



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:47 PM GMT

PDB ID : 4MLB
Title : Reverse polarity of binding pocket suggests different function of a MOP superfamily transporter from *Pyrococcus furiosus* Vc1 (DSM3638)
Authors : Malviya, V.N.; Nonaka, T.; Muenke, C.; Koepke, J.; Michel, H.
Deposited on : 2013-09-06
Resolution : 2.35 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

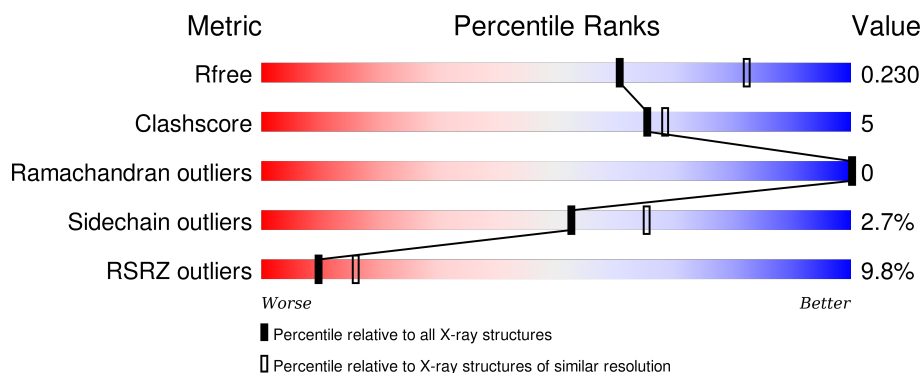
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1406 (2.36-2.32)
Clashscore	102246	1509 (2.36-2.32)
Ramachandran outliers	100387	1490 (2.36-2.32)
Sidechain outliers	100360	1491 (2.36-2.32)
RSRZ outliers	91569	1412 (2.36-2.32)

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

Mol	Chain	Length	Quality of chain
1	A	492	<div> <div>9%</div> <div>82%</div> <div>9%</div> <div>8%</div> </div>
1	B	492	<div> <div>6%</div> <div>84%</div> <div>8%</div> <div>8%</div> </div>
1	C	492	<div> <div>9%</div> <div>81%</div> <div>9%</div> <div>8%</div> </div>
1	D	492	<div> <div>11%</div> <div>81%</div> <div>11%</div> <div>8%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CXE	A	502	-	-	-	X
2	CXE	A	503	-	-	-	X
2	CXE	A	505	-	-	-	X
2	CXE	A	506	-	-	-	X
2	CXE	A	509	-	-	-	X
2	CXE	A	510	-	-	-	X
2	CXE	A	511	-	-	-	X
2	CXE	A	512	-	-	-	X
2	CXE	A	513	-	-	-	X
2	CXE	A	514	-	-	-	X
2	CXE	B	502	-	-	-	X
2	CXE	B	504	-	-	-	X
2	CXE	B	505	-	-	-	X
2	CXE	B	506	-	-	-	X
2	CXE	B	507	-	-	-	X
2	CXE	B	509	-	-	-	X
2	CXE	B	512	-	-	-	X
2	CXE	C	501	-	-	-	X
2	CXE	C	502	-	-	-	X
2	CXE	C	503	-	-	-	X
2	CXE	C	504	-	-	-	X
2	CXE	C	505	-	-	-	X
2	CXE	C	506	-	-	-	X
2	CXE	C	507	-	-	-	X
2	CXE	C	508	-	-	-	X
2	CXE	C	510	-	-	-	X
2	CXE	C	511	-	-	-	X
2	CXE	C	512	-	-	-	X
2	CXE	C	514	-	-	-	X
2	CXE	D	507	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14749 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 PF0708.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	0	1	0
			3412	2237	557	597	21			
1	B	454	Total	C	N	O	S	0	0	0
			3413	2237	555	600	21			
1	C	452	Total	C	N	O	S	0	2	0
			3418	2241	559	597	21			
1	D	452	Total	C	N	O	S	0	2	0
			3418	2241	559	597	21			

There are 128 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	EXPRESSION TAG	UNP Q8U2X0
A	-5	GLY	-	EXPRESSION TAG	UNP Q8U2X0
A	-4	GLY	-	EXPRESSION TAG	UNP Q8U2X0
A	-3	SER	-	EXPRESSION TAG	UNP Q8U2X0
A	-2	GLU	-	EXPRESSION TAG	UNP Q8U2X0
A	-1	ILE	-	EXPRESSION TAG	UNP Q8U2X0
A	0	PRO	-	EXPRESSION TAG	UNP Q8U2X0
A	298	THR	ALA	CONFLICT	UNP Q8U2X0
A	462	ARG	-	EXPRESSION TAG	UNP Q8U2X0
A	463	ASN	-	EXPRESSION TAG	UNP Q8U2X0
A	464	SER	-	EXPRESSION TAG	UNP Q8U2X0
A	465	GLU	-	EXPRESSION TAG	UNP Q8U2X0
A	466	ASN	-	EXPRESSION TAG	UNP Q8U2X0
A	467	LEU	-	EXPRESSION TAG	UNP Q8U2X0
A	468	TYR	-	EXPRESSION TAG	UNP Q8U2X0
A	469	PHE	-	EXPRESSION TAG	UNP Q8U2X0
A	470	GLN	-	EXPRESSION TAG	UNP Q8U2X0
A	471	GLY	-	EXPRESSION TAG	UNP Q8U2X0
A	472	GLY	-	EXPRESSION TAG	UNP Q8U2X0
A	473	ARG	-	EXPRESSION TAG	UNP Q8U2X0
A	474	GLY	-	EXPRESSION TAG	UNP Q8U2X0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	475	SER	-	EXPRESSION TAG	UNP Q8U2X0
A	476	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	477	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	478	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	479	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	480	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	481	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	482	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	483	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	484	HIS	-	EXPRESSION TAG	UNP Q8U2X0
A	485	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	-6	MET	-	EXPRESSION TAG	UNP Q8U2X0
B	-5	GLY	-	EXPRESSION TAG	UNP Q8U2X0
B	-4	GLY	-	EXPRESSION TAG	UNP Q8U2X0
B	-3	SER	-	EXPRESSION TAG	UNP Q8U2X0
B	-2	GLU	-	EXPRESSION TAG	UNP Q8U2X0
B	-1	ILE	-	EXPRESSION TAG	UNP Q8U2X0
B	0	PRO	-	EXPRESSION TAG	UNP Q8U2X0
B	298	THR	ALA	CONFLICT	UNP Q8U2X0
B	462	ARG	-	EXPRESSION TAG	UNP Q8U2X0
B	463	ASN	-	EXPRESSION TAG	UNP Q8U2X0
B	464	SER	-	EXPRESSION TAG	UNP Q8U2X0
B	465	GLU	-	EXPRESSION TAG	UNP Q8U2X0
B	466	ASN	-	EXPRESSION TAG	UNP Q8U2X0
B	467	LEU	-	EXPRESSION TAG	UNP Q8U2X0
B	468	TYR	-	EXPRESSION TAG	UNP Q8U2X0
B	469	PHE	-	EXPRESSION TAG	UNP Q8U2X0
B	470	GLN	-	EXPRESSION TAG	UNP Q8U2X0
B	471	GLY	-	EXPRESSION TAG	UNP Q8U2X0
B	472	GLY	-	EXPRESSION TAG	UNP Q8U2X0
B	473	ARG	-	EXPRESSION TAG	UNP Q8U2X0
B	474	GLY	-	EXPRESSION TAG	UNP Q8U2X0
B	475	SER	-	EXPRESSION TAG	UNP Q8U2X0
B	476	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	477	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	478	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	479	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	480	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	481	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	482	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	483	HIS	-	EXPRESSION TAG	UNP Q8U2X0
B	484	HIS	-	EXPRESSION TAG	UNP Q8U2X0

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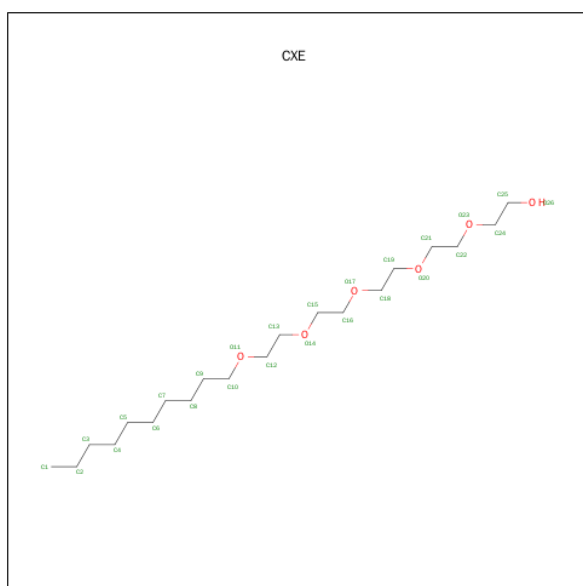
Chain	Residue	Modelled	Actual	Comment	Reference
B	485	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	-6	MET	-	EXPRESSION TAG	UNP Q8U2X0
C	-5	GLY	-	EXPRESSION TAG	UNP Q8U2X0
C	-4	GLY	-	EXPRESSION TAG	UNP Q8U2X0
C	-3	SER	-	EXPRESSION TAG	UNP Q8U2X0
C	-2	GLU	-	EXPRESSION TAG	UNP Q8U2X0
C	-1	ILE	-	EXPRESSION TAG	UNP Q8U2X0
C	0	PRO	-	EXPRESSION TAG	UNP Q8U2X0
C	298	THR	ALA	CONFLICT	UNP Q8U2X0
C	462	ARG	-	EXPRESSION TAG	UNP Q8U2X0
C	463	ASN	-	EXPRESSION TAG	UNP Q8U2X0
C	464	SER	-	EXPRESSION TAG	UNP Q8U2X0
C	465	GLU	-	EXPRESSION TAG	UNP Q8U2X0
C	466	ASN	-	EXPRESSION TAG	UNP Q8U2X0
C	467	LEU	-	EXPRESSION TAG	UNP Q8U2X0
C	468	TYR	-	EXPRESSION TAG	UNP Q8U2X0
C	469	PHE	-	EXPRESSION TAG	UNP Q8U2X0
C	470	GLN	-	EXPRESSION TAG	UNP Q8U2X0
C	471	GLY	-	EXPRESSION TAG	UNP Q8U2X0
C	472	GLY	-	EXPRESSION TAG	UNP Q8U2X0
C	473	ARG	-	EXPRESSION TAG	UNP Q8U2X0
C	474	GLY	-	EXPRESSION TAG	UNP Q8U2X0
C	475	SER	-	EXPRESSION TAG	UNP Q8U2X0
C	476	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	477	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	478	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	479	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	480	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	481	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	482	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	483	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	484	HIS	-	EXPRESSION TAG	UNP Q8U2X0
C	485	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	-6	MET	-	EXPRESSION TAG	UNP Q8U2X0
D	-5	GLY	-	EXPRESSION TAG	UNP Q8U2X0
D	-4	GLY	-	EXPRESSION TAG	UNP Q8U2X0
D	-3	SER	-	EXPRESSION TAG	UNP Q8U2X0
D	-2	GLU	-	EXPRESSION TAG	UNP Q8U2X0
D	-1	ILE	-	EXPRESSION TAG	UNP Q8U2X0
D	0	PRO	-	EXPRESSION TAG	UNP Q8U2X0
D	298	THR	ALA	CONFLICT	UNP Q8U2X0
D	462	ARG	-	EXPRESSION TAG	UNP Q8U2X0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	463	ASN	-	EXPRESSION TAG	UNP Q8U2X0
D	464	SER	-	EXPRESSION TAG	UNP Q8U2X0
D	465	GLU	-	EXPRESSION TAG	UNP Q8U2X0
D	466	ASN	-	EXPRESSION TAG	UNP Q8U2X0
D	467	LEU	-	EXPRESSION TAG	UNP Q8U2X0
D	468	TYR	-	EXPRESSION TAG	UNP Q8U2X0
D	469	PHE	-	EXPRESSION TAG	UNP Q8U2X0
D	470	GLN	-	EXPRESSION TAG	UNP Q8U2X0
D	471	GLY	-	EXPRESSION TAG	UNP Q8U2X0
D	472	GLY	-	EXPRESSION TAG	UNP Q8U2X0
D	473	ARG	-	EXPRESSION TAG	UNP Q8U2X0
D	474	GLY	-	EXPRESSION TAG	UNP Q8U2X0
D	475	SER	-	EXPRESSION TAG	UNP Q8U2X0
D	476	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	477	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	478	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	479	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	480	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	481	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	482	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	483	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	484	HIS	-	EXPRESSION TAG	UNP Q8U2X0
D	485	HIS	-	EXPRESSION TAG	UNP Q8U2X0

- Molecule 2 is PENTAETHYLENE GLYCOL MONODECYL ETHER (three-letter code: CXE) (formula: $C_{20}H_{42}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 26 20 6	0	0
2	A	1	Total C O 26 20 6	0	0
2	A	1	Total C O 26 20 6	0	0
2	A	1	Total C O 20 16 4	0	0
2	A	1	Total C 10 10	0	0
2	A	1	Total C O 20 16 4	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C O 14 12 2	0	0
2	A	1	Total C O 23 18 5	0	0
2	A	1	Total C 10 10	0	0
2	A	1	Total C 10 10	0	0
2	A	1	Total C 6 6	0	0
2	A	1	Total C O 20 16 4	0	0
2	A	1	Total C 9 9	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 7 7	0	0
2	A	1	Total C 5 5	0	0
2	B	1	Total C O 26 20 6	0	0
2	B	1	Total C O 20 16 4	0	0
2	B	1	Total C O 17 14 3	0	0
2	B	1	Total C O 11 10 1	0	0
2	B	1	Total C 10 10	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 17 14 3	0	0
2	B	1	Total C 9 9	0	0
2	B	1	Total C 7 7	0	0
2	B	1	Total C 6 6	0	0
2	B	1	Total C 6 6	0	0
2	B	1	Total C 6 6	0	0
2	B	1	Total C 9 9	0	0
2	C	1	Total C O 26 20 6	0	0
2	C	1	Total C O 26 20 6	0	0
2	C	1	Total C O 26 20 6	0	0
2	C	1	Total C O 26 20 6	0	0
2	C	1	Total C O 20 16 4	0	0
2	C	1	Total C O 15 13 2	0	0
2	C	1	Total C 10 10	0	0
2	C	1	Total C 7 7	0	0
2	C	1	Total C O 17 14 3	0	0
2	C	1	Total C O 23 18 5	0	0
2	C	1	Total C 10 10	0	0
2	C	1	Total C O 16 10 6	0	0
2	C	1	Total C O 23 18 5	0	0
2	C	1	Total C O 17 14 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total C 4 4	0	0
2	C	1	Total C 7 7	0	0
2	D	1	Total C O 11 10 1	0	0
2	D	1	Total C O 20 16 4	0	0
2	D	1	Total C O 14 12 2	0	0
2	D	1	Total C 10 10	0	0
2	D	1	Total C O 14 12 2	0	0
2	D	1	Total C O 11 10 1	0	0
2	D	1	Total C O 11 10 1	0	0
2	D	1	Total C 5 5	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Cl 2 2	0	0

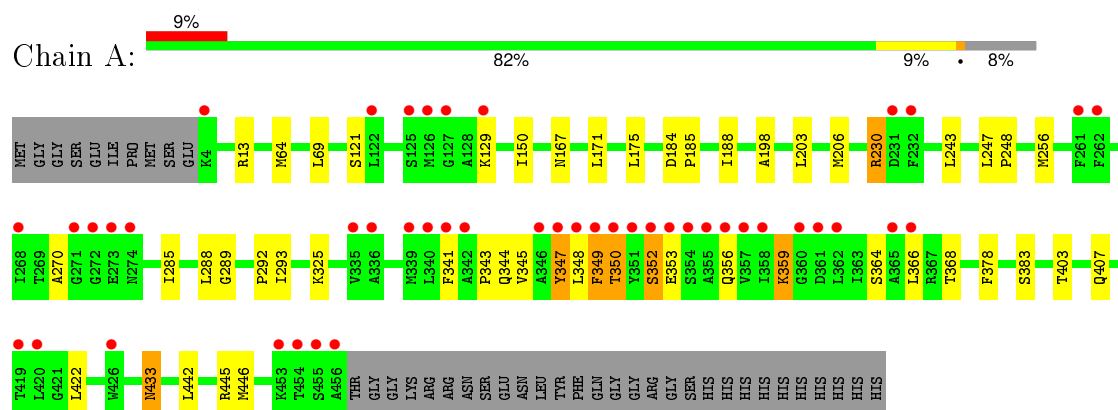
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	111	Total O 111 111	0	0
4	B	74	Total O 74 74	0	0
4	C	112	Total O 112 112	0	0
4	D	30	Total O 30 30	0	0

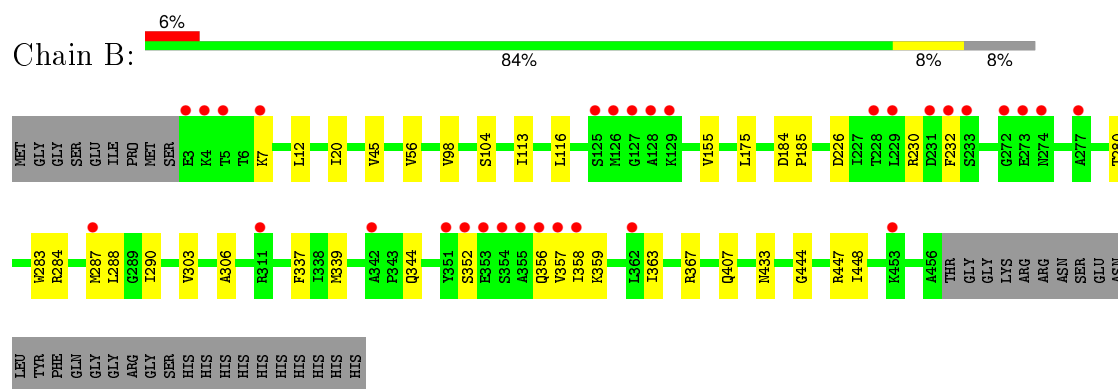
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

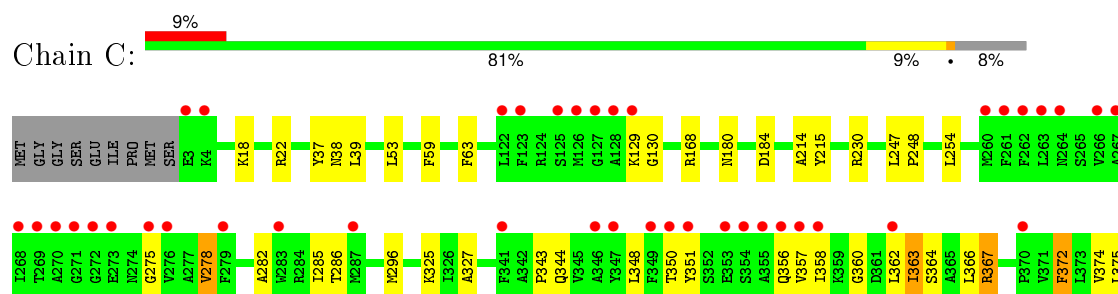
• Molecule 1: PF0708



• Molecule 1: PF0708

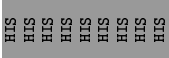
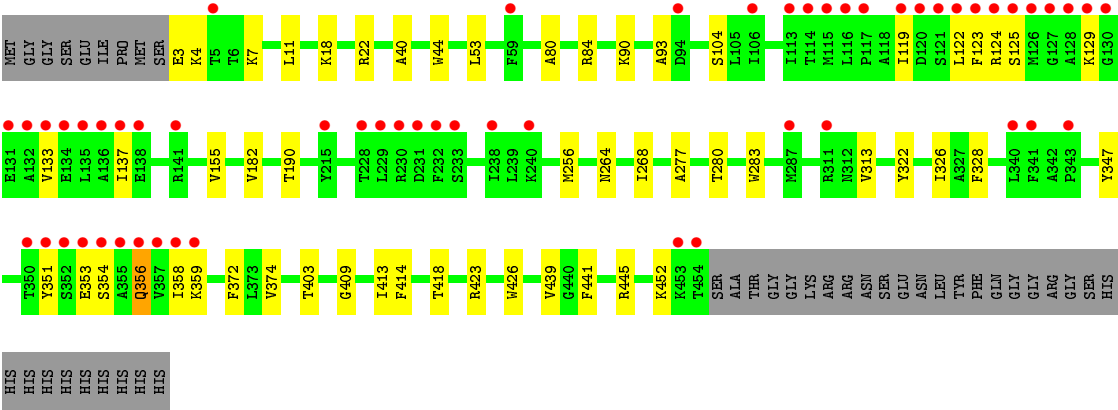
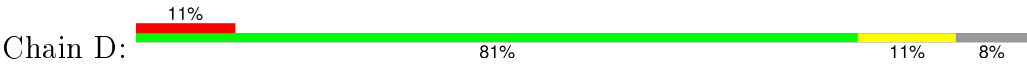


• Molecule 1: PF0708





● Molecule 1: PF0708



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	219.56 Å 94.55 Å 138.82 Å 90.00° 126.47° 90.00°	Depositor
Resolution (Å)	45.24 – 2.35 45.24 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.24-2.35) 99.7 (45.24-2.35)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.34 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.203 , 0.231 0.202 , 0.230	Depositor DCC
R_{free} test set	4737 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	38.1	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 68.5	EDS
Estimated twinning fraction	0.015 for -h-2*k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 95102 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14749	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.25	0/3476	0.43	0/4714
1	B	0.23	0/3474	0.40	0/4712
1	C	0.25	0/3485	0.43	0/4725
1	D	0.24	0/3485	0.43	0/4725
All	All	0.24	0/13920	0.42	0/18876

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 [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	3412	0	3601	33	0
1	B	3413	0	3594	26	0
1	C	3418	0	3610	40	0
1	D	3418	0	3610	33	0
2	A	246	0	420	21	0
2	B	144	0	253	11	0
2	C	273	0	450	23	0
2	D	96	0	174	8	0
3	A	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	111	0	0	4	0
4	B	74	0	0	1	0
4	C	112	0	0	0	0
4	D	30	0	0	1	0
All	All	14749	0	15712	152	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 5.

All (152) 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:B:344:GLN:HG2	2:B:506:CXE:H091	1.59	0.82
1:C:445:ARG:HG2	1:C:445:ARG:HH11	1.51	0.76
1:A:349:PHE:H	1:A:349:PHE:HD2	1.37	0.72
2:B:501:CXE:H222	1:C:39:LEU:HD11	1.72	0.72
2:A:501:CXE:H062	2:A:515:CXE:H022	1.74	0.70
1:D:356:GLN:HE22	1:D:359:LYS:HD2	1.57	0.67
1:A:407:GLN:OE1	1:A:433:ASN:ND2	2.27	0.67
1:C:278:VAL:HG11	1:C:422:LEU:HD11	1.77	0.66
1:A:325:LYS:NZ	4:A:706:HOH:O	2.29	0.66
1:A:353:GLU:HB3	1:A:356:GLN:HE21	1.61	0.66
1:A:175:LEU:HB2	2:A:506:CXE:H052	1.79	0.65
1:B:337:PHE:HZ	2:B:506:CXE:H032	1.62	0.64
1:C:348:LEU:HD11	2:C:513:CXE:H013	1.78	0.64
1:A:171:LEU:HD13	2:A:506:CXE:H091	1.80	0.63
2:A:503:CXE:H062	2:A:509:CXE:H032	1.82	0.61
1:C:445:ARG:NH1	1:C:445:ARG:HG2	2.15	0.61
1:D:414:PHE:O	1:D:418:THR:OG1	2.17	0.61
1:D:84:ARG:NH1	4:D:609:HOH:O	2.34	0.61
1:B:230:ARG:NH2	4:B:647:HOH:O	2.33	0.60
1:C:372:PHE:HA	1:C:375:LEU:HD12	1.82	0.60
1:A:13:ARG:NH2	4:A:609:HOH:O	2.30	0.59
1:C:343:PRO:HB2	2:C:513:CXE:H132	1.83	0.59
2:A:502:CXE:H101	1:B:175:LEU:HB2	1.84	0.59
1:A:348:LEU:O	1:A:352:SER:HB2	2.02	0.58
2:A:516:CXE:H061	1:D:190:THR:HA	1.85	0.58
1:C:357:VAL:HG13	1:C:358:ILE:HD12	1.85	0.58
1:B:339:MET:O	1:B:367:ARG:NE	2.34	0.57
1:C:275:GLY:HA2	1:C:278:VAL:HB	1.86	0.57
1:A:445:ARG:NH1	4:A:633:HOH:O	2.24	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:503:CXE:H071	2:D:505:CXE:H072	1.87	0.56
1:C:356:GLN:O	1:C:360:GLY:N	2.33	0.56
1:B:45:VAL:HG11	1:B:56:VAL:HG21	1.87	0.56
1:C:278:VAL:HG13	1:C:362:LEU:HD21	1.88	0.56
2:B:502:CXE:H021	2:C:505:CXE:H051	1.88	0.56
2:D:504:CXE:H082	2:D:505:CXE:H081	1.89	0.55
1:D:439:VAL:HG22	2:D:502:CXE:H051	1.88	0.55
2:A:506:CXE:H101	1:B:185:PRO:HB2	1.89	0.55
2:B:502:CXE:H072	2:C:505:CXE:H131	1.89	0.53
1:C:438:ILE:HD13	1:D:40:ALA:HB2	1.90	0.53
1:A:270:ALA:HB1	1:A:422:LEU:HA	1.90	0.53
1:A:185:PRO:HB2	2:A:502:CXE:H151	1.90	0.53
1:A:343:PRO:O	1:A:347:TYR:HB2	2.09	0.52
1:C:254:LEU:HB2	2:C:511:CXE:H061	1.92	0.52
1:B:352:SER:O	1:B:356:GLN:NE2	2.42	0.52
1:A:188:ILE:HD11	1:A:198:ALA:HB2	1.91	0.51
1:A:185:PRO:HG2	2:A:502:CXE:H131	1.93	0.51
1:C:358:ILE:O	1:C:362:LEU:HG	2.11	0.51
1:A:349:PHE:N	1:A:349:PHE:CD2	2.77	0.50
1:D:44:TRP:HZ3	2:D:507:CXE:H062	1.77	0.50
1:C:215:TYR:CD1	2:C:501:CXE:H132	2.46	0.50
1:D:123:PHE:HD2	1:D:137:ILE:HD13	1.77	0.49
1:A:203:LEU:HA	1:A:206:MET:HE2	1.93	0.49
1:A:64:MET:HB3	2:A:513:CXE:H101	1.94	0.49
1:A:344:GLN:OE1	1:A:344:GLN:N	2.45	0.49
2:C:505:CXE:H121	2:C:514:CXE:H013	1.94	0.49
1:C:129:LYS:HG2	1:C:130:GLY:H	1.78	0.48
1:B:287:MET:HA	1:B:290:ILE:HG23	1.95	0.48
1:B:337:PHE:CZ	2:B:506:CXE:H032	2.46	0.48
2:A:505:CXE:H032	2:B:511:CXE:H022	1.95	0.48
1:D:133:VAL:O	1:D:137:ILE:HG12	2.14	0.48
1:B:20:ILE:HD12	1:B:303:VAL:HG21	1.95	0.48
2:A:504:CXE:H091	2:A:517:CXE:H021	1.96	0.48
2:A:506:CXE:H031	1:B:185:PRO:HG3	1.96	0.48
1:C:37:TYR:HE2	2:C:512:CXE:H181	1.78	0.47
2:C:513:CXE:H062	2:C:513:CXE:H091	1.68	0.47
1:A:230:ARG:NE	1:A:230:ARG:HA	2.28	0.47
1:D:44:TRP:CZ3	2:D:507:CXE:H062	2.49	0.47
2:B:502:CXE:H092	2:C:505:CXE:H152	1.96	0.46
1:D:277:ALA:HB3	1:D:358:ILE:HD13	1.97	0.46
1:C:296:MET:HG3	1:C:327:ALA:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:PHE:O	1:A:345:VAL:HG23	2.15	0.46
1:A:350:THR:HG21	1:A:359:LYS:N	2.29	0.46
1:B:357:VAL:HG23	1:B:358:ILE:HG23	1.96	0.46
1:C:376:THR:HG22	1:C:380:MET:HG3	1.98	0.46
1:D:104:SER:HB3	1:D:155:VAL:HG21	1.95	0.46
1:C:230:ARG:HA	2:C:502:CXE:H162	1.98	0.46
1:B:113:ILE:HD11	2:C:503:CXE:H071	1.98	0.46
3:A:518:CL:CL	4:A:652:HOH:O	2.58	0.46
1:C:325:LYS:HG2	2:C:514:CXE:H032	1.98	0.46
1:C:374:VAL:HG11	1:D:182:VAL:HG13	1.97	0.46
1:A:353:GLU:HG2	1:A:356:GLN:HG3	1.98	0.46
1:A:256:MET:HG2	1:A:403:THR:HG21	1.98	0.45
1:C:362:LEU:O	1:C:366:LEU:HG	2.16	0.45
2:C:504:CXE:H242	2:C:504:CXE:H212	1.46	0.45
1:A:350:THR:HG21	1:A:359:LYS:HB3	1.99	0.45
1:B:407:GLN:OE1	1:B:433:ASN:ND2	2.46	0.45
1:A:69:LEU:HD21	2:A:513:CXE:H021	1.98	0.45
1:C:59:PHE:CZ	1:C:63:PHE:HB2	2.52	0.45
1:C:282:ALA:HA	1:C:285:ILE:HD12	1.99	0.45
1:A:378:PHE:CE2	2:A:507:CXE:H022	2.52	0.45
1:C:445:ARG:CG	1:C:445:ARG:HH11	2.25	0.44
1:D:354:SER:HA	1:D:358:ILE:HD12	1.99	0.44
1:A:289:GLY:O	1:A:292:PRO:HD2	2.18	0.44
2:A:501:CXE:H082	2:A:515:CXE:H041	2.00	0.44
1:C:129:LYS:HE3	1:C:129:LYS:HB2	1.89	0.44
1:D:3:GLU:HA	1:D:90:LYS:HE3	1.99	0.44
1:D:7:LYS:HA	1:D:7:LYS:HD2	1.89	0.44
1:C:363:ILE:O	1:C:367:ARG:HD3	2.17	0.44
1:D:441:PHE:O	1:D:445:ARG:HG2	2.17	0.44
2:A:503:CXE:H191	2:B:506:CXE:H151	1.98	0.43
1:C:360:GLY:HA2	1:C:363:ILE:HG13	2.00	0.43
1:B:444:GLY:O	1:B:448:ILE:HG12	2.18	0.43
1:C:180:ASN:O	1:C:184:ASP:HB2	2.19	0.43
1:C:344:GLN:NE2	2:C:513:CXE:H212	2.33	0.43
1:B:116:LEU:HD12	2:C:501:CXE:H121	1.99	0.43
1:D:328:PHE:HE1	1:D:374:VAL:HG13	1.84	0.43
2:A:506:CXE:H062	2:A:506:CXE:H092	1.75	0.42
2:C:504:CXE:H121	2:D:501:CXE:H081	2.01	0.42
1:A:442:LEU:O	1:A:446:MET:HB2	2.19	0.42
1:A:150:ILE:HG12	1:A:206:MET:SD	2.60	0.42
1:B:284:ARG:O	1:B:288:LEU:HD13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:501:CXE:H062	2:A:515:CXE:C2	2.48	0.42
1:D:80:ALA:O	1:D:84:ARG:HG2	2.19	0.42
1:B:7:LYS:HB2	2:B:503:CXE:H151	2.00	0.42
1:D:313:VAL:HG11	1:D:452:LYS:HG3	2.00	0.42
1:C:278:VAL:HG22	1:C:362:LEU:HD21	2.02	0.42
1:C:214:ALA:HB1	2:C:503:CXE:H181	2.01	0.42
1:C:247:LEU:HB3	1:C:248:PRO:HD3	2.02	0.42
1:D:423:ARG:HA	1:D:426:TRP:CD1	2.54	0.42
1:A:129:LYS:HD2	1:A:129:LYS:HA	1.92	0.42
1:C:38:ASN:OD1	2:C:512:CXE:H161	2.20	0.42
1:B:280:THR:HA	1:B:283:TRP:NE1	2.35	0.41
2:C:501:CXE:H131	2:C:503:CXE:C12	2.50	0.41
1:B:280:THR:HA	1:B:283:TRP:CD1	2.55	0.41
1:D:347:TYR:CD1	2:D:501:CXE:H071	2.55	0.41
1:A:167:ASN:HD21	2:A:501:CXE:H252	1.85	0.41
1:C:415:VAL:HG12	1:C:416:HIS:ND1	2.36	0.41
1:D:409:GLY:O	1:D:413:ILE:HG12	2.19	0.41
1:B:447:ARG:HD2	1:B:447:ARG:HA	1.93	0.41
2:C:503:CXE:H162	2:C:503:CXE:H192	1.34	0.41
1:A:285:ILE:HD12	1:A:366:LEU:HD21	2.03	0.41
1:C:18:LYS:HE2	1:C:22:ARG:HG3	2.03	0.41
1:A:247:LEU:HB3	1:A:248:PRO:HD3	2.02	0.41
1:D:11:LEU:HD21	1:D:22[A]:ARG:HB2	2.02	0.41
1:B:12:LEU:HG	1:B:306:ALA:HB2	2.03	0.41
1:D:84:ARG:HB2	1:D:93:ALA:HB2	2.03	0.41
1:D:280:THR:HA	1:D:283:TRP:CD1	2.56	0.41
1:D:356:GLN:NE2	1:D:359:LYS:HD2	2.30	0.41
1:C:446:MET:SD	1:D:351:TYR:HB3	2.61	0.41
1:D:4:LYS:HD2	1:D:4:LYS:HA	1.69	0.41
1:D:256:MET:HG2	1:D:403:THR:HG21	2.02	0.41
1:D:18:LYS:HE3	1:D:18:LYS:HB2	1.81	0.41
1:C:180:ASN:HD22	2:C:512:CXE:H222	1.86	0.40
1:B:104:SER:HB3	1:B:155:VAL:HG21	2.03	0.40
2:A:501:CXE:H041	2:A:506:CXE:H011	2.03	0.40
1:C:325:LYS:HD3	2:D:507:CXE:H042	2.02	0.40
1:D:264:ASN:O	1:D:268:ILE:HG13	2.22	0.40
2:B:506:CXE:H062	2:B:506:CXE:H092	1.75	0.40
2:C:506:CXE:H102	2:C:516:CXE:H042	2.04	0.40
1:B:359:LYS:NZ	1:B:363:ILE:HD11	2.37	0.40
1:B:98:VAL:HG11	1:B:232:PHE:HB2	2.03	0.40
1:D:322:TYR:CE2	1:D:326:ILE:HD11	2.56	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	452/492 (92%)	444 (98%)	8 (2%)	0	100	100
1	B	452/492 (92%)	446 (99%)	6 (1%)	0	100	100
1	C	452/492 (92%)	444 (98%)	8 (2%)	0	100	100
1	D	452/492 (92%)	445 (98%)	7 (2%)	0	100	100
All	All	1808/1968 (92%)	1779 (98%)	29 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	358/389 (92%)	343 (96%)	15 (4%)	36	46
1	B	358/389 (92%)	356 (99%)	2 (1%)	90	96
1	C	359/389 (92%)	347 (97%)	12 (3%)	45	57
1	D	359/389 (92%)	350 (98%)	9 (2%)	55	68
All	All	1434/1556 (92%)	1396 (97%)	38 (3%)	52	66

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	SER
1	A	184	ASP
1	A	230	ARG
1	A	243	LEU
1	A	288	LEU
1	A	293	ILE
1	A	347	TYR
1	A	349	PHE
1	A	350	THR
1	A	352	SER
1	A	359	LYS
1	A	364	SER
1	A	368	THR
1	A	383	SER
1	A	433	ASN
1	B	184	ASP
1	B	226	ASP
1	C	53	LEU
1	C	168	ARG
1	C	278	VAL
1	C	286	THR
1	C	350	THR
1	C	351	TYR
1	C	363	ILE
1	C	364	SER
1	C	367	ARG
1	C	372	PHE
1	C	415	VAL
1	C	445	ARG
1	D	53	LEU
1	D	119	ILE
1	D	122	LEU
1	D	124	ARG
1	D	125	SER
1	D	129	LYS
1	D	353	GLU
1	D	356	GLN
1	D	372	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	356	GLN

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Mol	Chain	Res	Type
1	A	407	GLN
1	A	433	ASN
1	B	167	ASN
1	B	407	GLN
1	B	433	ASN
1	C	407	GLN
1	D	356	GLN

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](#)

Of 55 ligands modelled in this entry, 2 are monoatomic - leaving 53 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	CXE	A	501	-	25,25,25	0.40	0	24,24,24	0.52	0
2	CXE	A	502	-	25,25,25	0.41	0	24,24,24	0.43	0
2	CXE	A	503	-	25,25,25	0.34	0	24,24,24	0.69	0
2	CXE	A	504	-	19,19,25	0.31	0	18,18,24	0.60	0
2	CXE	A	505	-	9,9,25	0.18	0	8,8,24	0.82	0
2	CXE	A	506	-	19,19,25	0.32	0	18,18,24	0.56	0
2	CXE	A	507	-	6,6,25	0.24	0	5,5,24	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CXE	A	508	-	13,13,25	0.29	0	12,12,24	0.52	0
2	CXE	A	509	-	22,22,25	0.39	0	21,21,24	0.41	0
2	CXE	A	510	-	9,9,25	0.23	0	8,8,24	0.55	0
2	CXE	A	511	-	9,9,25	0.23	0	8,8,24	0.57	0
2	CXE	A	512	-	5,5,25	0.24	0	4,4,24	0.39	0
2	CXE	A	513	-	19,19,25	0.33	0	18,18,24	0.53	0
2	CXE	A	514	-	8,8,25	0.24	0	7,7,24	0.52	0
2	CXE	A	515	-	6,6,25	0.24	0	5,5,24	0.41	0
2	CXE	A	516	-	6,6,25	0.21	0	5,5,24	0.61	0
2	CXE	A	517	-	4,4,25	0.22	0	3,3,24	0.50	0
2	CXE	B	501	-	25,25,25	0.40	0	24,24,24	0.45	0
2	CXE	B	502	-	19,19,25	0.42	0	18,18,24	0.48	0
2	CXE	B	503	-	16,16,25	0.33	0	15,15,24	0.60	0
2	CXE	B	504	-	10,10,25	0.25	0	9,9,24	0.51	0
2	CXE	B	505	-	9,9,25	0.24	0	8,8,24	0.55	0
2	CXE	B	506	-	16,16,25	0.36	0	15,15,24	0.52	0
2	CXE	B	507	-	8,8,25	0.21	0	7,7,24	0.59	0
2	CXE	B	508	-	6,6,25	0.25	0	5,5,24	0.40	0
2	CXE	B	509	-	5,5,25	0.24	0	4,4,24	0.34	0
2	CXE	B	510	-	5,5,25	0.23	0	4,4,24	0.39	0
2	CXE	B	511	-	5,5,25	0.25	0	4,4,24	0.39	0
2	CXE	B	512	-	8,8,25	0.25	0	7,7,24	0.45	0
2	CXE	C	501	-	25,25,25	0.41	0	24,24,24	0.44	0
2	CXE	C	502	-	25,25,25	0.38	0	24,24,24	0.59	0
2	CXE	C	503	-	25,25,25	0.39	0	24,24,24	0.61	0
2	CXE	C	504	-	25,25,25	0.40	0	24,24,24	0.49	0
2	CXE	C	505	-	19,19,25	0.38	0	18,18,24	0.76	0
2	CXE	C	506	-	14,14,25	0.33	0	13,13,24	0.56	0
2	CXE	C	507	-	9,9,25	0.25	0	8,8,24	0.49	0
2	CXE	C	508	-	6,6,25	0.23	0	5,5,24	0.52	0
2	CXE	C	509	-	16,16,25	0.37	0	15,15,24	0.58	0
2	CXE	C	510	-	22,22,25	0.37	0	21,21,24	0.50	0
2	CXE	C	511	-	9,9,25	0.23	0	8,8,24	0.57	0
2	CXE	C	512	-	15,15,25	0.45	0	14,14,24	0.45	0
2	CXE	C	513	-	22,22,25	0.35	0	21,21,24	0.68	0
2	CXE	C	514	-	16,16,25	0.34	0	15,15,24	0.47	0
2	CXE	C	515	-	3,3,25	0.47	0	2,2,24	0.65	0
2	CXE	C	516	-	6,6,25	0.25	0	5,5,24	0.49	0
2	CXE	D	501	-	10,10,25	0.21	0	9,9,24	0.58	0
2	CXE	D	502	-	19,19,25	0.30	0	18,18,24	0.58	0
2	CXE	D	503	-	13,13,25	0.31	0	12,12,24	0.49	0
2	CXE	D	504	-	9,9,25	0.22	0	8,8,24	0.62	0
2	CXE	D	505	-	13,13,25	0.27	0	12,12,24	0.51	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CXE	D	506	-	10,10,25	0.25	0	9,9,24	0.51	0
2	CXE	D	507	-	10,10,25	0.24	0	9,9,24	0.52	0
2	CXE	D	508	-	4,4,25	0.23	0	3,3,24	0.39	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
2	CXE	A	501	-	-	0/23/23/23	0/0/0/0
2	CXE	A	502	-	-	0/23/23/23	0/0/0/0
2	CXE	A	503	-	-	0/23/23/23	0/0/0/0
2	CXE	A	504	-	-	0/17/17/23	0/0/0/0
2	CXE	A	505	-	-	0/7/7/23	0/0/0/0
2	CXE	A	506	-	-	0/17/17/23	0/0/0/0
2	CXE	A	507	-	-	0/4/4/23	0/0/0/0
2	CXE	A	508	-	-	0/11/11/23	0/0/0/0
2	CXE	A	509	-	-	0/20/20/23	0/0/0/0
2	CXE	A	510	-	-	0/7/7/23	0/0/0/0
2	CXE	A	511	-	-	0/7/7/23	0/0/0/0
2	CXE	A	512	-	-	0/3/3/23	0/0/0/0
2	CXE	A	513	-	-	0/17/17/23	0/0/0/0
2	CXE	A	514	-	-	0/6/6/23	0/0/0/0
2	CXE	A	515	-	-	0/4/4/23	0/0/0/0
2	CXE	A	516	-	-	0/4/4/23	0/0/0/0
2	CXE	A	517	-	-	0/2/2/23	0/0/0/0
2	CXE	B	501	-	-	0/23/23/23	0/0/0/0
2	CXE	B	502	-	-	0/17/17/23	0/0/0/0
2	CXE	B	503	-	-	0/14/14/23	0/0/0/0
2	CXE	B	504	-	-	0/8/8/23	0/0/0/0
2	CXE	B	505	-	-	0/7/7/23	0/0/0/0
2	CXE	B	506	-	-	0/14/14/23	0/0/0/0
2	CXE	B	507	-	-	0/6/6/23	0/0/0/0
2	CXE	B	508	-	-	0/4/4/23	0/0/0/0
2	CXE	B	509	-	-	0/3/3/23	0/0/0/0
2	CXE	B	510	-	-	0/3/3/23	0/0/0/0
2	CXE	B	511	-	-	0/3/3/23	0/0/0/0
2	CXE	B	512	-	-	0/6/6/23	0/0/0/0
2	CXE	C	501	-	-	0/23/23/23	0/0/0/0
2	CXE	C	502	-	-	0/23/23/23	0/0/0/0
2	CXE	C	503	-	-	0/23/23/23	0/0/0/0
2	CXE	C	504	-	-	0/23/23/23	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CXE	C	505	-	-	0/17/17/23	0/0/0/0
2	CXE	C	506	-	-	0/12/12/23	0/0/0/0
2	CXE	C	507	-	-	0/7/7/23	0/0/0/0
2	CXE	C	508	-	-	0/4/4/23	0/0/0/0
2	CXE	C	509	-	-	0/14/14/23	0/0/0/0
2	CXE	C	510	-	-	0/20/20/23	0/0/0/0
2	CXE	C	511	-	-	0/7/7/23	0/0/0/0
2	CXE	C	512	-	-	0/13/13/23	0/0/0/0
2	CXE	C	513	-	-	0/20/20/23	0/0/0/0
2	CXE	C	514	-	-	0/14/14/23	0/0/0/0
2	CXE	C	515	-	-	0/1/1/23	0/0/0/0
2	CXE	C	516	-	-	0/4/4/23	0/0/0/0
2	CXE	D	501	-	-	0/8/8/23	0/0/0/0
2	CXE	D	502	-	-	0/17/17/23	0/0/0/0
2	CXE	D	503	-	-	0/11/11/23	0/0/0/0
2	CXE	D	504	-	-	0/7/7/23	0/0/0/0
2	CXE	D	505	-	-	0/11/11/23	0/0/0/0
2	CXE	D	506	-	-	0/8/8/23	0/0/0/0
2	CXE	D	507	-	-	0/8/8/23	0/0/0/0
2	CXE	D	508	-	-	0/2/2/23	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

34 monomers are involved in 57 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	CXE	5	0
2	A	502	CXE	3	0
2	A	503	CXE	2	0
2	A	504	CXE	1	0
2	A	505	CXE	1	0
2	A	506	CXE	6	0
2	A	507	CXE	1	0
2	A	509	CXE	1	0
2	A	513	CXE	2	0
2	A	515	CXE	3	0
2	A	516	CXE	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	517	CXE	1	0
2	B	501	CXE	1	0
2	B	502	CXE	3	0
2	B	503	CXE	1	0
2	B	506	CXE	5	0
2	B	511	CXE	1	0
2	C	501	CXE	3	0
2	C	502	CXE	1	0
2	C	503	CXE	4	0
2	C	504	CXE	2	0
2	C	505	CXE	4	0
2	C	506	CXE	1	0
2	C	511	CXE	1	0
2	C	512	CXE	3	0
2	C	513	CXE	4	0
2	C	514	CXE	2	0
2	C	516	CXE	1	0
2	D	501	CXE	2	0
2	D	502	CXE	1	0
2	D	503	CXE	1	0
2	D	504	CXE	1	0
2	D	505	CXE	2	0
2	D	507	CXE	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	453/492 (92%)	0.32	46 (10%) 9 15	19, 37, 89, 146	0
1	B	454/492 (92%)	0.34	31 (6%) 20 30	21, 42, 76, 113	0
1	C	452/492 (91%)	0.47	44 (9%) 10 16	19, 35, 105, 142	0
1	D	452/492 (91%)	0.71	56 (12%) 5 9	33, 53, 97, 129	0
All	All	1811/1968 (92%)	0.46	177 (9%) 10 16	19, 44, 91, 146	0

All (177) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	354	SER	11.3
1	A	456	ALA	9.1
1	D	352	SER	8.3
1	A	454	THR	8.0
1	D	355	ALA	7.6
1	C	353	GLU	7.4
1	D	357	VAL	7.3
1	A	351	TYR	7.2
1	A	347	TYR	7.0
1	C	350	THR	7.0
1	A	352	SER	6.9
1	B	357	VAL	6.7
1	D	454	THR	6.4
1	A	455	SER	6.4
1	C	357	VAL	6.3
1	C	4	LYS	6.1
1	C	267	ALA	5.9
1	A	126	MET	5.9
1	C	270	ALA	5.9
1	A	355	ALA	5.8
1	A	350	THR	5.8

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Mol	Chain	Res	Type	RSRZ
1	D	231	ASP	5.8
1	C	355	ALA	5.8
1	D	356	GLN	5.7
1	C	127	GLY	5.6
1	D	228	THR	5.5
1	D	59	PHE	5.4
1	D	128	ALA	5.2
1	D	232	PHE	5.2
1	D	129	LYS	5.1
1	C	271	GLY	5.1
1	C	276	VAL	5.1
1	D	126	MET	5.0
1	B	273	GLU	5.0
1	D	130	GLY	4.9
1	C	358	ILE	4.9
1	D	354	SER	4.9
1	C	261	PHE	4.9
1	B	352	SER	4.9
1	C	264	ASN	4.7
1	C	126	MET	4.7
1	D	353	GLU	4.7
1	C	275	GLY	4.6
1	C	263	LEU	4.6
1	C	279	PHE	4.5
1	D	133	VAL	4.4
1	A	273	GLU	4.3
1	B	354	SER	4.2
1	D	131	GLU	4.2
1	B	232	PHE	4.1
1	C	283	TRP	4.1
1	A	357	VAL	4.1
1	A	340	LEU	4.1
1	D	229	LEU	4.0
1	C	266	VAL	4.0
1	B	355	ALA	4.0
1	A	271	GLY	3.9
1	B	129	LYS	3.9
1	B	3	GLU	3.8
1	D	124	ARG	3.8
1	B	126	MET	3.8
1	B	127	GLY	3.7
1	D	123	PHE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	231	ASP	3.7
1	D	127	GLY	3.7
1	B	272	GLY	3.6
1	B	233	SER	3.6
1	A	358	ILE	3.6
1	A	353	GLU	3.5
1	A	272	GLY	3.5
1	C	351	TYR	3.5
1	C	125	SER	3.5
1	A	346	ALA	3.5
1	D	135	LEU	3.5
1	D	138	GLU	3.5
1	A	361	ASP	3.5
1	D	240	LYS	3.5
1	D	122	LEU	3.4
1	C	454	THR	3.4
1	C	268	ILE	3.4
1	D	340	LEU	3.4
1	D	351	TYR	3.3
1	B	311	ARG	3.3
1	B	287	MET	3.3
1	C	370	PRO	3.3
1	C	426	TRP	3.3
1	C	273	GLU	3.2
1	C	341	PHE	3.2
1	A	453	LYS	3.2
1	D	132	ALA	3.2
1	A	232	PHE	3.2
1	A	419	THR	3.2
1	A	268	ILE	3.2
1	D	116	LEU	3.2
1	D	113	ILE	3.2
1	A	127	GLY	3.2
1	B	231	ASP	3.1
1	B	353	GLU	3.1
1	A	261	PHE	3.1
1	C	349	PHE	3.1
1	A	339	MET	3.1
1	D	121	SER	3.1
1	C	128	ALA	3.1
1	D	137	ILE	3.0
1	D	350	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	359	LYS	3.0
1	B	125	SER	3.0
1	A	362	LEU	3.0
1	A	356	GLN	3.0
1	A	354	SER	3.0
1	A	360	GLY	3.0
1	A	4	LYS	2.9
1	D	311	ARG	2.9
1	C	272	GLY	2.9
1	B	4	LYS	2.9
1	D	230	ARG	2.9
1	D	233	SER	2.9
1	D	119	ILE	2.9
1	B	342	ALA	2.9
1	B	351	TYR	2.9
1	C	3	GLU	2.8
1	A	122	LEU	2.8
1	A	349	PHE	2.8
1	B	358	ILE	2.8
1	D	453	LYS	2.7
1	A	420	LEU	2.7
1	C	421	GLY	2.6
1	C	260	MET	2.6
1	D	141	ARG	2.6
1	D	117	PRO	2.6
1	B	453	LYS	2.5
1	A	274	ASN	2.5
1	C	262	PHE	2.5
1	A	426	TRP	2.5
1	B	128	ALA	2.5
1	D	215	TYR	2.5
1	B	356	GLN	2.5
1	A	262	PHE	2.5
1	C	287	MET	2.4
1	C	123	PHE	2.4
1	B	229	LEU	2.4
1	A	125	SER	2.4
1	D	114	THR	2.4
1	C	356	GLN	2.4
1	B	7	LYS	2.4
1	A	365	ALA	2.4
1	D	125	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	269	THR	2.3
1	A	348	LEU	2.3
1	C	347	TYR	2.3
1	D	120	ASP	2.3
1	C	122	LEU	2.3
1	C	362	LEU	2.3
1	D	358	ILE	2.3
1	A	336	ALA	2.3
1	A	342	ALA	2.3
1	D	5	THR	2.3
1	D	343	PRO	2.3
1	D	115	MET	2.3
1	D	136	ALA	2.2
1	B	274	ASN	2.2
1	A	129	LYS	2.2
1	D	341	PHE	2.2
1	D	287	MET	2.2
1	D	238	ILE	2.1
1	B	362	LEU	2.1
1	D	94	ASP	2.1
1	A	335	VAL	2.1
1	A	366	LEU	2.1
1	B	5	THR	2.1
1	D	106	ILE	2.1
1	A	341	PHE	2.1
1	B	228	THR	2.1
1	C	129	LYS	2.1
1	D	134	GLU	2.1
1	B	277	ALA	2.1
1	C	346	ALA	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å ²)	Q<0.9
2	CXE	A	510	10/26	0.81	0.36	23.41	36,63,68,69	0
2	CXE	C	504	26/26	0.74	0.38	17.90	50,72,102,105	0
2	CXE	B	504	11/26	0.80	0.24	7.87	36,74,78,81	0
2	CXE	A	509	23/26	0.63	0.39	7.81	56,83,102,104	0
2	CXE	C	512	16/26	0.83	0.25	7.40	38,57,82,89	0
2	CXE	C	506	15/26	0.84	0.21	7.33	37,47,71,75	0
2	CXE	A	503	26/26	0.63	0.35	6.78	65,77,83,85	0
2	CXE	B	507	9/26	0.83	0.24	6.61	36,61,73,84	0
2	CXE	A	512	6/26	0.88	0.23	6.52	34,49,53,65	0
2	CXE	C	511	10/26	0.86	0.23	6.17	48,56,65,67	0
2	CXE	B	505	10/26	0.77	0.21	6.15	46,60,72,77	0
2	CXE	B	512	9/26	0.77	0.23	6.14	44,53,62,65	0
2	CXE	C	505	20/26	0.73	0.27	5.98	46,62,82,83	0
2	CXE	B	509	6/26	0.87	1.03	5.86	32,36,42,45	6
2	CXE	A	505	10/26	0.87	0.83	5.61	38,42,47,63	10
2	CXE	C	501	26/26	0.78	0.28	5.38	26,43,88,95	0
2	CXE	C	514	17/26	0.65	0.34	5.19	50,70,93,93	0
2	CXE	B	502	20/26	0.81	0.24	5.13	36,50,62,65	0
2	CXE	C	507	10/26	0.85	0.28	4.84	60,68,79,80	0
2	CXE	A	513	20/26	0.73	0.26	4.38	42,74,102,106	0
2	CXE	C	503	26/26	0.75	0.24	4.15	47,57,74,78	0
2	CXE	A	514	9/26	0.83	0.21	3.99	55,62,69,73	0
2	CXE	C	508	7/26	0.83	0.28	3.63	52,59,64,66	0
2	CXE	A	506	20/26	0.87	0.22	3.59	24,39,57,58	0
2	CXE	A	502	26/26	0.87	0.25	3.40	29,48,74,81	0
2	CXE	B	506	17/26	0.81	0.22	3.11	56,70,84,84	0
2	CXE	C	510	23/26	0.83	0.24	2.98	49,73,80,88	0
2	CXE	C	502	26/26	0.78	0.30	2.86	40,76,83,87	0
2	CXE	D	507	11/26	0.83	0.23	2.78	48,58,67,70	0
2	CXE	A	511	10/26	0.80	0.23	2.34	58,66,74,74	0
2	CXE	D	505	14/26	0.76	0.24	1.94	49,66,77,78	0
2	CXE	D	502	20/26	0.90	0.19	1.89	38,48,56,58	10
2	CXE	A	516	7/26	0.83	0.22	1.51	52,57,70,73	0
2	CXE	A	515	7/26	0.86	0.23	1.47	38,53,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CXE	A	504	20/26	0.88	0.17	1.38	43,61,77,81	0
2	CXE	C	513	23/26	0.79	0.25	1.33	57,67,81,85	0
2	CXE	D	504	10/26	0.81	0.22	1.11	55,59,73,74	0
2	CXE	A	508	14/26	0.71	0.29	1.00	63,78,100,100	0
2	CXE	B	503	17/26	0.85	0.21	0.76	46,53,66,68	3
2	CXE	B	501	26/26	0.88	0.19	0.59	35,50,77,86	0
2	CXE	A	501	26/26	0.83	0.18	0.53	35,49,60,64	0
2	CXE	D	508	5/26	0.83	0.20	0.37	56,57,57,58	0
2	CXE	D	503	14/26	0.93	0.17	0.10	53,61,65,76	0
2	CXE	D	501	11/26	0.91	0.15	-0.14	41,46,65,65	0
2	CXE	A	517	5/26	0.87	0.22	-	56,60,63,68	0
2	CXE	C	515	4/26	0.86	0.15	-	48,50,54,66	0
2	CXE	A	507	7/26	0.81	0.17	-	42,52,59,62	0
3	CL	A	518	1/1	0.97	0.08	-	29,29,29,29	0
2	CXE	C	516	7/26	0.86	0.29	-	51,65,67,68	0
2	CXE	B	508	7/26	0.85	0.22	-	44,52,67,68	0
2	CXE	D	506	11/26	0.78	0.23	-	64,68,87,91	0
2	CXE	B	511	6/26	0.71	1.05	-	34,38,39,42	6
2	CXE	B	510	6/26	0.88	0.14	-	62,69,71,72	0
2	CXE	C	509	17/26	0.81	0.20	-	54,76,85,95	0
3	CL	A	519	1/1	0.98	0.13	-	37,37,37,37	0

6.5 Other polymers

There are no such residues in this entry.