



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 02:55 pm BST

PDB ID : 3F56
Title : The structure of a previously undetected carboxysome shell protein: CsoS1D from *Prochlorococcus marinus* MED4
Authors : Klein, M.G.; Zwart, P.; Kerfeld, C.A.
Deposited on : 2008-11-03
Resolution : 2.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

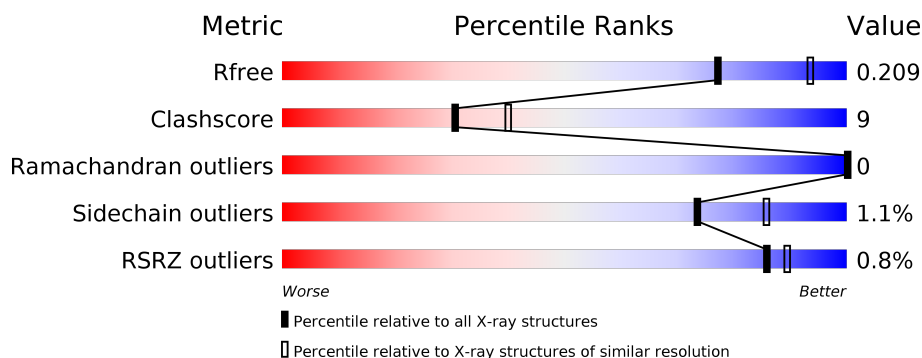
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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	281	<div> <div>60%</div> <div>12%</div> <div>•</div> <div>26%</div> </div>
1	B	281	<div> <div>68%</div> <div>6%</div> <div>26%</div> </div>
1	C	281	<div> <div>%</div> <div>59%</div> <div>15%</div> <div>•</div> <div>26%</div> </div>
1	D	281	<div> <div>64%</div> <div>8%</div> <div>27%</div> </div>
1	E	281	<div> <div>%</div> <div>55%</div> <div>16%</div> <div>29%</div> </div>
1	F	281	<div> <div>63%</div> <div>9%</div> <div>27%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9951 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 CsoS1D.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	Se	0	0	0
			1568	985	273	301	2	7			
1	B	209	Total	C	N	O	S	Se	0	0	0
			1563	982	272	300	2	7			
1	C	208	Total	C	N	O	S	Se	0	0	0
			1560	981	270	300	2	7			
1	D	204	Total	C	N	O	S	Se	0	0	0
			1536	967	267	293	2	7			
1	E	200	Total	C	N	O	S	Se	0	0	0
			1502	945	262	286	2	7			
1	F	204	Total	C	N	O	S	Se	0	0	0
			1540	969	268	294	2	7			

There are 150 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MSE	-	EXPRESSION TAG	UNP Q7V2D3
A	-23	SER	-	EXPRESSION TAG	UNP Q7V2D3
A	-22	TYR	-	EXPRESSION TAG	UNP Q7V2D3
A	-21	TYR	-	EXPRESSION TAG	UNP Q7V2D3
A	-20	HIS	-	EXPRESSION TAG	UNP Q7V2D3
A	-19	HIS	-	EXPRESSION TAG	UNP Q7V2D3
A	-18	HIS	-	EXPRESSION TAG	UNP Q7V2D3
A	-17	HIS	-	EXPRESSION TAG	UNP Q7V2D3
A	-16	HIS	-	EXPRESSION TAG	UNP Q7V2D3
A	-15	HIS	-	EXPRESSION TAG	UNP Q7V2D3
A	-14	ASP	-	EXPRESSION TAG	UNP Q7V2D3
A	-13	TYR	-	EXPRESSION TAG	UNP Q7V2D3
A	-12	ASP	-	EXPRESSION TAG	UNP Q7V2D3
A	-11	ILE	-	EXPRESSION TAG	UNP Q7V2D3
A	-10	PRO	-	EXPRESSION TAG	UNP Q7V2D3
A	-9	THR	-	EXPRESSION TAG	UNP Q7V2D3
A	-8	THR	-	EXPRESSION TAG	UNP Q7V2D3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLU	-	EXPRESSION TAG	UNP Q7V2D3
A	-6	ASN	-	EXPRESSION TAG	UNP Q7V2D3
A	-5	LEU	-	EXPRESSION TAG	UNP Q7V2D3
A	-4	THR	-	EXPRESSION TAG	UNP Q7V2D3
A	-3	PHE	-	EXPRESSION TAG	UNP Q7V2D3
A	-2	GLN	-	EXPRESSION TAG	UNP Q7V2D3
A	-1	GLY	-	EXPRESSION TAG	UNP Q7V2D3
A	0	ALA	-	EXPRESSION TAG	UNP Q7V2D3
B	-24	MSE	-	EXPRESSION TAG	UNP Q7V2D3
B	-23	SER	-	EXPRESSION TAG	UNP Q7V2D3
B	-22	TYR	-	EXPRESSION TAG	UNP Q7V2D3
B	-21	TYR	-	EXPRESSION TAG	UNP Q7V2D3
B	-20	HIS	-	EXPRESSION TAG	UNP Q7V2D3
B	-19	HIS	-	EXPRESSION TAG	UNP Q7V2D3
B	-18	HIS	-	EXPRESSION TAG	UNP Q7V2D3
B	-17	HIS	-	EXPRESSION TAG	UNP Q7V2D3
B	-16	HIS	-	EXPRESSION TAG	UNP Q7V2D3
B	-15	HIS	-	EXPRESSION TAG	UNP Q7V2D3
B	-14	ASP	-	EXPRESSION TAG	UNP Q7V2D3
B	-13	TYR	-	EXPRESSION TAG	UNP Q7V2D3
B	-12	ASP	-	EXPRESSION TAG	UNP Q7V2D3
B	-11	ILE	-	EXPRESSION TAG	UNP Q7V2D3
B	-10	PRO	-	EXPRESSION TAG	UNP Q7V2D3
B	-9	THR	-	EXPRESSION TAG	UNP Q7V2D3
B	-8	THR	-	EXPRESSION TAG	UNP Q7V2D3
B	-7	GLU	-	EXPRESSION TAG	UNP Q7V2D3
B	-6	ASN	-	EXPRESSION TAG	UNP Q7V2D3
B	-5	LEU	-	EXPRESSION TAG	UNP Q7V2D3
B	-4	THR	-	EXPRESSION TAG	UNP Q7V2D3
B	-3	PHE	-	EXPRESSION TAG	UNP Q7V2D3
B	-2	GLN	-	EXPRESSION TAG	UNP Q7V2D3
B	-1	GLY	-	EXPRESSION TAG	UNP Q7V2D3
B	0	ALA	-	EXPRESSION TAG	UNP Q7V2D3
C	-24	MSE	-	EXPRESSION TAG	UNP Q7V2D3
C	-23	SER	-	EXPRESSION TAG	UNP Q7V2D3
C	-22	TYR	-	EXPRESSION TAG	UNP Q7V2D3
C	-21	TYR	-	EXPRESSION TAG	UNP Q7V2D3
C	-20	HIS	-	EXPRESSION TAG	UNP Q7V2D3
C	-19	HIS	-	EXPRESSION TAG	UNP Q7V2D3
C	-18	HIS	-	EXPRESSION TAG	UNP Q7V2D3
C	-17	HIS	-	EXPRESSION TAG	UNP Q7V2D3
C	-16	HIS	-	EXPRESSION TAG	UNP Q7V2D3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-15	HIS	-	EXPRESSION TAG	UNP Q7V2D3
C	-14	ASP	-	EXPRESSION TAG	UNP Q7V2D3
C	-13	TYR	-	EXPRESSION TAG	UNP Q7V2D3
C	-12	ASP	-	EXPRESSION TAG	UNP Q7V2D3
C	-11	ILE	-	EXPRESSION TAG	UNP Q7V2D3
C	-10	PRO	-	EXPRESSION TAG	UNP Q7V2D3
C	-9	THR	-	EXPRESSION TAG	UNP Q7V2D3
C	-8	THR	-	EXPRESSION TAG	UNP Q7V2D3
C	-7	GLU	-	EXPRESSION TAG	UNP Q7V2D3
C	-6	ASN	-	EXPRESSION TAG	UNP Q7V2D3
C	-5	LEU	-	EXPRESSION TAG	UNP Q7V2D3
C	-4	THR	-	EXPRESSION TAG	UNP Q7V2D3
C	-3	PHE	-	EXPRESSION TAG	UNP Q7V2D3
C	-2	GLN	-	EXPRESSION TAG	UNP Q7V2D3
C	-1	GLY	-	EXPRESSION TAG	UNP Q7V2D3
C	0	ALA	-	EXPRESSION TAG	UNP Q7V2D3
D	-24	MSE	-	EXPRESSION TAG	UNP Q7V2D3
D	-23	SER	-	EXPRESSION TAG	UNP Q7V2D3
D	-22	TYR	-	EXPRESSION TAG	UNP Q7V2D3
D	-21	TYR	-	EXPRESSION TAG	UNP Q7V2D3
D	-20	HIS	-	EXPRESSION TAG	UNP Q7V2D3
D	-19	HIS	-	EXPRESSION TAG	UNP Q7V2D3
D	-18	HIS	-	EXPRESSION TAG	UNP Q7V2D3
D	-17	HIS	-	EXPRESSION TAG	UNP Q7V2D3
D	-16	HIS	-	EXPRESSION TAG	UNP Q7V2D3
D	-15	HIS	-	EXPRESSION TAG	UNP Q7V2D3
D	-14	ASP	-	EXPRESSION TAG	UNP Q7V2D3
D	-13	TYR	-	EXPRESSION TAG	UNP Q7V2D3
D	-12	ASP	-	EXPRESSION TAG	UNP Q7V2D3
D	-11	ILE	-	EXPRESSION TAG	UNP Q7V2D3
D	-10	PRO	-	EXPRESSION TAG	UNP Q7V2D3
D	-9	THR	-	EXPRESSION TAG	UNP Q7V2D3
D	-8	THR	-	EXPRESSION TAG	UNP Q7V2D3
D	-7	GLU	-	EXPRESSION TAG	UNP Q7V2D3
D	-6	ASN	-	EXPRESSION TAG	UNP Q7V2D3
D	-5	LEU	-	EXPRESSION TAG	UNP Q7V2D3
D	-4	THR	-	EXPRESSION TAG	UNP Q7V2D3
D	-3	PHE	-	EXPRESSION TAG	UNP Q7V2D3
D	-2	GLN	-	EXPRESSION TAG	UNP Q7V2D3
D	-1	GLY	-	EXPRESSION TAG	UNP Q7V2D3
D	0	ALA	-	EXPRESSION TAG	UNP Q7V2D3
E	-24	MSE	-	EXPRESSION TAG	UNP Q7V2D3

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-23	SER	-	EXPRESSION TAG	UNP Q7V2D3
E	-22	TYR	-	EXPRESSION TAG	UNP Q7V2D3
E	-21	TYR	-	EXPRESSION TAG	UNP Q7V2D3
E	-20	HIS	-	EXPRESSION TAG	UNP Q7V2D3
E	-19	HIS	-	EXPRESSION TAG	UNP Q7V2D3
E	-18	HIS	-	EXPRESSION TAG	UNP Q7V2D3
E	-17	HIS	-	EXPRESSION TAG	UNP Q7V2D3
E	-16	HIS	-	EXPRESSION TAG	UNP Q7V2D3
E	-15	HIS	-	EXPRESSION TAG	UNP Q7V2D3
E	-14	ASP	-	EXPRESSION TAG	UNP Q7V2D3
E	-13	TYR	-	EXPRESSION TAG	UNP Q7V2D3
E	-12	ASP	-	EXPRESSION TAG	UNP Q7V2D3
E	-11	ILE	-	EXPRESSION TAG	UNP Q7V2D3
E	-10	PRO	-	EXPRESSION TAG	UNP Q7V2D3
E	-9	THR	-	EXPRESSION TAG	UNP Q7V2D3
E	-8	THR	-	EXPRESSION TAG	UNP Q7V2D3
E	-7	GLU	-	EXPRESSION TAG	UNP Q7V2D3
E	-6	ASN	-	EXPRESSION TAG	UNP Q7V2D3
E	-5	LEU	-	EXPRESSION TAG	UNP Q7V2D3
E	-4	THR	-	EXPRESSION TAG	UNP Q7V2D3
E	-3	PHE	-	EXPRESSION TAG	UNP Q7V2D3
E	-2	GLN	-	EXPRESSION TAG	UNP Q7V2D3
E	-1	GLY	-	EXPRESSION TAG	UNP Q7V2D3
E	0	ALA	-	EXPRESSION TAG	UNP Q7V2D3
F	-24	MSE	-	EXPRESSION TAG	UNP Q7V2D3
F	-23	SER	-	EXPRESSION TAG	UNP Q7V2D3
F	-22	TYR	-	EXPRESSION TAG	UNP Q7V2D3
F	-21	TYR	-	EXPRESSION TAG	UNP Q7V2D3
F	-20	HIS	-	EXPRESSION TAG	UNP Q7V2D3
F	-19	HIS	-	EXPRESSION TAG	UNP Q7V2D3
F	-18	HIS	-	EXPRESSION TAG	UNP Q7V2D3
F	-17	HIS	-	EXPRESSION TAG	UNP Q7V2D3
F	-16	HIS	-	EXPRESSION TAG	UNP Q7V2D3
F	-15	HIS	-	EXPRESSION TAG	UNP Q7V2D3
F	-14	ASP	-	EXPRESSION TAG	UNP Q7V2D3
F	-13	TYR	-	EXPRESSION TAG	UNP Q7V2D3
F	-12	ASP	-	EXPRESSION TAG	UNP Q7V2D3
F	-11	ILE	-	EXPRESSION TAG	UNP Q7V2D3
F	-10	PRO	-	EXPRESSION TAG	UNP Q7V2D3
F	-9	THR	-	EXPRESSION TAG	UNP Q7V2D3
F	-8	THR	-	EXPRESSION TAG	UNP Q7V2D3
F	-7	GLU	-	EXPRESSION TAG	UNP Q7V2D3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-6	ASN	-	EXPRESSION TAG	UNP Q7V2D3
F	-5	LEU	-	EXPRESSION TAG	UNP Q7V2D3
F	-4	THR	-	EXPRESSION TAG	UNP Q7V2D3
F	-3	PHE	-	EXPRESSION TAG	UNP Q7V2D3
F	-2	GLN	-	EXPRESSION TAG	UNP Q7V2D3
F	-1	GLY	-	EXPRESSION TAG	UNP Q7V2D3
F	0	ALA	-	EXPRESSION TAG	UNP Q7V2D3

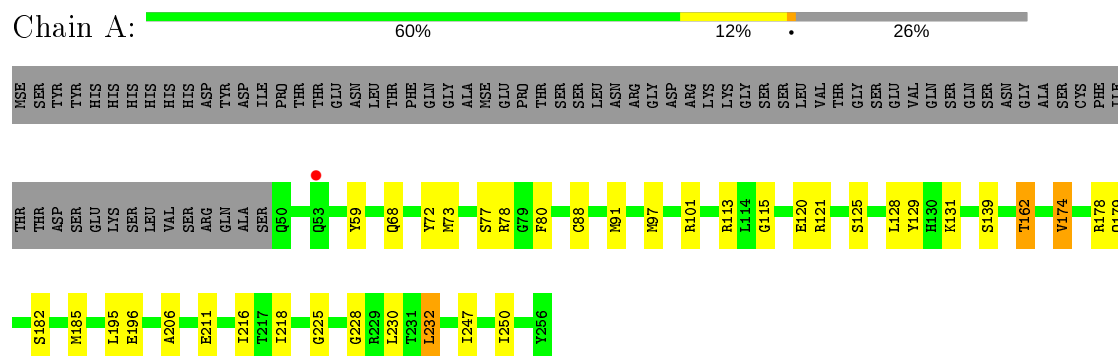
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	148	Total	O	0	0
			148	148		
2	B	128	Total	O	0	0
			128	128		
2	C	98	Total	O	0	0
			98	98		
2	D	126	Total	O	0	0
			126	126		
2	E	75	Total	O	0	0
			75	75		
2	F	107	Total	O	0	0
			107	107		

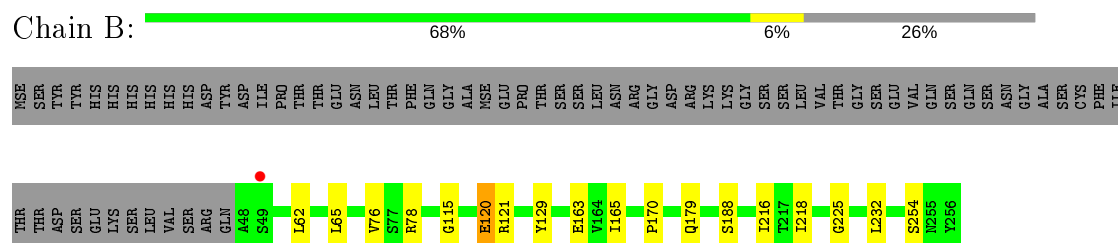
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

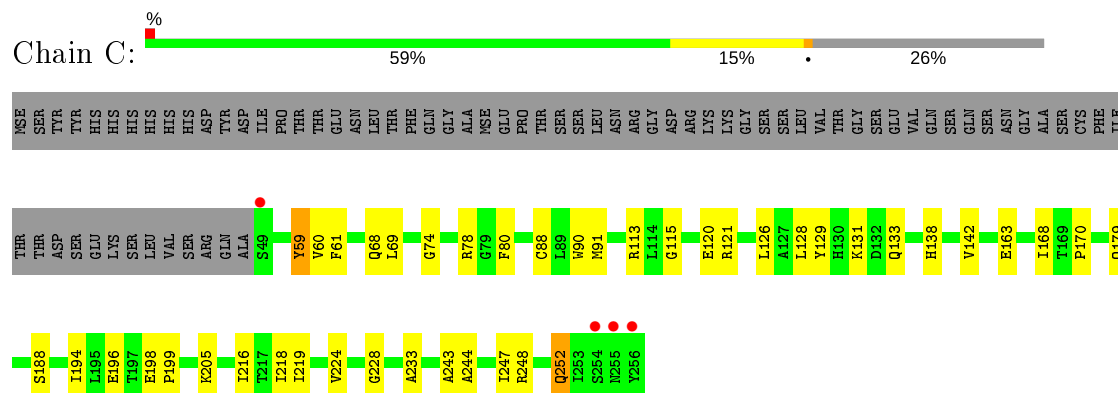
• Molecule 1: CsoS1D



• Molecule 1: CsoS1D

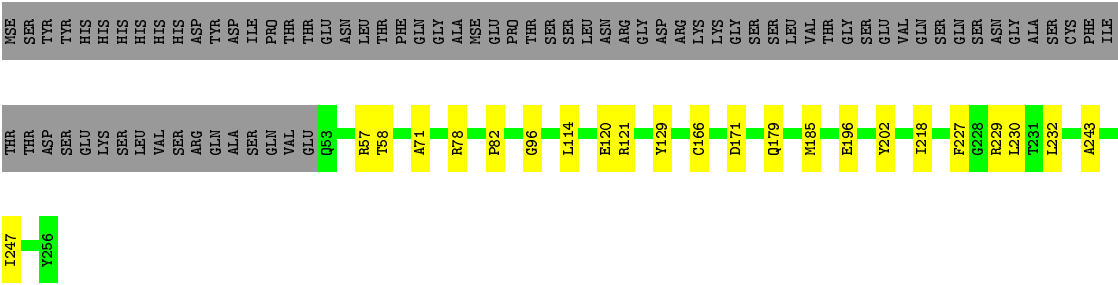


• Molecule 1: CsoS1D

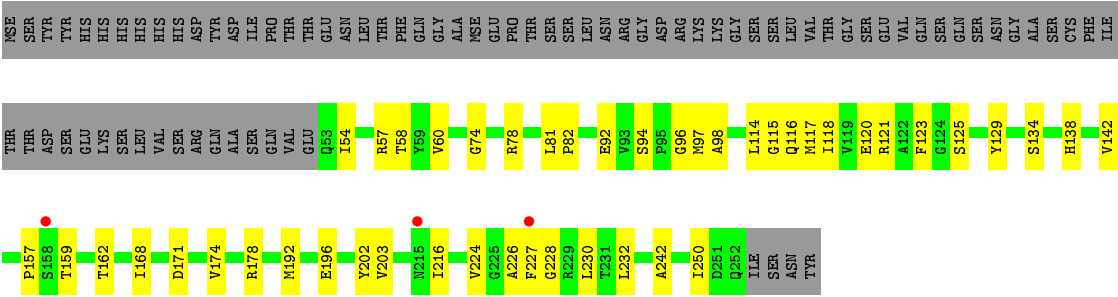


• Molecule 1: CsoS1D

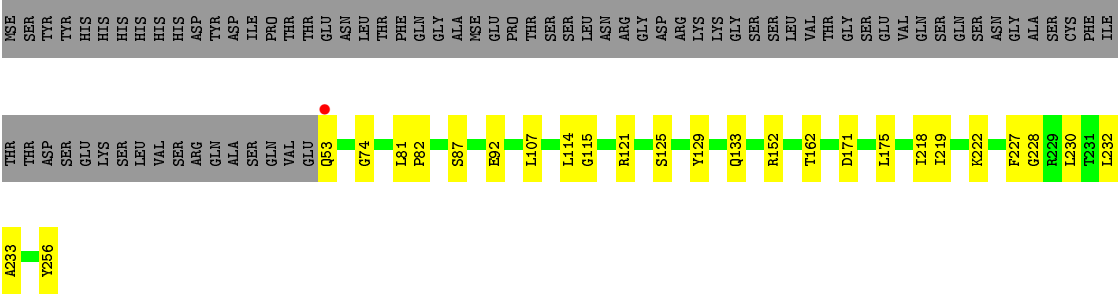




• Molecule 1: CsoS1D



• Molecule 1: CsoS1D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	122.41Å 131.29Å 131.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.50 – 2.30 46.50 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.9 (46.50-2.30) 98.9 (46.50-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.73 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.188 , 0.217 0.180 , 0.209	Depositor DCC
R_{free} test set	4678 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.006 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9951	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.89% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.48	0/1585	0.69	2/2136 (0.1%)
1	B	0.43	0/1580	0.58	0/2132
1	C	0.42	0/1577	0.58	0/2127
1	D	0.47	0/1553	0.62	0/2093
1	E	0.43	0/1518	0.57	0/2045
1	F	0.45	0/1557	0.63	0/2098
All	All	0.45	0/9370	0.61	2/12631 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	113	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	A	174	VAL	CB-CA-C	-5.35	101.23	111.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1568	0	1584	40	0
1	B	1563	0	1567	21	0
1	C	1560	0	1568	37	0
1	D	1536	0	1551	32	0
1	E	1502	0	1520	51	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1540	0	1557	29	0
2	A	148	0	0	2	0
2	B	128	0	0	3	0
2	C	98	0	0	2	0
2	D	126	0	0	3	0
2	E	75	0	0	0	0
2	F	107	0	0	0	0
All	All	9951	0	9347	171	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (171) 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:D:229:ARG:HE	1:E:97:MSE:HE1	1.14	1.06
1:C:60:VAL:HG21	1:C:205:LYS:HB2	1.47	0.95
1:D:229:ARG:NE	1:E:97:MSE:HE1	1.82	0.94
1:E:216:ILE:HD12	1:E:232:LEU:HD22	1.53	0.89
1:A:72:TYR:HA	1:D:185:MSE:HE1	1.56	0.86
1:A:185:MSE:HE1	1:D:71:ALA:C	1.97	0.85
1:A:185:MSE:HE1	1:D:71:ALA:O	1.77	0.84
1:B:120:GLU:HG2	1:B:121:ARG:H	1.46	0.80
1:C:60:VAL:CG2	1:C:205:LYS:HB2	2.15	0.77
1:E:227:PHE:HE2	1:F:121:ARG:NE	1.82	0.76
1:A:179:GLN:OE1	1:B:78:ARG:HG3	1.87	0.75
1:F:53:GLN:OE1	1:F:53:GLN:HA	1.86	0.75
1:A:120:GLU:HG2	1:A:121:ARG:H	1.51	0.74
1:C:61:PHE:HZ	1:C:133:GLN:HG3	1.52	0.73
1:F:230:LEU:HD11	1:F:232:LEU:HD21	1.73	0.70
1:D:179:GLN:HG2	1:E:78:ARG:HE	1.58	0.68
1:B:120:GLU:HG3	2:B:274:HOH:O	1.95	0.67
1:A:115:GLY:HA3	1:A:129:TYR:CE2	2.30	0.66
1:D:78:ARG:HG2	1:D:78:ARG:HH11	1.62	0.65
1:F:218:ILE:HD13	1:F:232:LEU:HD22	1.77	0.65
1:A:73:MSE:HE2	1:A:129:TYR:OH	1.97	0.65
1:D:78:ARG:HG2	1:D:78:ARG:NH1	2.12	0.64
1:F:121:ARG:HD2	1:F:121:ARG:O	1.98	0.64
1:D:196:GLU:CD	1:E:97:MSE:HE3	2.19	0.64
1:E:227:PHE:CE2	1:F:121:ARG:CD	2.81	0.63
1:E:174:VAL:HG13	1:E:178:ARG:HD2	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:THR:HB	1:E:92:GLU:HB3	1.80	0.63
1:C:243:ALA:O	1:C:247:ILE:HG12	2.00	0.62
1:A:68:GLN:HB3	1:A:218:ILE:HD12	1.81	0.62
1:B:218:ILE:HD13	1:B:232:LEU:HD22	1.82	0.62
1:B:120:GLU:OE2	1:C:121:ARG:NH1	2.30	0.61
1:E:227:PHE:CE2	1:F:121:ARG:HG2	2.36	0.61
1:D:166:CYS:SG	2:D:304:HOH:O	2.56	0.61
1:E:227:PHE:CE2	1:F:121:ARG:NE	2.68	0.60
1:E:227:PHE:HE2	1:F:121:ARG:CD	2.13	0.60
1:E:216:ILE:CD1	1:E:232:LEU:HD22	2.31	0.60
1:D:230:LEU:HD11	1:D:232:LEU:HD21	1.84	0.59
1:A:80:PHE:CE1	1:E:81:LEU:HB2	2.37	0.59
1:B:120:GLU:HG2	1:B:121:ARG:N	2.16	0.59
1:D:196:GLU:OE2	1:E:97:MSE:HE3	2.03	0.58
1:A:179:GLN:HB2	2:A:282:HOH:O	2.03	0.58
1:A:162:THR:HG21	1:A:247:ILE:HD11	1.85	0.58
1:C:248:ARG:O	1:C:252:GLN:HG3	2.03	0.58
1:D:229:ARG:HE	1:E:97:MSE:CE	2.01	0.58
1:F:219:ILE:HD11	1:F:233:ALA:HB3	1.86	0.57
1:A:120:GLU:OE2	1:A:225:GLY:HA2	2.02	0.57
1:B:218:ILE:HD13	1:B:232:LEU:CD2	2.35	0.57
1:D:57:ARG:NH1	2:D:262:HOH:O	2.37	0.57
1:D:227:PHE:CZ	1:E:121:ARG:HG2	2.40	0.57
1:F:219:ILE:HD11	1:F:233:ALA:CB	2.35	0.57
1:E:226:ALA:C	1:E:227:PHE:HD1	2.08	0.56
1:E:54:ILE:HG12	1:E:98:ALA:HB1	1.88	0.55
1:F:53:GLN:OE1	1:F:53:GLN:CA	2.54	0.55
1:E:57:ARG:HD2	1:E:123:PHE:CE1	2.41	0.55
1:E:82:PRO:HG3	1:E:129:TYR:CZ	2.42	0.54
1:B:120:GLU:CG	1:B:121:ARG:H	2.18	0.54
1:B:115:GLY:HA3	1:B:129:TYR:CE2	2.43	0.54
1:D:82:PRO:HG3	1:D:129:TYR:CZ	2.43	0.54
1:E:174:VAL:CG1	1:E:178:ARG:HD2	2.39	0.53
1:C:60:VAL:HG12	1:C:90:TRP:HB3	1.89	0.53
1:A:72:TYR:HA	1:D:185:MSE:CE	2.32	0.53
1:A:162:THR:HG23	1:A:195:LEU:CD1	2.38	0.53
1:D:120:GLU:HG2	2:D:284:HOH:O	2.09	0.53
1:F:74:GLY:HA2	1:F:82:PRO:HD2	1.91	0.53
1:E:96:GLY:HA3	1:E:120:GLU:O	2.09	0.52
1:C:131:LYS:HG2	2:C:277:HOH:O	2.09	0.52
1:E:159:THR:HG22	1:E:250:ILE:HG21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:92:GLU:HG2	1:F:125:SER:OG	2.10	0.52
1:A:182:SER:O	1:D:185:MSE:HE3	2.10	0.52
1:C:68:GLN:HB3	1:C:218:ILE:HD12	1.92	0.52
1:D:196:GLU:OE2	1:E:97:MSE:CE	2.58	0.52
1:E:196:GLU:HA	1:E:228:GLY:O	2.10	0.52
1:E:57:ARG:HD3	1:E:92:GLU:CD	2.30	0.52
1:F:121:ARG:HD2	1:F:121:ARG:C	2.30	0.52
1:A:120:GLU:CG	1:A:121:ARG:H	2.20	0.51
1:B:120:GLU:OE2	1:B:225:GLY:HA2	2.09	0.51
1:D:243:ALA:O	1:D:247:ILE:HG12	2.10	0.51
1:B:120:GLU:CG	1:B:121:ARG:N	2.74	0.51
1:A:120:GLU:HG2	1:A:121:ARG:N	2.23	0.51
1:E:227:PHE:CE2	1:F:121:ARG:CG	2.95	0.50
1:C:60:VAL:CG1	1:C:90:TRP:HB3	2.42	0.50
1:F:152:ARG:NH1	1:F:256:TYR:C	2.65	0.49
1:E:118:ILE:HD13	1:E:224:VAL:CG1	2.42	0.49
1:D:121:ARG:HG2	1:F:227:PHE:CZ	2.48	0.49
1:E:159:THR:CG2	1:E:250:ILE:HG21	2.43	0.48
1:C:244:ALA:O	1:C:248:ARG:HG3	2.13	0.48
1:A:230:LEU:HD11	1:A:232:LEU:HD13	1.96	0.48
1:C:198:GLU:HA	1:C:199:PRO:C	2.33	0.48
1:B:163:GLU:CD	1:B:165:ILE:HD11	2.34	0.48
1:A:196:GLU:HA	1:A:228:GLY:O	2.13	0.48
1:F:82:PRO:HG3	1:F:129:TYR:CZ	2.48	0.48
1:A:97:MSE:CE	1:C:194:ILE:HD12	2.43	0.48
1:C:61:PHE:CZ	1:C:133:GLN:HG3	2.40	0.48
1:E:57:ARG:HD2	1:E:123:PHE:CD1	2.49	0.48
1:C:115:GLY:HA3	1:C:129:TYR:CE2	2.48	0.47
1:C:74:GLY:O	1:E:178:ARG:NH1	2.48	0.47
1:F:87:SER:OG	1:F:133:GLN:HG2	2.14	0.47
1:B:163:GLU:HG3	1:B:165:ILE:HD12	1.97	0.47
1:F:53:GLN:N	1:F:53:GLN:CD	2.64	0.47
1:B:62:LEU:HD23	1:B:65:LEU:CD2	2.45	0.47
1:C:59:TYR:C	1:C:59:TYR:CD2	2.88	0.47
1:A:179:GLN:OE1	1:B:78:ARG:CG	2.60	0.47
1:C:120:GLU:HG3	1:C:224:VAL:HG12	1.97	0.47
1:D:96:GLY:HA3	1:D:120:GLU:O	2.15	0.47
1:F:115:GLY:HA3	1:F:129:TYR:CE2	2.50	0.47
1:A:78:ARG:HG3	1:C:179:GLN:NE2	2.30	0.46
1:A:97:MSE:SE	1:C:194:ILE:HG23	2.66	0.46
1:E:171:ASP:HB3	1:F:114:LEU:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:168:ILE:HD11	1:E:192:MSE:HE2	1.97	0.46
1:C:216:ILE:HD12	1:C:216:ILE:C	2.36	0.46
1:F:222:LYS:O	1:F:228:GLY:HA2	2.15	0.46
1:D:218:ILE:CD1	1:D:232:LEU:HD22	2.46	0.46
1:D:218:ILE:HD13	1:D:232:LEU:HD22	1.96	0.46
1:C:138:HIS:O	1:C:142:VAL:HG23	2.16	0.46
1:C:196:GLU:HA	1:C:228:GLY:O	2.16	0.46
1:E:138:HIS:O	1:E:142:VAL:HG23	2.15	0.46
1:A:206:ALA:HB2	1:A:250:ILE:CD1	2.46	0.45
1:A:68:GLN:HB2	1:A:211:GLU:OE2	2.16	0.45
1:A:120:GLU:CG	1:A:121:ARG:N	2.79	0.45
1:D:171:ASP:HB3	1:E:114:LEU:HB3	1.98	0.45
1:D:114:LEU:HB3	1:F:171:ASP:HB3	1.98	0.45
1:C:113:ARG:NH2	2:C:362:HOH:O	2.26	0.45
1:E:216:ILE:HD13	1:E:242:ALA:HB2	1.99	0.45
1:A:88:CYS:HA	1:A:128:LEU:O	2.17	0.45
1:B:170:PRO:HA	1:B:188:SER:HB3	1.98	0.45
1:A:131:LYS:HE2	1:A:131:LYS:HB3	1.55	0.44
1:A:185:MSE:HE2	1:D:71:ALA:HB1	1.99	0.44
1:E:157:PRO:HG3	1:E:202:TYR:CG	2.53	0.44
1:A:230:LEU:HD11	1:A:232:LEU:CD1	2.47	0.44
1:A:91:MSE:O	1:A:125:SER:HA	2.18	0.44
1:A:121:ARG:NH1	1:C:120:GLU:OE2	2.37	0.44
1:A:185:MSE:HE2	1:A:185:MSE:HB3	1.73	0.44
1:D:229:ARG:CD	1:E:97:MSE:HE1	2.47	0.43
1:B:179:GLN:CB	1:C:78:ARG:NH1	2.81	0.43
1:F:162:THR:O	1:F:162:THR:HG23	2.18	0.43
1:A:101:ARG:HH21	1:C:163:GLU:HG3	1.84	0.43
1:D:82:PRO:HG3	1:D:129:TYR:CE2	2.53	0.43
1:E:115:GLY:HA3	1:E:129:TYR:CE2	2.54	0.43
2:B:830:HOH:O	1:C:78:ARG:HG2	2.18	0.43
1:D:78:ARG:CG	1:D:78:ARG:HH11	2.29	0.43
1:A:178:ARG:O	1:B:78:ARG:NH2	2.52	0.43
1:B:120:GLU:HG2	2:B:276:HOH:O	2.18	0.43
1:E:117:MSE:HA	1:E:125:SER:O	2.18	0.42
1:E:216:ILE:HD13	1:E:242:ALA:CB	2.49	0.42
1:F:107:LEU:HD21	1:F:114:LEU:HB2	2.02	0.42
1:C:170:PRO:HA	1:C:188:SER:HB3	2.02	0.42
1:C:219:ILE:HD11	1:C:233:ALA:CB	2.50	0.42
1:C:88:CYS:HA	1:C:128:LEU:O	2.19	0.42
1:F:121:ARG:CD	1:F:121:ARG:C	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:SER:HB2	2:A:315:HOH:O	2.19	0.42
1:E:162:THR:O	1:E:162:THR:HG23	2.20	0.42
1:E:115:GLY:O	1:E:116:GLN:HG3	2.20	0.41
1:C:80:PHE:CE1	1:F:81:LEU:HB2	2.55	0.41
1:C:91:MSE:HE3	1:C:126:LEU:HD21	2.02	0.41
1:A:162:THR:HG23	1:A:195:LEU:HD12	2.03	0.41
1:C:248:ARG:O	1:C:252:GLN:CG	2.67	0.41
1:C:69:LEU:HA	1:C:69:LEU:HD12	1.87	0.41
1:E:94:SER:HB3	1:E:123:PHE:CD1	2.56	0.41
1:A:97:MSE:HE2	1:C:194:ILE:HD12	2.00	0.41
1:B:216:ILE:HD12	1:B:216:ILE:C	2.40	0.41
1:E:203:VAL:CG2	1:E:230:LEU:HB2	2.51	0.41
1:E:74:GLY:HA2	1:E:82:PRO:HD2	2.02	0.41
1:E:60:VAL:HG22	1:E:202:TYR:CD1	2.56	0.41
1:E:203:VAL:HG22	1:E:230:LEU:HB2	2.02	0.41
1:C:168:ILE:HA	1:C:168:ILE:HD13	1.75	0.41
1:D:58:THR:HG23	1:D:202:TYR:CZ	2.56	0.41
1:E:118:ILE:HD13	1:E:224:VAL:HG13	2.02	0.41
1:A:216:ILE:HD12	1:A:216:ILE:C	2.40	0.40
1:E:157:PRO:HB2	1:E:250:ILE:HG23	2.02	0.40
1:B:62:LEU:HD23	1:B:65:LEU:HD21	2.02	0.40
1:A:59:TYR:CD2	1:A:59:TYR:C	2.95	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	205/281 (73%)	202 (98%)	3 (2%)	0	100	100
1	B	207/281 (74%)	202 (98%)	5 (2%)	0	100	100
1	C	206/281 (73%)	201 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	202/281 (72%)	199 (98%)	3 (2%)	0	100	100
1	E	198/281 (70%)	194 (98%)	4 (2%)	0	100	100
1	F	202/281 (72%)	200 (99%)	2 (1%)	0	100	100
All	All	1220/1686 (72%)	1198 (98%)	22 (2%)	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	168/225 (75%)	164 (98%)	4 (2%)	49	66
1	B	165/225 (73%)	162 (98%)	3 (2%)	59	75
1	C	166/225 (74%)	164 (99%)	2 (1%)	71	84
1	D	163/225 (72%)	163 (100%)	0	100	100
1	E	159/225 (71%)	158 (99%)	1 (1%)	86	94
1	F	164/225 (73%)	163 (99%)	1 (1%)	86	94
All	All	985/1350 (73%)	974 (99%)	11 (1%)	73	86

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	SER
1	A	162	THR
1	A	174	VAL
1	A	232	LEU
1	B	76	VAL
1	B	120	GLU
1	B	254	SER
1	C	59	TYR
1	C	252	GLN
1	E	134	SER

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Mol	Chain	Res	Type
1	F	175	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	200/281 (71%)	-0.49	1 (0%) 91 94	18, 25, 37, 59	0
1	B	202/281 (71%)	-0.47	1 (0%) 91 94	19, 28, 41, 47	0
1	C	201/281 (71%)	-0.30	4 (1%) 65 71	23, 32, 49, 64	0
1	D	197/281 (70%)	-0.62	0 100 100	18, 26, 38, 42	0
1	E	193/281 (68%)	-0.35	3 (1%) 72 77	24, 34, 47, 59	0
1	F	197/281 (70%)	-0.56	1 (0%) 91 94	23, 28, 40, 50	0
All	All	1190/1686 (70%)	-0.46	10 (0%) 86 89	18, 28, 43, 64	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	255	ASN	4.3
1	C	256	TYR	3.1
1	E	215	ASN	2.4
1	F	53	GLN	2.4
1	C	49	SER	2.4
1	E	158	SER	2.3
1	C	254	SER	2.2
1	E	227	PHE	2.1
1	B	49	SER	2.0
1	A	53	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.