



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 09:34 am BST

PDB ID : 5V3J
Title : mouseZFP568-ZnF1-10 in complex with DNA
Authors : Patel, A.; Cheng, X.
Deposited on : 2017-03-07
Resolution : 2.06 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

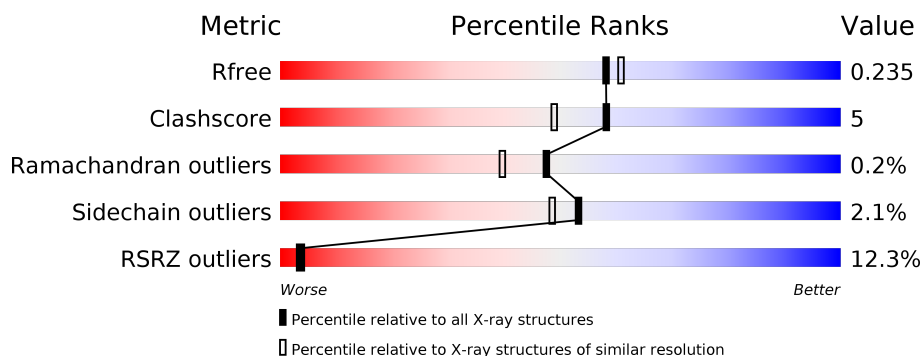
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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	26	<div> <div>73%</div> <div>23%</div> <div>.</div> </div>
1	C	26	<div> <div>81%</div> <div>15%</div> <div>.</div> </div>
2	B	26	<div> <div>81%</div> <div>19%</div> <div>.</div> </div>
2	D	26	<div> <div>58%</div> <div>38%</div> <div>.</div> </div>
3	E	284	<div> <div>12%</div> <div>86%</div> <div>11%</div> <div>.</div> </div>
3	F	284	<div> <div>16%</div> <div>86%</div> <div>11%</div> <div>..</div> </div>

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6727 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 DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	26	Total	C	N	O	P	0	0	0
			544	256	113	150	25			
1	C	26	Total	C	N	O	P	0	0	0
			544	256	113	150	25			

- Molecule 2 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	26	Total	C	N	O	P	0	0	0
			519	248	85	160	26			
2	D	26	Total	C	N	O	P	0	0	0
			516	248	85	158	25			

- Molecule 3 is a protein called Zinc finger protein 568.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	277	Total	C	N	O	S	0	0	0
			2093	1278	416	374	25			
3	F	278	Total	C	N	O	S	0	2	0
			2115	1291	421	378	25			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	358	GLY	-	expression tag	UNP E9PYI1
E	359	PRO	-	expression tag	UNP E9PYI1
E	360	GLY	-	expression tag	UNP E9PYI1
E	361	SER	-	expression tag	UNP E9PYI1
E	641	LYS	-	expression tag	UNP E9PYI1
F	358	GLY	-	expression tag	UNP E9PYI1
F	359	PRO	-	expression tag	UNP E9PYI1
F	360	GLY	-	expression tag	UNP E9PYI1

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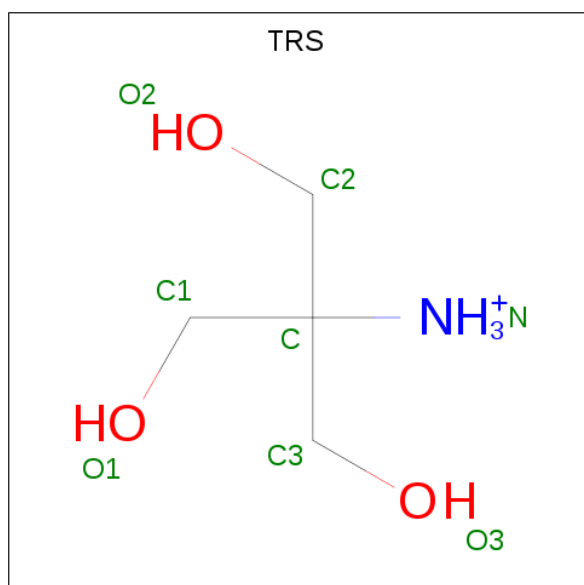
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Chain	Residue	Modelled	Actual	Comment	Reference
F	361	SER	-	expression tag	UNP E9PYI1
F	641	LYS	-	expression tag	UNP E9PYI1

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	10	Total	Zn	0	0
			10	10		
4	E	10	Total	Zn	0	0
			10	10		

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	E	1	Total	C	N	O	0	0
			8	4	1	3		
5	F	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	1	Total	Mg	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	38	Total	O	0	0
			38	38		
7	B	28	Total	O	0	0
			28	28		
7	C	39	Total	O	0	0
			39	39		
7	D	31	Total	O	0	0
			31	31		
7	E	87	Total	O	0	0
			87	87		
7	F	135	Total	O	0	0
			135	135		

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: DNA (26-MER)

Chain A: 




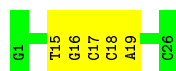
- Molecule 1: DNA (26-MER)

Chain C: 



- Molecule 2: DNA (26-MER)

Chain B: 




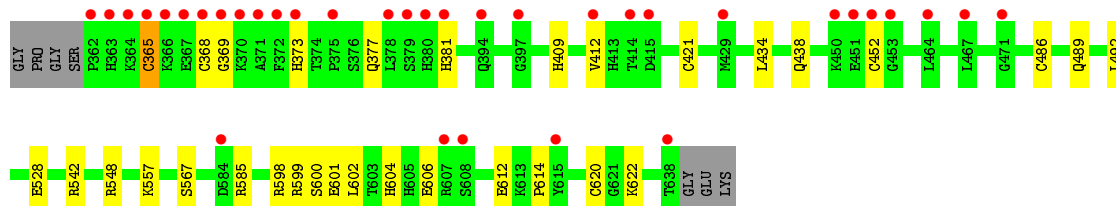
- Molecule 2: DNA (26-MER)

Chain D: 

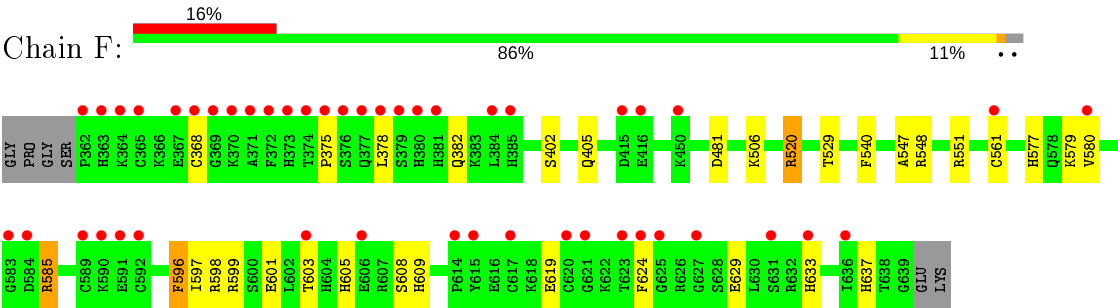


- Molecule 3: Zinc finger protein 568

Chain E: 



● Molecule 3: Zinc finger protein 568



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.79Å 65.71Å 73.02Å 100.52° 104.25° 97.25°	Depositor
Resolution (Å)	34.50 – 2.06 34.50 – 2.06	Depositor EDS
% Data completeness (in resolution range)	97.3 (34.50-2.06) 97.4 (34.50-2.06)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.06Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, R_{free}	0.192 , 0.237 0.192 , 0.235	Depositor DCC
R_{free} test set	1996 reflections (3.43%)	wwPDB-VP
Wilson B-factor (Å ²)	38.7	Xtriage
Anisotropy	0.262	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6727	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.91	0/614	0.96	1/949 (0.1%)
1	C	0.93	0/614	1.06	2/949 (0.2%)
2	B	0.84	0/577	0.99	0/885
2	D	1.01	1/574 (0.2%)	1.08	0/881
3	E	0.39	0/2148	0.55	0/2887
3	F	0.44	0/2175	0.63	2/2919 (0.1%)
All	All	0.65	1/6702 (0.0%)	0.78	5/9470 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	15	DT	C4'-O4'	-5.24	1.39	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	16	DG	O5'-P-OP1	9.93	122.62	110.70
3	F	520	ARG	NE-CZ-NH2	-7.09	116.75	120.30
1	A	16	DG	O5'-P-OP1	5.58	117.39	110.70
3	F	520	ARG	CG-CD-NE	-5.41	100.45	111.80
1	C	13	DC	O4'-C4'-C3'	-5.25	102.40	104.50

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	544	0	291	5	0
1	C	544	0	291	2	0
2	B	519	0	294	3	0
2	D	516	0	295	6	0
3	E	2093	0	1880	18	0
3	F	2115	0	1915	21	0
4	E	10	0	0	0	0
4	F	10	0	0	0	0
5	E	8	0	11	0	0
5	F	8	0	12	2	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
7	A	38	0	0	1	1
7	B	28	0	0	1	0
7	C	39	0	0	0	0
7	D	31	0	0	0	0
7	E	87	0	0	1	0
7	F	135	0	0	3	1
All	All	6727	0	4989	54	1

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 (54) 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)
3:F:405[B]:GLN:NE2	7:F:1101:HOH:O	2.05	0.89
2:D:15:DT:H2'	2:D:16:DG:C8	2.23	0.74
3:E:598:ARG:HG3	3:E:601:GLU:OE1	1.93	0.68
3:E:602:LEU:O	3:E:606:GLU:HG2	1.92	0.68
3:F:624:PHE:CD2	3:F:629:GLU:HB3	2.29	0.66
3:E:599:ARG:NH2	7:E:1103:HOH:O	2.28	0.66
3:F:624:PHE:HD2	3:F:629:GLU:HB3	1.62	0.64
3:E:486:CYS:SG	3:E:489:GLN:HG3	2.37	0.64
3:F:579:LYS:HD2	3:F:597:ILE:HG23	1.82	0.61
3:E:600:SER:O	3:E:604:HIS:ND1	2.36	0.58
3:F:596:PHE:CD2	3:F:596:PHE:N	2.72	0.57
3:F:375:PRO:HA	3:F:378:LEU:HB3	1.87	0.57
3:F:605:HIS:CE1	3:F:609:HIS:HE2	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:598:ARG:HG3	3:F:601:GLU:OE1	2.05	0.56
3:F:378:LEU:O	3:F:382:GLN:N	2.35	0.55
2:D:22:DC:H2'	2:D:23:DC:C6	2.42	0.55
2:D:17:DC:H2'	2:D:18:DC:C6	2.42	0.54
2:B:17:DC:H2'	2:B:18:DC:C6	2.44	0.52
3:F:619:GLU:HB3	3:F:637:HIS:CD2	2.44	0.52
2:B:19:DA:OP2	7:B:101:HOH:O	2.19	0.52
3:E:368:CYS:SG	3:E:381:HIS:NE2	2.83	0.49
2:B:15:DT:H2'	2:B:16:DG:C8	2.48	0.48
1:C:16:DG:H2'	1:C:17:DT:C6	2.49	0.48
3:F:548:ARG:NH1	7:F:1105:HOH:O	2.42	0.47
1:C:2:DT:H2''	1:C:3:DG:C8	2.50	0.47
1:A:8:DT:OP1	3:E:585:ARG:NH2	2.48	0.47
3:E:373:HIS:HB2	3:E:377:GLN:OE1	2.16	0.46
3:F:585:ARG:HD2	3:F:597:ILE:HD13	1.97	0.46
1:A:2:DT:H2''	1:A:3:DG:C8	2.51	0.46
3:E:409:HIS:O	3:E:412:VAL:HG22	2.16	0.45
3:F:577:HIS:O	3:F:580:VAL:HG22	2.17	0.45
3:F:605:HIS:O	3:F:608:SER:HB3	2.17	0.44
3:F:529:THR:HB	3:F:540:PHE:N	2.33	0.44
2:D:4:DC:H2'	2:D:5:DT:H72	1.99	0.44
3:F:481:ASP:OD2	5:F:1011:TRS:O2	2.35	0.44
3:F:585:ARG:NH1	3:F:597:ILE:HD11	2.33	0.44
3:F:633:HIS:CE1	3:F:637:HIS:CE1	3.06	0.44
3:F:599:ARG:O	3:F:603:THR:HG23	2.18	0.43
3:E:557:LYS:HD3	3:E:567:SER:O	2.19	0.43
2:D:20:DC:H2''	2:D:21:DG:C8	2.53	0.43
7:A:114:HOH:O	3:E:542:ARG:HG3	2.18	0.43
2:D:23:DC:H2'	2:D:24:DC:C6	2.53	0.43
3:E:421:CYS:HB2	3:E:434:LEU:CD1	2.49	0.42
1:A:12:DA:OP2	3:E:548:ARG:NH2	2.35	0.42
3:E:434:LEU:O	3:E:438:GLN:HG3	2.19	0.42
3:E:612:GLU:O	3:E:614:PRO:HD3	2.20	0.42
1:A:16:DG:H2'	1:A:17:DT:C6	2.54	0.42
3:E:365:CYS:O	3:E:369:GLY:HA2	2.20	0.42
3:F:402:SER:OG	3:F:405[B]:GLN:HG2	2.19	0.41
3:F:547:ALA:O	3:F:551:ARG:HG3	2.20	0.41
5:F:1011:TRS:H22	7:F:1141:HOH:O	2.20	0.41
3:E:606:GLU:OE2	3:E:606:GLU:HA	2.20	0.41
3:E:620:CYS:SG	3:E:622:LYS:HD2	2.61	0.41
1:A:1:DG:H1'	1:A:2:DT:H5'	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:134:HOH:O	7:F:1151:HOH:O[1_455]	2.18	0.02

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	
3	E	275/284 (97%)	270 (98%)	5 (2%)	0	100	100
3	F	278/284 (98%)	272 (98%)	5 (2%)	1 (0%)	34	25
All	All	553/568 (97%)	542 (98%)	10 (2%)	1 (0%)	47	39

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	368	CYS

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	
3	E	210/247 (85%)	206 (98%)	4 (2%)	57	53
3	F	213/247 (86%)	208 (98%)	5 (2%)	50	45
All	All	423/494 (86%)	414 (98%)	9 (2%)	53	48

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	365	CYS
3	E	452	CYS
3	E	492	LEU
3	E	528	GLU
3	F	506	LYS
3	F	520	ARG
3	F	561	CYS
3	F	585	ARG
3	F	596	PHE

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

Mol	Chain	Res	Type
3	E	503	HIS
3	F	438	GLN
3	F	494	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 24 ligands modelled in this entry, 22 are monoatomic - leaving 2 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	$\# Z > 2$
5	TRS	F	1011	-	7,7,7	0.28	0	9,9,9	0.36	0
5	TRS	E	1011	6	7,7,7	0.30	0	9,9,9	0.26	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
5	TRS	F	1011	-	-	5/9/9/9	-
5	TRS	E	1011	6	-	3/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	1011	TRS	N-C-C3-O3
5	F	1011	TRS	N-C-C2-O2
5	E	1011	TRS	C2-C-C3-O3
5	E	1011	TRS	N-C-C3-O3
5	F	1011	TRS	C1-C-C2-O2
5	F	1011	TRS	C3-C-C2-O2
5	E	1011	TRS	C1-C-C3-O3
5	F	1011	TRS	C1-C-C3-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	1011	TRS	2	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 ⓘ

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	26/26 (100%)	0.05	0	100 100	36, 49, 87, 98	0
1	C	26/26 (100%)	0.20	0	100 100	28, 49, 104, 120	0
2	B	26/26 (100%)	0.04	0	100 100	35, 59, 93, 102	0
2	D	26/26 (100%)	0.14	0	100 100	27, 63, 107, 113	0
3	E	277/284 (97%)	0.64	35 (12%)	3 3	35, 59, 100, 140	0
3	F	278/284 (97%)	0.81	46 (16%)	1 1	29, 55, 120, 140	0
All	All	659/672 (98%)	0.62	81 (12%)	4 3	27, 58, 110, 140	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	380	HIS	14.5
3	E	371	ALA	7.5
3	F	363	HIS	7.3
3	E	372	PHE	6.4
3	F	362	PRO	6.0
3	E	368	CYS	5.9
3	F	371	ALA	5.7
3	F	378	LEU	5.7
3	F	373	HIS	5.6
3	F	374	THR	5.6
3	F	368	CYS	5.6
3	F	384	LEU	5.2
3	E	365	CYS	5.1
3	F	372	PHE	5.0
3	E	363	HIS	4.9
3	E	380	HIS	4.9
3	F	369	GLY	4.8
3	E	452	CYS	4.8
3	F	615	TYR	4.8

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Mol	Chain	Res	Type	RSRZ
3	F	620	CYS	4.8
3	E	373	HIS	4.7
3	F	377	GLN	4.6
3	E	362	PRO	4.5
3	E	415	ASP	4.5
3	E	375	PRO	4.4
3	F	364	LYS	4.3
3	F	625	GLY	4.2
3	F	415	ASP	4.0
3	E	429	MET	3.7
3	F	603	THR	3.7
3	E	364	LYS	3.7
3	F	590	LYS	3.7
3	F	375	PRO	3.6
3	E	367	GLU	3.6
3	F	365	CYS	3.5
3	F	589	CYS	3.5
3	E	370	LYS	3.5
3	E	378	LEU	3.5
3	F	636	ILE	3.4
3	F	379	SER	3.3
3	E	366	LYS	3.3
3	E	369	GLY	3.3
3	E	450	LYS	3.3
3	E	397	GLY	3.2
3	F	580	VAL	3.2
3	E	381	HIS	3.1
3	F	614	PRO	3.1
3	E	412	VAL	3.1
3	F	381	HIS	3.0
3	F	561	CYS	3.0
3	F	367	GLU	3.0
3	F	621	GLY	3.0
3	F	624	PHE	2.9
3	F	385	HIS	2.9
3	E	414	THR	2.9
3	F	370	LYS	2.9
3	F	633	HIS	2.8
3	E	453	GLY	2.8
3	E	471	GLY	2.8
3	F	606	GLU	2.8
3	F	631[A]	SER	2.7

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Mol	Chain	Res	Type	RSRZ
3	E	464	LEU	2.7
3	F	376	SER	2.6
3	F	591	GLU	2.6
3	E	638	THR	2.6
3	E	451	GLU	2.6
3	E	584	ASP	2.5
3	E	607	ARG	2.5
3	F	592	CYS	2.5
3	F	450	LYS	2.5
3	F	627	GLY	2.4
3	E	394	GLN	2.4
3	E	615	TYR	2.4
3	F	623	THR	2.3
3	F	416	GLU	2.3
3	E	467	LEU	2.2
3	F	617	CYS	2.2
3	F	583	GLY	2.1
3	E	379	SER	2.1
3	E	608	SER	2.1
3	F	584	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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(\AA^2)	Q<0.9
5	TRS	F	1011	8/8	0.60	0.27	69,82,85,86	0
4	ZN	F	1009	1/1	0.78	0.05	74,74,74,74	0
5	TRS	E	1011	8/8	0.79	0.21	92,101,102,109	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	ZN	E	1001	1/1	0.80	0.07	97,97,97,97	0
4	ZN	F	1008	1/1	0.94	0.06	70,70,70,70	0
4	ZN	F	1010	1/1	0.94	0.05	85,85,85,85	0
6	MG	E	1012	1/1	0.95	0.10	60,60,60,60	0
4	ZN	E	1003	1/1	0.96	0.10	51,51,51,51	0
4	ZN	F	1001	1/1	0.96	0.09	94,94,94,94	0
4	ZN	E	1008	1/1	0.97	0.07	57,57,57,57	0
4	ZN	F	1003	1/1	0.98	0.11	39,39,39,39	0
6	MG	F	1012	1/1	0.98	0.07	55,55,55,55	0
4	ZN	E	1002	1/1	0.98	0.07	70,70,70,70	0
4	ZN	F	1007	1/1	0.98	0.06	55,55,55,55	0
4	ZN	F	1005	1/1	0.99	0.10	37,37,37,37	0
4	ZN	E	1004	1/1	0.99	0.06	69,69,69,69	0
4	ZN	F	1006	1/1	0.99	0.10	45,45,45,45	0
4	ZN	F	1002	1/1	0.99	0.09	40,40,40,40	0
4	ZN	E	1010	1/1	0.99	0.06	44,44,44,44	0
4	ZN	E	1005	1/1	0.99	0.12	46,46,46,46	0
4	ZN	E	1009	1/1	0.99	0.08	64,64,64,64	0
4	ZN	E	1007	1/1	0.99	0.06	56,56,56,56	0
4	ZN	E	1006	1/1	1.00	0.07	46,46,46,46	0
4	ZN	F	1004	1/1	1.00	0.09	42,42,42,42	0

6.5 Other polymers

There are no such residues in this entry.