



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 02:20 PM UTC

PDB ID : 3BB5 / pdb_00003bb5
Title : CRYSTAL STRUCTURE OF A DIMERIC FERREDOXIN-LIKE PROTEIN OF UNKNOWN FUNCTION (JANN_3925) FROM JANNASCHIA SP. CCS1 AT 2.30 Å RESOLUTION
Authors : Joint Center for Structural Genomics (JCSG)
Deposited on : 2007-11-09
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 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

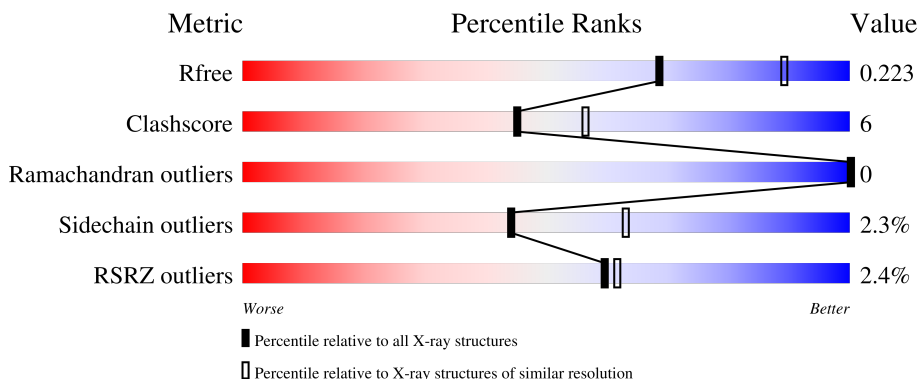
1 Overall quality at a glance i

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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	121	 2% 76% 8% • 15%
1	B	121	 2% 75% 9% • 15%
1	C	121	 77% 7% • 15%
1	D	121	 2% 70% 18% • 11%
1	E	121	 4% 75% 11% 14%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	121	 A horizontal bar chart showing the quality of chain. The bar is divided into four segments: a small red segment at the beginning labeled '2%', a large green segment labeled '76%', a small yellow segment labeled '7%', and a grey segment at the end labeled '15%'. The segments are separated by small black dots.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5027 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 Stress responsive alpha-beta protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	103	791	501	133	149	2	6	0	2	0
1	B	103	789	496	135	150	2	6	0	0	0
1	C	103	787	496	135	148	2	6	0	0	0
1	D	108	828	526	141	153	2	6	0	0	0
1	E	104	793	502	136	147	2	6	0	1	0
1	F	103	783	494	135	146	2	6	0	0	0

There are 114 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MSE	-	expression tag	UNP Q28KC0
A	-17	GLY	-	expression tag	UNP Q28KC0
A	-16	SER	-	expression tag	UNP Q28KC0
A	-15	ASP	-	expression tag	UNP Q28KC0
A	-14	LYS	-	expression tag	UNP Q28KC0
A	-13	ILE	-	expression tag	UNP Q28KC0
A	-12	HIS	-	expression tag	UNP Q28KC0
A	-11	HIS	-	expression tag	UNP Q28KC0
A	-10	HIS	-	expression tag	UNP Q28KC0
A	-9	HIS	-	expression tag	UNP Q28KC0
A	-8	HIS	-	expression tag	UNP Q28KC0
A	-7	HIS	-	expression tag	UNP Q28KC0
A	-6	GLU	-	expression tag	UNP Q28KC0
A	-5	ASN	-	expression tag	UNP Q28KC0
A	-4	LEU	-	expression tag	UNP Q28KC0
A	-3	TYR	-	expression tag	UNP Q28KC0
A	-2	PHE	-	expression tag	UNP Q28KC0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLN	-	expression tag	UNP Q28KC0
A	0	GLY	-	expression tag	UNP Q28KC0
B	-18	MSE	-	expression tag	UNP Q28KC0
B	-17	GLY	-	expression tag	UNP Q28KC0
B	-16	SER	-	expression tag	UNP Q28KC0
B	-15	ASP	-	expression tag	UNP Q28KC0
B	-14	LYS	-	expression tag	UNP Q28KC0
B	-13	ILE	-	expression tag	UNP Q28KC0
B	-12	HIS	-	expression tag	UNP Q28KC0
B	-11	HIS	-	expression tag	UNP Q28KC0
B	-10	HIS	-	expression tag	UNP Q28KC0
B	-9	HIS	-	expression tag	UNP Q28KC0
B	-8	HIS	-	expression tag	UNP Q28KC0
B	-7	HIS	-	expression tag	UNP Q28KC0
B	-6	GLU	-	expression tag	UNP Q28KC0
B	-5	ASN	-	expression tag	UNP Q28KC0
B	-4	LEU	-	expression tag	UNP Q28KC0
B	-3	TYR	-	expression tag	UNP Q28KC0
B	-2	PHE	-	expression tag	UNP Q28KC0
B	-1	GLN	-	expression tag	UNP Q28KC0
B	0	GLY	-	expression tag	UNP Q28KC0
C	-18	MSE	-	expression tag	UNP Q28KC0
C	-17	GLY	-	expression tag	UNP Q28KC0
C	-16	SER	-	expression tag	UNP Q28KC0
C	-15	ASP	-	expression tag	UNP Q28KC0
C	-14	LYS	-	expression tag	UNP Q28KC0
C	-13	ILE	-	expression tag	UNP Q28KC0
C	-12	HIS	-	expression tag	UNP Q28KC0
C	-11	HIS	-	expression tag	UNP Q28KC0
C	-10	HIS	-	expression tag	UNP Q28KC0
C	-9	HIS	-	expression tag	UNP Q28KC0
C	-8	HIS	-	expression tag	UNP Q28KC0
C	-7	HIS	-	expression tag	UNP Q28KC0
C	-6	GLU	-	expression tag	UNP Q28KC0
C	-5	ASN	-	expression tag	UNP Q28KC0
C	-4	LEU	-	expression tag	UNP Q28KC0
C	-3	TYR	-	expression tag	UNP Q28KC0
C	-2	PHE	-	expression tag	UNP Q28KC0
C	-1	GLN	-	expression tag	UNP Q28KC0
C	0	GLY	-	expression tag	UNP Q28KC0
D	-18	MSE	-	expression tag	UNP Q28KC0
D	-17	GLY	-	expression tag	UNP Q28KC0

Continued on next page...

Continued from previous page...

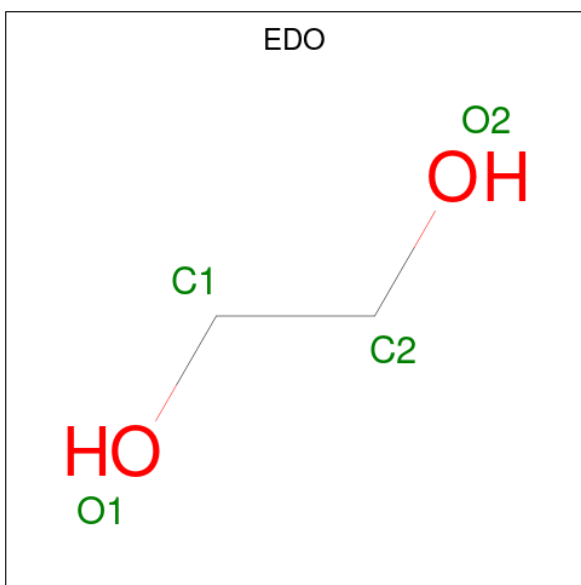
Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP Q28KC0
D	-15	ASP	-	expression tag	UNP Q28KC0
D	-14	LYS	-	expression tag	UNP Q28KC0
D	-13	ILE	-	expression tag	UNP Q28KC0
D	-12	HIS	-	expression tag	UNP Q28KC0
D	-11	HIS	-	expression tag	UNP Q28KC0
D	-10	HIS	-	expression tag	UNP Q28KC0
D	-9	HIS	-	expression tag	UNP Q28KC0
D	-8	HIS	-	expression tag	UNP Q28KC0
D	-7	HIS	-	expression tag	UNP Q28KC0
D	-6	GLU	-	expression tag	UNP Q28KC0
D	-5	ASN	-	expression tag	UNP Q28KC0
D	-4	LEU	-	expression tag	UNP Q28KC0
D	-3	TYR	-	expression tag	UNP Q28KC0
D	-2	PHE	-	expression tag	UNP Q28KC0
D	-1	GLN	-	expression tag	UNP Q28KC0
D	0	GLY	-	expression tag	UNP Q28KC0
E	-18	MSE	-	expression tag	UNP Q28KC0
E	-17	GLY	-	expression tag	UNP Q28KC0
E	-16	SER	-	expression tag	UNP Q28KC0
E	-15	ASP	-	expression tag	UNP Q28KC0
E	-14	LYS	-	expression tag	UNP Q28KC0
E	-13	ILE	-	expression tag	UNP Q28KC0
E	-12	HIS	-	expression tag	UNP Q28KC0
E	-11	HIS	-	expression tag	UNP Q28KC0
E	-10	HIS	-	expression tag	UNP Q28KC0
E	-9	HIS	-	expression tag	UNP Q28KC0
E	-8	HIS	-	expression tag	UNP Q28KC0
E	-7	HIS	-	expression tag	UNP Q28KC0
E	-6	GLU	-	expression tag	UNP Q28KC0
E	-5	ASN	-	expression tag	UNP Q28KC0
E	-4	LEU	-	expression tag	UNP Q28KC0
E	-3	TYR	-	expression tag	UNP Q28KC0
E	-2	PHE	-	expression tag	UNP Q28KC0
E	-1	GLN	-	expression tag	UNP Q28KC0
E	0	GLY	-	expression tag	UNP Q28KC0
F	-18	MSE	-	expression tag	UNP Q28KC0
F	-17	GLY	-	expression tag	UNP Q28KC0
F	-16	SER	-	expression tag	UNP Q28KC0
F	-15	ASP	-	expression tag	UNP Q28KC0
F	-14	LYS	-	expression tag	UNP Q28KC0
F	-13	ILE	-	expression tag	UNP Q28KC0

Continued on next page...

Continued from previous page...

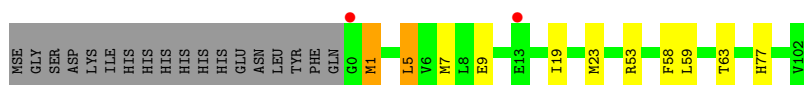
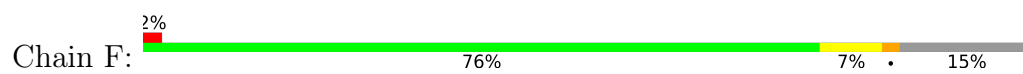
Chain	Residue	Modelled	Actual	Comment	Reference
F	-12	HIS	-	expression tag	UNP Q28KC0
F	-11	HIS	-	expression tag	UNP Q28KC0
F	-10	HIS	-	expression tag	UNP Q28KC0
F	-9	HIS	-	expression tag	UNP Q28KC0
F	-8	HIS	-	expression tag	UNP Q28KC0
F	-7	HIS	-	expression tag	UNP Q28KC0
F	-6	GLU	-	expression tag	UNP Q28KC0
F	-5	ASN	-	expression tag	UNP Q28KC0
F	-4	LEU	-	expression tag	UNP Q28KC0
F	-3	TYR	-	expression tag	UNP Q28KC0
F	-2	PHE	-	expression tag	UNP Q28KC0
F	-1	GLN	-	expression tag	UNP Q28KC0
F	0	GLY	-	expression tag	UNP Q28KC0

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	E	1	Total	C	O	0	0
			4	2	2		
2	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: C₆H₈O₇).



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	147.72Å 66.32Å 110.45Å 90.00° 93.41° 90.00°	Depositor
Resolution (Å)	29.84 – 2.30 29.84 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.84-2.30) 99.9 (29.84-2.30)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.31Å)	Xtrriage
Refinement program	REFMAC 5.2.0019, PHENIX	Depositor
R, R_{free}	0.179 , 0.222 0.181 , 0.223	Depositor DCC
R_{free} test set	2409 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtrriage
Anisotropy	0.709	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5027	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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](#)

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

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	0.97	1/808 (0.1%)	0.97	0/1082
1	B	0.96	0/800	0.99	0/1070
1	C	0.96	0/798	0.99	0/1068
1	D	1.06	3/841 (0.4%)	1.09	3/1127 (0.3%)
1	E	0.94	0/807	1.02	0/1081
1	F	0.93	0/794	0.97	0/1063
All	All	0.97	4/4848 (0.1%)	1.01	3/6491 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	0	GLY	CA-C	7.01	1.60	1.51
1	D	0	GLY	N-CA	5.46	1.51	1.45
1	A	30	ALA	CA-CB	-5.18	1.49	1.54
1	D	-1	GLN	CA-C	5.16	1.59	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	-1	GLN	CA-C-N	5.44	129.68	120.86
1	D	-1	GLN	C-N-CA	5.44	129.68	120.86
1	D	29	LEU	N-CA-C	5.28	117.12	111.36

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	791	0	769	8	0
1	B	789	0	760	7	0
1	C	787	0	763	11	0
1	D	828	0	798	17	0
1	E	793	0	772	12	0
1	F	783	0	759	12	0
2	A	4	0	6	0	0
2	C	4	0	6	0	0
2	E	4	0	6	0	0
2	F	4	0	6	0	0
3	B	13	0	5	1	0
3	C	13	0	5	0	0
3	D	13	0	5	1	0
3	E	13	0	5	0	0
3	F	13	0	5	2	0
4	A	27	0	0	0	0
4	B	36	0	0	0	0
4	C	28	0	0	0	0
4	D	22	0	0	0	0
4	E	33	0	0	0	0
4	F	29	0	0	0	0
All	All	5027	0	4670	56	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 6.

All (56) 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:C:1:MSE:HE2	1:C:61:THR:HG22	1.57	0.84
1:F:1:MSE:HE2	1:F:63:THR:HA	1.61	0.81
1:D:1:MSE:HE2	1:D:61:THR:CG2	2.10	0.81
1:C:1:MSE:HE2	1:C:61:THR:CG2	2.21	0.71
1:F:1:MSE:CE	1:F:63:THR:HG22	2.24	0.67
1:F:1:MSE:HE1	1:F:63:THR:HG22	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1:MSE:HE2	1:D:61:THR:HG22	1.79	0.64
1:D:-2:PHE:O	1:D:-1:GLN:C	2.40	0.63
1:F:1:MSE:CE	1:F:63:THR:HA	2.32	0.60
1:A:5:LEU:HD11	1:A:7:MSE:SE	2.52	0.59
1:C:5:LEU:HD22	1:D:5:LEU:HD22	1.84	0.58
1:E:21:GLU:HB2	1:E:83:MSE:HE1	1.86	0.58
1:B:30:ALA:HB3	1:B:31:PRO:HD3	1.87	0.57
1:A:30:ALA:HB3	1:A:31:PRO:HD3	1.86	0.56
1:E:5:LEU:HD22	1:F:5:LEU:HD22	1.88	0.56
1:D:3:TYR:CE1	1:D:61:THR:HG23	2.41	0.55
1:D:-2:PHE:O	1:D:101:GLU:OE2	2.25	0.54
1:C:50:LYS:O	1:D:96:LEU:HD12	2.07	0.53
1:F:77:HIS:HE2	3:F:104:CIT:C1	2.22	0.53
1:D:95:ILE:HG21	3:D:103:CIT:H42	1.94	0.49
1:D:3:TYR:HE1	1:D:61:THR:HG23	1.77	0.49
1:D:-5:ASN:O	1:D:-5:ASN:CG	2.56	0.48
1:E:30:ALA:HB3	1:E:31:PRO:HD3	1.95	0.48
1:E:98:VAL:HG11	1:F:7:MSE:SE	2.63	0.48
1:C:5:LEU:HD12	1:C:59:LEU:HD13	1.94	0.48
1:C:5:LEU:HD13	1:D:5:LEU:HD13	1.96	0.48
1:F:77:HIS:NE2	3:F:104:CIT:O1	2.45	0.48
1:A:5:LEU:HD22	1:B:5:LEU:CG	2.45	0.47
1:F:9:GLU:HG2	1:F:53:ARG:O	2.14	0.47
1:B:13:GLU:HA	1:B:13:GLU:OE1	2.15	0.47
1:E:36[B]:LEU:HD13	1:E:62:PHE:CE1	2.51	0.46
1:F:23:MSE:HE1	1:F:58:PHE:CE2	2.50	0.46
1:A:65:LYS:HE2	1:B:47:PHE:CD1	2.52	0.45
1:B:1:MSE:HE2	1:B:63:THR:HA	1.99	0.44
1:E:41:HIS:HB3	1:E:58:PHE:HB3	1.98	0.44
1:A:21:GLU:HB3	1:A:83:MSE:HE1	1.99	0.44
1:A:100:LEU:HD21	1:B:7:MSE:HE1	1.99	0.43
1:C:86:ALA:HA	1:E:18:ARG:CD	2.49	0.43
1:B:45:ARG:O	1:B:46:ASP:C	2.62	0.43
1:C:7:MSE:HE1	1:D:100:LEU:HD21	2.00	0.43
1:C:5:LEU:HD13	1:D:5:LEU:HD22	2.01	0.42
1:C:5:LEU:CD1	1:C:59:LEU:HD13	2.49	0.42
1:A:45:ARG:O	1:A:46:ASP:C	2.60	0.42
1:D:30:ALA:HB3	1:D:31:PRO:HD3	2.00	0.42
1:E:36[B]:LEU:CD1	1:E:60:CYS:HB3	2.49	0.42
1:F:19:ILE:O	1:F:23:MSE:HG2	2.19	0.42
1:F:5:LEU:HG	1:F:59:LEU:HD13	2.00	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:5:LEU:HD11	1:E:7:MSE:SE	2.71	0.41
1:C:16:MSE:O	1:C:20:MSE:HG2	2.20	0.41
1:D:62:PHE:CE2	1:D:68:LEU:HD13	2.56	0.41
1:D:36:LEU:HD23	1:D:36:LEU:C	2.45	0.41
1:A:48:GLU:OE1	3:B:103:CIT:O6	2.39	0.41
1:E:36[B]:LEU:HD11	1:E:60:CYS:HB3	2.03	0.41
1:D:21:GLU:HB3	1:D:83:MSE:HE1	2.02	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	103/121 (85%)	101 (98%)	2 (2%)	0	100	100
1	B	101/121 (84%)	98 (97%)	3 (3%)	0	100	100
1	C	101/121 (84%)	98 (97%)	3 (3%)	0	100	100
1	D	106/121 (88%)	102 (96%)	4 (4%)	0	100	100
1	E	103/121 (85%)	100 (97%)	3 (3%)	0	100	100
1	F	101/121 (84%)	99 (98%)	2 (2%)	0	100	100
All	All	615/726 (85%)	598 (97%)	17 (3%)	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	80/91 (88%)	80 (100%)	0	100	100
1	B	80/91 (88%)	77 (96%)	3 (4%)	29	44
1	C	80/91 (88%)	77 (96%)	3 (4%)	29	44
1	D	83/91 (91%)	80 (96%)	3 (4%)	31	47
1	E	80/91 (88%)	80 (100%)	0	100	100
1	F	79/91 (87%)	77 (98%)	2 (2%)	42	60
All	All	482/546 (88%)	471 (98%)	11 (2%)	44	63

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

Mol	Chain	Res	Type
1	B	13	GLU
1	B	49	GLN
1	B	89	ARG
1	C	1	MSE
1	C	5	LEU
1	C	49	GLN
1	D	-4	LEU
1	D	37	THR
1	D	49	GLN
1	F	1	MSE
1	F	5	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	GLN
1	C	77	HIS
1	D	-5	ASN
1	D	49	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	E	103	-	3,3,3	0.35	0	2,2,2	0.48	0
3	CIT	C	104	-	12,12,12	1.11	0	17,17,17	1.77	5 (29%)
2	EDO	F	103	-	3,3,3	0.51	0	2,2,2	0.40	0
3	CIT	F	104	-	12,12,12	1.18	0	17,17,17	2.00	7 (41%)
3	CIT	D	103	-	12,12,12	1.08	0	17,17,17	1.66	6 (35%)
3	CIT	B	103	-	12,12,12	1.16	0	17,17,17	2.23	9 (52%)
3	CIT	E	104	-	12,12,12	1.18	0	17,17,17	2.26	8 (47%)
2	EDO	A	103	-	3,3,3	0.58	0	2,2,2	0.06	0
2	EDO	C	103	-	3,3,3	0.69	0	2,2,2	0.23	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	EDO	E	103	-	-	0/1/1/1	-
3	CIT	C	104	-	-	2/16/16/16	-
2	EDO	F	103	-	-	0/1/1/1	-
3	CIT	F	104	-	-	6/16/16/16	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CIT	D	103	-	-	0/16/16/16	-
3	CIT	B	103	-	-	7/16/16/16	-
3	CIT	E	104	-	-	0/16/16/16	-
2	EDO	A	103	-	-	1/1/1/1	-
2	EDO	C	103	-	-	1/1/1/1	-

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	103	CIT	O6-C6-C3	3.84	120.50	113.14
3	B	103	CIT	O2-C1-O1	-3.81	113.54	123.33
3	E	104	CIT	C4-C3-C2	3.80	119.07	109.31
3	F	104	CIT	O2-C1-C2	3.71	126.10	114.35
3	E	104	CIT	O6-C6-C3	3.55	119.95	113.14
3	B	103	CIT	O2-C1-C2	3.51	125.47	114.35
3	F	104	CIT	O6-C6-C3	3.49	119.84	113.14
3	B	103	CIT	C4-C3-C2	3.40	118.04	109.31
3	C	104	CIT	O2-C1-O1	-3.36	114.68	123.33
3	C	104	CIT	O6-C6-C3	3.24	119.35	113.14
3	E	104	CIT	O4-C5-O3	-3.22	115.06	123.33
3	B	103	CIT	O7-C3-C6	3.21	113.51	108.96
3	E	104	CIT	C4-C3-C6	-3.18	102.99	110.03
3	E	104	CIT	O4-C5-C4	3.16	124.37	114.35
3	E	104	CIT	O2-C1-O1	-3.07	115.44	123.33
3	B	103	CIT	O4-C5-O3	-3.06	115.47	123.33
3	F	104	CIT	C2-C3-C6	2.81	116.25	110.03
3	B	103	CIT	O6-C6-C3	2.77	118.46	113.14
3	F	104	CIT	O4-C5-C4	2.62	122.66	114.35
3	F	104	CIT	O2-C1-O1	-2.42	117.12	123.33
3	E	104	CIT	O2-C1-C2	2.40	121.94	114.35
3	D	103	CIT	O4-C5-C4	2.38	121.88	114.35
3	E	104	CIT	O7-C3-C6	2.36	112.31	108.96
3	D	103	CIT	O7-C3-C6	2.30	112.23	108.96
3	C	104	CIT	O2-C1-C2	2.30	121.64	114.35
3	B	103	CIT	O7-C3-C4	-2.28	104.17	109.38
3	F	104	CIT	O1-C1-C2	-2.18	116.77	122.95
3	B	103	CIT	O7-C3-C2	-2.18	104.41	109.38
3	B	103	CIT	O4-C5-C4	2.17	121.23	114.35
3	D	103	CIT	O2-C1-C2	2.15	121.15	114.35
3	D	103	CIT	O4-C5-O3	-2.14	117.83	123.33
3	C	104	CIT	C4-C3-C2	2.13	114.77	109.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	104	CIT	C4-C3-C6	-2.12	105.35	110.03
3	D	103	CIT	O6-C6-O5	-2.09	117.18	123.86
3	C	104	CIT	O4-C5-O3	-2.00	118.18	123.33

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	104	CIT	C2-C3-C6-O5
3	F	104	CIT	C2-C3-C6-O6
3	F	104	CIT	O7-C3-C6-O5
3	F	104	CIT	O7-C3-C6-O6
3	B	103	CIT	C4-C3-C6-O6
3	F	104	CIT	O7-C3-C4-C5
3	F	104	CIT	C2-C3-C4-C5
3	B	103	CIT	C4-C3-C6-O5
2	A	103	EDO	O1-C1-C2-O2
3	B	103	CIT	O7-C3-C4-C5
3	B	103	CIT	O2-C1-C2-C3
3	B	103	CIT	C6-C3-C4-C5
3	C	104	CIT	O1-C1-C2-C3
3	C	104	CIT	O2-C1-C2-C3
3	B	103	CIT	O1-C1-C2-C3
2	C	103	EDO	O1-C1-C2-O2
3	B	103	CIT	C2-C3-C6-O6

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	104	CIT	2	0
3	D	103	CIT	1	0
3	B	103	CIT	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	97/121 (80%)	-0.05	3 (3%) 51 53	19, 37, 52, 57	2 (2%)
1	B	97/121 (80%)	-0.08	2 (2%) 63 65	32, 38, 53, 61	0
1	C	97/121 (80%)	-0.16	0 100 100	32, 37, 53, 57	0
1	D	102/121 (84%)	0.02	2 (1%) 65 66	32, 38, 52, 58	0
1	E	98/121 (80%)	-0.01	5 (5%) 33 35	22, 38, 54, 63	1 (1%)
1	F	97/121 (80%)	0.01	2 (2%) 63 65	32, 37, 52, 57	0
All	All	588/726 (80%)	-0.04	14 (2%) 59 62	19, 38, 53, 63	3 (0%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	-1	GLN	4.6
1	E	13	GLU	3.6
1	F	13	GLU	3.5
1	A	0	GLY	3.2
1	E	12	GLY	3.1
1	F	0	GLY	3.0
1	B	13	GLU	2.9
1	E	11	GLU	2.6
1	D	0	GLY	2.6
1	D	-1	GLN	2.5
1	B	52	GLU	2.2
1	E	0	GLY	2.2
1	A	13	GLU	2.1
1	A	52	GLU	2.1

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	EDO	F	103	4/4	0.82	0.20	59,65,67,67	0
2	EDO	A	103	4/4	0.85	0.22	48,52,52,56	0
3	CIT	F	104	13/13	0.87	0.15	49,74,87,89	0
3	CIT	B	103	13/13	0.88	0.12	48,58,67,67	0
2	EDO	C	103	4/4	0.88	0.25	54,57,62,67	0
3	CIT	C	104	13/13	0.89	0.15	51,74,84,87	0
3	CIT	D	103	13/13	0.91	0.12	55,76,86,89	0
3	CIT	E	104	13/13	0.91	0.13	45,63,74,82	0
2	EDO	E	103	4/4	0.91	0.19	47,48,54,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.