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.41 – 2.25 48.41 – 2.25	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.41-2.25) 99.0 (48.41-2.25)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.24Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.179 , 0.240 0.181 , 0.243	Depositor DCC
R_{free} test set	2319 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	32.6	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 35.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14566	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 52.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.7017e-05.*

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

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PGE

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	0.54	0/738	0.67	0/1005
1	B	0.53	0/748	0.63	0/1019
1	C	0.51	0/738	0.66	0/1005
1	D	0.50	0/732	0.62	0/997
1	E	0.54	0/743	0.62	0/1012
1	F	0.57	0/738	0.65	0/1005
1	G	0.56	0/748	0.64	0/1019
1	H	0.59	0/743	0.69	0/1012
1	I	0.57	0/748	0.65	0/1019
1	J	0.57	0/743	0.67	0/1012
All	All	0.55	0/7419	0.65	0/10105

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	723	695	695	3	0
1	B	733	705	705	2	0
1	C	723	695	695	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	717	691	690	11	0
1	E	728	700	700	8	0
1	F	723	695	695	4	0
1	G	733	705	705	8	0
1	H	728	700	700	5	0
1	I	733	705	705	5	0
1	J	728	700	700	6	0
2	B	2	0	0	0	0
2	D	2	0	0	0	0
2	F	2	0	0	0	0
2	G	3	0	0	0	0
2	J	1	0	0	0	0
3	G	10	14	14	0	0
4	A	31	0	0	1	0
4	B	22	0	0	0	0
4	C	16	0	0	0	0
4	D	19	0	0	1	0
4	E	22	0	0	2	0
4	F	24	0	0	0	0
4	G	39	0	0	2	0
4	H	29	0	0	2	0
4	I	29	0	0	1	0
4	J	41	0	0	1	0
All	All	7561	7005	7004	40	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 (40) 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:G:97:ALA:O	4:G:301:HOH:O	1.91	0.89
1:G:46:SER:O	4:G:302:HOH:O	2.01	0.77
1:D:8:THR:N	4:D:301:HOH:O	2.20	0.75
1:I:85:ARG:NH2	4:I:301:HOH:O	2.21	0.72
1:H:61:GLU:OE1	4:H:301:HOH:O	2.10	0.69
1:E:16:LYS:NZ	4:E:303:HOH:O	2.29	0.64
1:A:61:GLU:OE1	4:A:201:HOH:O	2.15	0.61
1:E:82:GLU:OE2	4:E:301:HOH:O	2.16	0.60
1:G:88:LEU:CD2	1:H:88:LEU:HD23	2.31	0.60
1:G:54:ILE:HG23	1:I:68:MET:HE2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:LEU:CD2	1:D:70:LEU:HD21	2.35	0.56
1:D:68:MET:HE2	1:E:54:ILE:HG23	1.90	0.54
1:E:74:ARG:HD2	1:F:89:PHE:CE1	2.44	0.53
1:B:68:MET:HE2	1:C:54:ILE:HG23	1.90	0.52
1:E:70:LEU:HD21	1:F:70:LEU:HD13	1.92	0.52
1:G:88:LEU:CD2	1:H:88:LEU:CD2	2.88	0.51
1:E:94:ILE:O	1:E:96:ALA:N	2.40	0.51
1:A:68:MET:HE2	1:J:54:ILE:HG23	1.93	0.49
1:A:54:ILE:HG23	1:J:68:MET:HE2	1.96	0.48
1:J:18:GLU:HA	4:J:307:HOH:O	2.15	0.46
1:C:88:LEU:CD2	1:D:88:LEU:CD2	2.95	0.45
1:E:68:MET:HG2	1:F:87:TYR:CE1	2.51	0.45
1:G:20:VAL:O	1:G:24:ARG:HG3	2.17	0.44
1:J:25:ALA:O	1:J:29:VAL:HG23	2.19	0.43
1:C:88:LEU:HA	1:D:71:GLU:OE1	2.19	0.43
1:I:88:LEU:HA	1:J:71:GLU:OE1	2.19	0.42
1:B:20:VAL:O	1:B:24:ARG:HG3	2.20	0.42
1:C:74:ARG:HD2	1:D:89:PHE:CE1	2.55	0.42
1:E:38:TRP:CE2	1:F:9:HIS:CE1	3.08	0.42
1:C:70:LEU:CD2	1:D:70:LEU:CD2	2.97	0.41
1:C:88:LEU:HD23	1:D:88:LEU:CD2	2.50	0.41
1:C:70:LEU:HD21	1:D:70:LEU:CD2	2.51	0.41
1:G:26:ILE:HG23	1:H:33:LEU:HB3	2.03	0.41
1:G:51:LEU:O	1:G:55:LEU:HG	2.21	0.41
1:C:85:ARG:HG3	1:D:89:PHE:CE1	2.55	0.41
1:D:39:TYR:HB3	1:D:59:ARG:HB2	2.02	0.41
1:I:11:PRO:O	1:I:14:VAL:HG22	2.20	0.41
1:I:70:LEU:HD13	1:J:70:LEU:HD21	2.03	0.40
1:C:77:ASP:HB3	1:C:80:TRP:HB2	2.02	0.40
1:H:85:ARG:NE	4:H:303:HOH:O	2.38	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	87/116 (75%)	87 (100%)	0	0	100	100
1	B	89/116 (77%)	89 (100%)	0	0	100	100
1	C	87/116 (75%)	87 (100%)	0	0	100	100
1	D	86/116 (74%)	85 (99%)	1 (1%)	0	100	100
1	E	88/116 (76%)	87 (99%)	1 (1%)	0	100	100
1	F	87/116 (75%)	87 (100%)	0	0	100	100
1	G	89/116 (77%)	88 (99%)	1 (1%)	0	100	100
1	H	88/116 (76%)	88 (100%)	0	0	100	100
1	I	89/116 (77%)	89 (100%)	0	0	100	100
1	J	88/116 (76%)	88 (100%)	0	0	100	100
All	All	878/1160 (76%)	875 (100%)	3 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	76/97 (78%)	76 (100%)	0	100	100
1	B	76/97 (78%)	75 (99%)	1 (1%)	61	71
1	C	76/97 (78%)	76 (100%)	0	100	100
1	D	75/97 (77%)	74 (99%)	1 (1%)	61	71
1	E	76/97 (78%)	75 (99%)	1 (1%)	61	71
1	F	76/97 (78%)	76 (100%)	0	100	100
1	G	76/97 (78%)	75 (99%)	1 (1%)	61	71
1	H	76/97 (78%)	74 (97%)	2 (3%)	40	48
1	I	76/97 (78%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	76/97 (78%)	75 (99%)	1 (1%)	61	71
All	All	759/970 (78%)	752 (99%)	7 (1%)	70	78

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	9	HIS
1	D	9	HIS
1	E	9	HIS
1	G	9	HIS
1	H	9	HIS
1	H	50	GLU
1	J	9	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	9	HIS
1	G	9	HIS
1	J	76	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	PGE	G	203	-	9,9,9	0.51	0	8,8,8	0.50	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PGE	G	203	-	-	2/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	203	PGE	C4-C3-O2-C2
3	G	203	PGE	C3-C4-O3-C5

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	89/116 (76%)	-0.17	0 100 100	31, 41, 65, 74	0
1	B	91/116 (78%)	-0.04	2 (2%) 62 64	32, 44, 66, 91	0
1	C	89/116 (76%)	-0.12	0 100 100	35, 44, 70, 82	0
1	D	88/116 (75%)	-0.15	0 100 100	36, 46, 68, 96	0
1	E	90/116 (77%)	-0.06	1 (1%) 78 79	33, 44, 65, 78	0
1	F	89/116 (76%)	-0.21	0 100 100	29, 41, 64, 80	0
1	G	91/116 (78%)	-0.25	0 100 100	30, 39, 61, 76	0
1	H	90/116 (77%)	-0.30	0 100 100	28, 38, 63, 71	0
1	I	91/116 (78%)	-0.14	0 100 100	32, 40, 62, 88	0
1	J	90/116 (77%)	-0.19	1 (1%) 78 79	29, 40, 61, 76	0
All	All	898/1160 (77%)	-0.16	4 (0%) 88 90	28, 42, 66, 96	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	97	ALA	3.7
1	B	96	ALA	2.7
1	E	96	ALA	2.6
1	J	96	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MG	D	201	1/1	0.85	0.20	60,60,60,60	0
2	MG	B	202	1/1	0.89	0.17	54,54,54,54	0
2	MG	B	201	1/1	0.89	0.15	57,57,57,57	0
2	MG	D	202	1/1	0.89	0.17	53,53,53,53	0
2	MG	G	204	1/1	0.89	0.08	46,46,46,46	0
3	PGE	G	203	10/10	0.90	0.10	31,45,54,55	0
2	MG	F	202	1/1	0.91	0.17	47,47,47,47	0
2	MG	G	201	1/1	0.93	0.06	56,56,56,56	0
2	MG	F	201	1/1	0.95	0.14	48,48,48,48	0
2	MG	J	201	1/1	0.97	0.08	47,47,47,47	0
2	MG	G	202	1/1	0.98	0.06	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.