Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 07:48 PM GMT

PDB ID	:	4PZO
Title	:	Crystal structure of PHC3 SAM L967R
Authors	:	Nanyes, D.R.; Junco, S.E.; Taylor, A.B.; Robinson, A.K.; Patterson, N.L.; Shivarajpur, A.; Halloran, J.; Hale, S.M.; Kaur, Y.; Hart, P.J.; Kim, C.A.
Deposited on	:	2014-03-31
Resolution	:	2.25 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

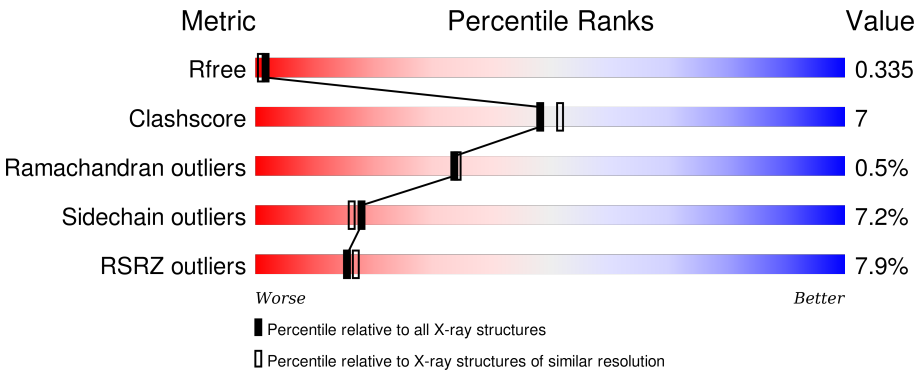
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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 <=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	82	9% 72% 15% 13%
1	B	82	5% 68% 12% 6% 13%
1	C	82	10% 67% 15% 5% 13%
1	D	82	9% 71% 13% • 15%
1	E	82	76% 11% • 12%

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Mol	Chain	Length	Quality of chain
1	F	82	9% 66% 20% • 13%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3488 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 Polyhomeotic-like protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	71	564	355	98	106	5	0	0	0
1	B	71	564	355	98	106	5	0	0	0
1	C	71	565	356	98	106	5	0	0	0
1	D	70	553	349	94	105	5	0	0	0
1	E	72	571	359	99	108	5	0	0	0
1	F	71	564	355	98	106	5	0	0	0

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	909	MET	-	INITIATING METHIONINE	UNP Q8NDX5
A	910	GLU	-	EXPRESSION TAG	UNP Q8NDX5
A	911	LYS	-	EXPRESSION TAG	UNP Q8NDX5
A	912	THR	-	EXPRESSION TAG	UNP Q8NDX5
A	913	ARG	-	EXPRESSION TAG	UNP Q8NDX5
A	967	ARG	LEU	ENGINEERED MUTATION	UNP Q8NDX5
A	984	ARG	-	EXPRESSION TAG	UNP Q8NDX5
A	985	HIS	-	EXPRESSION TAG	UNP Q8NDX5
A	986	HIS	-	EXPRESSION TAG	UNP Q8NDX5
A	987	HIS	-	EXPRESSION TAG	UNP Q8NDX5
A	988	HIS	-	EXPRESSION TAG	UNP Q8NDX5
A	989	HIS	-	EXPRESSION TAG	UNP Q8NDX5
A	990	HIS	-	EXPRESSION TAG	UNP Q8NDX5
B	909	MET	-	INITIATING METHIONINE	UNP Q8NDX5
B	910	GLU	-	EXPRESSION TAG	UNP Q8NDX5
B	911	LYS	-	EXPRESSION TAG	UNP Q8NDX5
B	912	THR	-	EXPRESSION TAG	UNP Q8NDX5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	913	ARG	-	EXPRESSION TAG	UNP Q8NDX5
B	967	ARG	LEU	ENGINEERED MUTATION	UNP Q8NDX5
B	984	ARG	-	EXPRESSION TAG	UNP Q8NDX5
B	985	HIS	-	EXPRESSION TAG	UNP Q8NDX5
B	986	HIS	-	EXPRESSION TAG	UNP Q8NDX5
B	987	HIS	-	EXPRESSION TAG	UNP Q8NDX5
B	988	HIS	-	EXPRESSION TAG	UNP Q8NDX5
B	989	HIS	-	EXPRESSION TAG	UNP Q8NDX5
B	990	HIS	-	EXPRESSION TAG	UNP Q8NDX5
C	909	MET	-	INITIATING METHIONINE	UNP Q8NDX5
C	910	GLU	-	EXPRESSION TAG	UNP Q8NDX5
C	911	LYS	-	EXPRESSION TAG	UNP Q8NDX5
C	912	THR	-	EXPRESSION TAG	UNP Q8NDX5
C	913	ARG	-	EXPRESSION TAG	UNP Q8NDX5
C	967	ARG	LEU	ENGINEERED MUTATION	UNP Q8NDX5
C	984	ARG	-	EXPRESSION TAG	UNP Q8NDX5
C	985	HIS	-	EXPRESSION TAG	UNP Q8NDX5
C	986	HIS	-	EXPRESSION TAG	UNP Q8NDX5
C	987	HIS	-	EXPRESSION TAG	UNP Q8NDX5
C	988	HIS	-	EXPRESSION TAG	UNP Q8NDX5
C	989	HIS	-	EXPRESSION TAG	UNP Q8NDX5
C	990	HIS	-	EXPRESSION TAG	UNP Q8NDX5
D	909	MET	-	INITIATING METHIONINE	UNP Q8NDX5
D	910	GLU	-	EXPRESSION TAG	UNP Q8NDX5
D	911	LYS	-	EXPRESSION TAG	UNP Q8NDX5
D	912	THR	-	EXPRESSION TAG	UNP Q8NDX5
D	913	ARG	-	EXPRESSION TAG	UNP Q8NDX5
D	967	ARG	LEU	ENGINEERED MUTATION	UNP Q8NDX5
D	984	ARG	-	EXPRESSION TAG	UNP Q8NDX5
D	985	HIS	-	EXPRESSION TAG	UNP Q8NDX5
D	986	HIS	-	EXPRESSION TAG	UNP Q8NDX5
D	987	HIS	-	EXPRESSION TAG	UNP Q8NDX5
D	988	HIS	-	EXPRESSION TAG	UNP Q8NDX5
D	989	HIS	-	EXPRESSION TAG	UNP Q8NDX5
D	990	HIS	-	EXPRESSION TAG	UNP Q8NDX5
E	909	MET	-	INITIATING METHIONINE	UNP Q8NDX5
E	910	GLU	-	EXPRESSION TAG	UNP Q8NDX5
E	911	LYS	-	EXPRESSION TAG	UNP Q8NDX5
E	912	THR	-	EXPRESSION TAG	UNP Q8NDX5
E	913	ARG	-	EXPRESSION TAG	UNP Q8NDX5
E	967	ARG	LEU	ENGINEERED MUTATION	UNP Q8NDX5
E	984	ARG	-	EXPRESSION TAG	UNP Q8NDX5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	985	HIS	-	EXPRESSION TAG	UNP Q8NDX5
E	986	HIS	-	EXPRESSION TAG	UNP Q8NDX5
E	987	HIS	-	EXPRESSION TAG	UNP Q8NDX5
E	988	HIS	-	EXPRESSION TAG	UNP Q8NDX5
E	989	HIS	-	EXPRESSION TAG	UNP Q8NDX5
E	990	HIS	-	EXPRESSION TAG	UNP Q8NDX5
F	909	MET	-	INITIATING METHIONINE	UNP Q8NDX5
F	910	GLU	-	EXPRESSION TAG	UNP Q8NDX5
F	911	LYS	-	EXPRESSION TAG	UNP Q8NDX5
F	912	THR	-	EXPRESSION TAG	UNP Q8NDX5
F	913	ARG	-	EXPRESSION TAG	UNP Q8NDX5
F	967	ARG	LEU	ENGINEERED MUTATION	UNP Q8NDX5
F	984	ARG	-	EXPRESSION TAG	UNP Q8NDX5
F	985	HIS	-	EXPRESSION TAG	UNP Q8NDX5
F	986	HIS	-	EXPRESSION TAG	UNP Q8NDX5
F	987	HIS	-	EXPRESSION TAG	UNP Q8NDX5
F	988	HIS	-	EXPRESSION TAG	UNP Q8NDX5
F	989	HIS	-	EXPRESSION TAG	UNP Q8NDX5
F	990	HIS	-	EXPRESSION TAG	UNP Q8NDX5

- Molecule 2 is water.

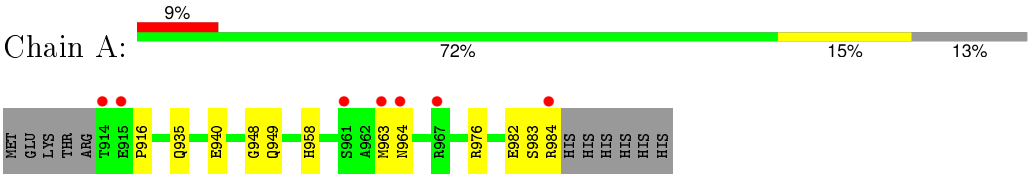
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	17	17	17	0	0
			Total	O		
2	B	22	22	22	0	0
			Total	O		
2	C	12	12	12	0	0
			Total	O		
2	D	14	14	14	0	0
			Total	O		
2	E	25	25	25	0	0
			Total	O		
2	F	17	17	17	0	0

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 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 (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.

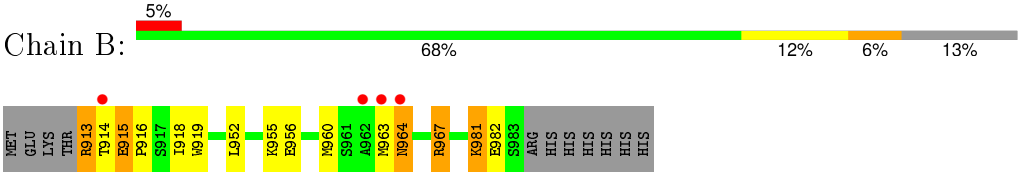
- Molecule 1: Polyhomeotic-like protein 3

Chain A:



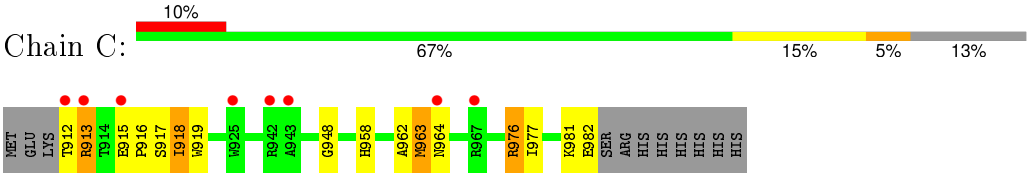
- Molecule 1: Polyhomeotic-like protein 3

Chain B:



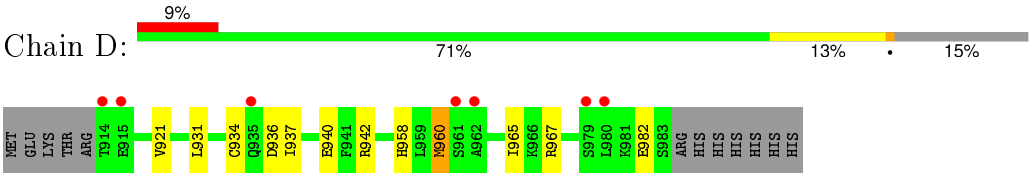
- Molecule 1: Polyhomeotic-like protein 3

Chain C:



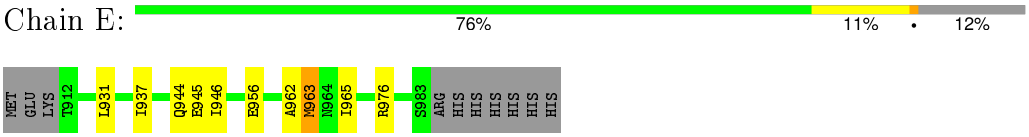
- Molecule 1: Polyhomeotic-like protein 3

Chain D:



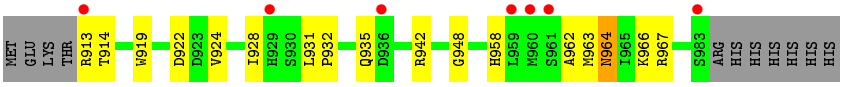
- Molecule 1: Polyhomeotic-like protein 3

Chain E:



- Molecule 1: Polyhomeotic-like protein 3

Chain F:


MET
GLU
LYS
THR
R913
T914
W919
D922
D923
V924
I928
H929
S930
L931
P932
Q935
D936
R942
G948
H958
L959
N960
S961
A962
N963
N964
I965
K966
R967
S983
ARG
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	123.94Å 51.74Å 124.02Å 90.00° 119.71° 90.00°	Depositor
Resolution (Å)	40.56 – 2.25 40.56 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.56-2.25) 99.8 (40.56-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	2.04 (at 2.24Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.282 , 0.335 0.282 , 0.335	Depositor DCC
R_{free} test set	1998 reflections (6.11%)	DCC
Wilson B-factor (Å^2)	38.9	Xtriage
Anisotropy	0.687	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 48.6	EDS
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Outliers	1 of 32704 reflections (0.003%)	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	3488	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 73.16 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.9334e-06.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: CME

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	0.24	0/563	0.43	0/759
1	B	0.21	0/563	0.35	0/759
1	C	0.21	0/564	0.38	0/761
1	D	0.21	0/552	0.35	0/745
1	E	0.20	0/570	0.35	0/769
1	F	0.21	0/563	0.40	0/759
All	All	0.22	0/3375	0.38	0/4552

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	564	0	564	6	0
1	B	564	0	564	11	0
1	C	565	0	566	14	0
1	D	553	0	551	12	0
1	E	571	0	571	8	0
1	F	564	0	564	11	0
2	A	17	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	22	0	0	1	0
2	C	12	0	0	0	0
2	D	14	0	0	0	0
2	E	25	0	0	0	0
2	F	17	0	0	0	0
All	All	3488	0	3380	49	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 7.

All (49) 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:A:958:HIS:NE2	1:B:956:GLU:OE2	2.24	0.70
1:C:915:GLU:HG3	1:C:917:SER:H	1.57	0.70
1:E:963:MET:HB2	1:E:965:ILE:HG13	1.80	0.63
1:E:944:GLN:HE21	1:F:967:ARG:HG2	1.66	0.61
1:B:963:MET:O	1:B:964:ASN:ND2	2.34	0.60
1:B:952:LEU:HD22	1:B:981:LYS:HD2	1.82	0.60
1:E:944:GLN:HA	1:F:966:LYS:HG2	1.83	0.60
1:B:915:GLU:HG2	1:B:916:PRO:HD2	1.83	0.59
1:D:958:HIS:NE2	1:E:956:GLU:OE2	2.35	0.59
1:D:937:ILE:HD12	1:D:940:GLU:HB3	1.86	0.57
1:C:976:ARG:HA	1:C:976:ARG:HE	1.69	0.56
1:B:914:THR:HG23	1:B:919:TRP:HE1	1.69	0.56
1:C:963:MET:CE	1:D:967:ARG:HD2	2.37	0.55
1:C:963:MET:CE	1:D:967:ARG:CD	2.85	0.55
1:F:922:ASP:OD1	1:F:942:ARG:NH2	2.40	0.54
1:F:958:HIS:HA	1:F:962:ALA:HB3	1.88	0.54
1:C:919:TRP:HB2	1:C:948:GLY:HA3	1.91	0.52
1:E:962:ALA:O	1:F:967:ARG:NH2	2.42	0.52
1:D:931:LEU:HB2	1:D:934:CYS:HB2	1.92	0.51
1:B:913:ARG:HA	1:B:913:ARG:HH11	1.78	0.49
1:C:977:ILE:HG22	1:C:981:LYS:HE3	1.96	0.47
1:B:960:MET:SD	1:B:967:ARG:HG2	2.53	0.47
1:E:931:LEU:HD22	1:E:976:ARG:HG3	1.96	0.47
1:F:919:TRP:HB2	1:F:948:GLY:HA3	1.96	0.47
1:C:958:HIS:O	1:C:962:ALA:HB3	2.14	0.46
1:D:937:ILE:HD13	1:D:965:ILE:CD1	2.45	0.46
1:A:916:PRO:O	1:A:948:GLY:HA3	2.16	0.46
1:C:963:MET:HE3	1:D:967:ARG:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:913:ARG:HB2	1:C:918:ILE:HD11	1.97	0.46
1:A:940:GLU:OE2	2:A:1008:HOH:O	2.20	0.45
1:F:964:ASN:ND2	1:F:964:ASN:O	2.43	0.45
1:E:946:ILE:HD11	1:E:963:MET:HE3	1.99	0.45
1:D:921:VAL:HG12	1:D:942:ARG:HG3	1.98	0.45
1:A:976:ARG:HD3	1:A:976:ARG:HA	1.69	0.45
1:C:916:PRO:HA	1:C:919:TRP:CD1	2.51	0.44
1:B:955:LYS:HD3	1:B:955:LYS:HA	1.81	0.44
1:C:963:MET:CE	1:D:967:ARG:HD3	2.48	0.43
1:B:915:GLU:O	1:B:918:ILE:HG12	2.19	0.42
1:A:963:MET:SD	1:B:967:ARG:HG3	2.59	0.42
1:F:942:ARG:HH11	1:F:942:ARG:HB3	1.84	0.41
1:C:912:THR:OG1	1:C:913:ARG:N	2.53	0.41
1:C:963:MET:HE1	1:D:967:ARG:HD2	2.02	0.41
1:D:937:ILE:HD13	1:D:965:ILE:HD11	2.02	0.41
1:E:945:GLU:HG3	1:F:966:LYS:HD2	2.02	0.41
1:F:931:LEU:HA	1:F:932:PRO:HD3	1.88	0.41
1:A:949:GLN:NE2	2:A:1007:HOH:O	2.49	0.41
1:B:981:LYS:NZ	2:B:1001:HOH:O	2.54	0.41
1:F:924:VAL:O	1:F:928:ILE:HG12	2.20	0.41
1:C:963:MET:HE3	1:D:967:ARG:CD	2.50	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	68/82 (83%)	64 (94%)	3 (4%)	1 (2%)	13 8
1	B	68/82 (83%)	65 (96%)	3 (4%)	0	100 100
1	C	68/82 (83%)	65 (96%)	3 (4%)	0	100 100
1	D	67/82 (82%)	66 (98%)	0	1 (2%)	13 8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	69/82 (84%)	69 (100%)	0	0	100	100
1	F	68/82 (83%)	67 (98%)	1 (2%)	0	100	100
All	All	408/492 (83%)	396 (97%)	10 (2%)	2 (0%)	34	34

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	982	GLU
1	D	960	MET

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	60/71 (84%)	56 (93%)	4 (7%)	20	19
1	B	60/71 (84%)	54 (90%)	6 (10%)	9	7
1	C	60/71 (84%)	54 (90%)	6 (10%)	9	7
1	D	59/71 (83%)	56 (95%)	3 (5%)	29	32
1	E	61/71 (86%)	59 (97%)	2 (3%)	45	56
1	F	60/71 (84%)	55 (92%)	5 (8%)	14	12
All	All	360/426 (84%)	334 (93%)	26 (7%)	18	16

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	935	GLN
1	A	964	ASN
1	A	983	SER
1	A	984	ARG
1	B	913	ARG
1	B	915	GLU
1	B	964	ASN
1	B	967	ARG

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Mol	Chain	Res	Type
1	B	981	LYS
1	B	982	GLU
1	C	913	ARG
1	C	918	ILE
1	C	963	MET
1	C	964	ASN
1	C	976	ARG
1	C	982	GLU
1	D	936	ASP
1	D	960	MET
1	D	982	GLU
1	E	937	ILE
1	E	963	MET
1	F	913	ARG
1	F	914	THR
1	F	935	GLN
1	F	963	MET
1	F	964	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	944	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)

6 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	CME	A	974	1	8,9,10	0.85	0	6,9,11	0.90	0
1	CME	B	974	1	8,9,10	0.86	0	6,9,11	0.79	0
1	CME	C	974	1	8,9,10	0.85	0	6,9,11	0.70	0
1	CME	D	974	1	8,9,10	0.87	0	6,9,11	0.78	0
1	CME	E	974	1	8,9,10	0.84	0	6,9,11	0.81	0
1	CME	F	974	1	8,9,10	0.86	0	6,9,11	0.74	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
1	CME	A	974	1	-	0/5/8/10	0/0/0/0
1	CME	B	974	1	-	0/5/8/10	0/0/0/0
1	CME	C	974	1	-	0/5/8/10	0/0/0/0
1	CME	D	974	1	-	0/5/8/10	0/0/0/0
1	CME	E	974	1	-	0/5/8/10	0/0/0/0
1	CME	F	974	1	-	0/5/8/10	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.

No monomer is involved in short contacts.

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 (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	70/82 (85%)	0.64	7 (10%) 9 10	24, 44, 79, 98	0
1	B	70/82 (85%)	0.62	4 (5%) 27 30	30, 41, 81, 105	0
1	C	70/82 (85%)	0.69	8 (11%) 7 6	35, 53, 82, 106	0
1	D	69/82 (84%)	0.73	7 (10%) 9 10	29, 48, 79, 99	0
1	E	71/82 (86%)	0.61	0 100 100	30, 44, 83, 89	0
1	F	70/82 (85%)	0.76	7 (10%) 9 10	36, 54, 85, 106	0
All	All	420/492 (85%)	0.67	33 (7%) 15 17	24, 48, 84, 106	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	914	THR	8.7
1	D	961	SER	7.1
1	F	961	SER	5.8
1	A	984	ARG	4.9
1	B	964	ASN	4.5
1	B	962	ALA	4.3
1	A	964	ASN	4.3
1	C	964	ASN	4.3
1	F	983	SER	3.9
1	F	913	ARG	3.7
1	F	960	MET	3.7
1	F	959	LEU	3.5
1	C	912	THR	3.3
1	D	980	LEU	3.1
1	F	936	ASP	2.9
1	B	914	THR	2.9
1	C	925	TRP	2.9
1	C	942	ARG	2.9
1	D	979	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	914	THR	2.8
1	C	967	ARG	2.8
1	D	962	ALA	2.6
1	A	963	MET	2.6
1	A	961	SER	2.5
1	C	915	GLU	2.4
1	F	929	HIS	2.3
1	A	967	ARG	2.3
1	A	915	GLU	2.2
1	D	915	GLU	2.2
1	D	935	GLN	2.2
1	C	943	ALA	2.1
1	B	963	MET	2.1
1	C	913	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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. 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
1	CME	A	974	10/11	0.93	0.11	-	32,44,59,60	0
1	CME	C	974	10/11	0.95	0.12	-	38,42,53,55	0
1	CME	E	974	10/11	0.95	0.12	-	33,47,56,57	0
1	CME	D	974	10/11	0.95	0.12	-	31,42,59,70	0
1	CME	F	974	10/11	0.89	0.13	-	33,46,66,70	0
1	CME	B	974	10/11	0.94	0.12	-	27,41,55,59	0

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.