



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 2, 2017 – 12:18 AM EDT

PDB ID : 4I5N
Title : Structural mechanism of trimeric PP2A holoenzyme involving PR70: insight for Cdc6 dephosphorylation
Authors : Wlodarchak, N.; Satyshur, K.A.; Guo, F.; Xing, Y.
Deposited on : unknown
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029824
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20029824

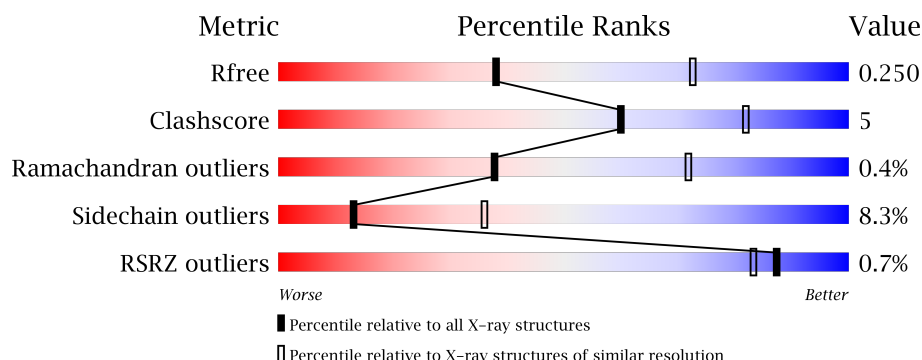
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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	584	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 100%; height: 10px; background-color: green; position: relative;"> % 81% 17% • </div> </div>
1	D	584	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 100%; height: 10px; background-color: green; position: relative;"> % 82% 17% • </div> </div>
2	B	413	<div> <div style="width: 100%; height: 10px; background-color: green; position: relative;"> 69% 15% • 14% </div> </div>
2	E	413	<div> <div style="width: 100%; height: 10px; background-color: green; position: relative;"> 69% 16% • 14% </div> </div>
3	C	311	<div> <div style="width: 100%; height: 10px; background-color: green; position: relative;"> 78% 14% • 6% </div> </div>

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Mol	Chain	Length	Quality of chain
3	F	311	<div><div></div><div>79%</div><div>13%</div><div>• • 5%</div></div>
4	G	7	<div><div></div><div>71%</div><div>29%</div></div>
4	H	7	<div><div></div><div>43%</div><div>57%</div></div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 19926 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 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	Se	0	0	0
			4534	2882	764	860	14	14			
1	D	582	Total	C	N	O	S	Se	0	0	0
			4534	2882	764	860	14	14			

- Molecule 2 is a protein called Serine/threonine-protein phosphatase 2A regulatory subunit B" subunit beta - Cell division control protein 6 homolog chimeric construct.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	355	Total	C	N	O	S	Se	0	0	0
			2890	1854	485	531	11	9			
2	E	357	Total	C	N	O	S	Se	0	0	0
			2906	1865	487	534	11	9			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	491	SER	-	LINKER	UNP Q9Y5P8
B	492	THR	-	LINKER	UNP Q9Y5P8
B	493	GLY	-	LINKER	UNP Q9Y5P8
B	494	ASN	-	LINKER	UNP Q9Y5P8
B	495	ALA	-	LINKER	UNP Q9Y5P8
B	496	SER	-	LINKER	UNP Q9Y5P8
B	497	ASP	-	LINKER	UNP Q9Y5P8
B	498	SER	-	LINKER	UNP Q9Y5P8
B	499	SER	-	LINKER	UNP Q9Y5P8
B	500	SER	-	LINKER	UNP Q9Y5P8
B	501	ASP	-	LINKER	UNP Q9Y5P8
B	502	SER	-	LINKER	UNP Q9Y5P8
B	503	SER	-	LINKER	UNP Q9Y5P8
B	504	SER	-	LINKER	UNP Q9Y5P8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	505	SER	-	LINKER	UNP Q9Y5P8
B	506	GLU	-	LINKER	UNP Q9Y5P8
B	507	GLY	-	LINKER	UNP Q9Y5P8
B	508	ASP	-	LINKER	UNP Q9Y5P8
B	509	GLY	-	LINKER	UNP Q9Y5P8
B	510	THR	-	LINKER	UNP Q9Y5P8
B	511	VAL	-	LINKER	UNP Q9Y5P8
E	491	SER	-	LINKER	UNP Q9Y5P8
E	492	THR	-	LINKER	UNP Q9Y5P8
E	493	GLY	-	LINKER	UNP Q9Y5P8
E	494	ASN	-	LINKER	UNP Q9Y5P8
E	495	ALA	-	LINKER	UNP Q9Y5P8
E	496	SER	-	LINKER	UNP Q9Y5P8
E	497	ASP	-	LINKER	UNP Q9Y5P8
E	498	SER	-	LINKER	UNP Q9Y5P8
E	499	SER	-	LINKER	UNP Q9Y5P8
E	500	SER	-	LINKER	UNP Q9Y5P8
E	501	ASP	-	LINKER	UNP Q9Y5P8
E	502	SER	-	LINKER	UNP Q9Y5P8
E	503	SER	-	LINKER	UNP Q9Y5P8
E	504	SER	-	LINKER	UNP Q9Y5P8
E	505	SER	-	LINKER	UNP Q9Y5P8
E	506	GLU	-	LINKER	UNP Q9Y5P8
E	507	GLY	-	LINKER	UNP Q9Y5P8
E	508	ASP	-	LINKER	UNP Q9Y5P8
E	509	GLY	-	LINKER	UNP Q9Y5P8
E	510	THR	-	LINKER	UNP Q9Y5P8
E	511	VAL	-	LINKER	UNP Q9Y5P8

- Molecule 3 is a protein called Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform, PP2A-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	293	Total	C	N	O	S	0	0	0
			2366	1497	405	449	15			
3	F	294	Total	C	N	O	S	0	0	0
			2373	1501	409	448	15			

- Molecule 4 is a protein called Microcystin-LR (MCLR) bound form.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	7	Total	C	N	O	0	0	0
			71	49	10	12			
4	H	7	Total	C	N	O	0	0	0
			71	49	10	12			

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Ca	0	0
			2	2		
5	E	2	Total	Ca	0	0
			2	2		

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	2	Total	Mn	0	0
			2	2		
6	F	2	Total	Mn	0	0
			2	2		

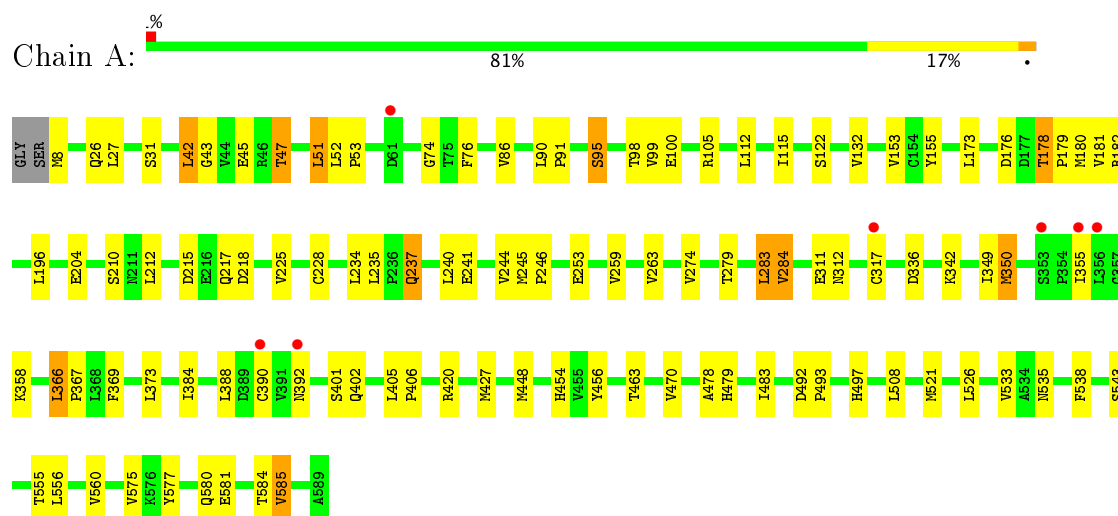
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	30	Total	O	0	0
			30	30		
7	B	27	Total	O	0	0
			27	27		
7	C	34	Total	O	0	0
			34	34		
7	D	25	Total	O	0	0
			25	25		
7	E	25	Total	O	0	0
			25	25		
7	F	31	Total	O	0	0
			31	31		
7	H	1	Total	O	0	0
			1	1		

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: Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform



- Molecule 4: Microcystin-LR (MCLR) bound form

Chain G:  71% 29%



- Molecule 4: Microcystin-LR (MCLR) bound form

Chain H:  43% 57%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.10Å 101.08Å 347.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.08 – 2.80 49.04 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.08-2.80) 99.9 (49.04-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.183 , 0.250 0.192 , 0.250	Depositor DCC
R_{free} test set	4109 reflections (5.18%)	DCC
Wilson B-factor (Å ²)	54.0	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19926	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.30% 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: ACB, DAL, CA, MN, MAA, 1ZN, FGA

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	0.45	0/4595	0.68	1/6217 (0.0%)
1	D	0.46	0/4595	0.67	1/6217 (0.0%)
2	B	0.50	0/2954	0.77	3/3976 (0.1%)
2	E	0.49	0/2971	0.73	2/3999 (0.1%)
3	C	0.49	0/2423	0.75	1/3285 (0.0%)
3	F	0.51	0/2430	0.82	6/3293 (0.2%)
4	G	0.47	0/17	1.16	0/19
4	H	0.55	0/17	0.89	0/19
All	All	0.48	0/20002	0.73	14/27025 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	E	0	1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	57	ASP	CB-CG-OD1	15.44	132.19	118.30
2	B	412	GLU	OE1-CD-OE2	9.29	134.45	123.30
2	E	412	GLU	OE1-CD-OE2	6.80	131.46	123.30
3	C	97	VAL	CB-CA-C	-6.32	99.39	111.40
3	F	239	ARG	NE-CZ-NH1	6.13	123.37	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	139	VAL	Peptide

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	4534	0	4642	43	0
1	D	4534	0	4642	46	0
2	B	2890	0	2798	32	0
2	E	2906	0	2810	33	0
3	C	2366	0	2268	30	0
3	F	2373	0	2280	28	0
4	G	71	0	68	2	0
4	H	71	0	69	5	0
5	B	2	0	0	0	0
5	E	2	0	0	0	0
6	C	2	0	0	0	0
6	F	2	0	0	0	0
7	A	30	0	0	4	0
7	B	27	0	0	2	0
7	C	34	0	0	1	0
7	D	25	0	0	1	0
7	E	25	0	0	0	0
7	F	31	0	0	0	0
7	H	1	0	0	0	0
All	All	19926	0	19577	209	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.

The worst 5 of 209 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:477:TRP:CE2	1:D:481:THR:HG21	2.06	0.91
3:F:223:ASP:O	3:F:227:THR:HG22	1.77	0.83
3:F:168:GLY:O	3:F:239:ARG:NH1	2.15	0.79
3:C:72:GLY:O	3:C:78:THR:HG21	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:1:DAL:H	4:G:7:MAA:HM2	1.54	0.72

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	580/584 (99%)	548 (94%)	31 (5%)	1 (0%)	51	83
1	D	580/584 (99%)	554 (96%)	23 (4%)	3 (0%)	32	67
2	B	351/413 (85%)	332 (95%)	18 (5%)	1 (0%)	44	77
2	E	353/413 (86%)	328 (93%)	22 (6%)	3 (1%)	22	55
3	C	291/311 (94%)	274 (94%)	16 (6%)	1 (0%)	44	77
3	F	292/311 (94%)	274 (94%)	17 (6%)	1 (0%)	44	77
4	G	1/7 (14%)	1 (100%)	0	0	100	100
4	H	1/7 (14%)	1 (100%)	0	0	100	100
All	All	2449/2630 (93%)	2312 (94%)	127 (5%)	10 (0%)	38	72

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	294	ARG
1	D	390	CYS
2	E	121	SER
2	E	426	SER
1	A	401	SER

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	509/496 (103%)	459 (90%)	50 (10%)	9	27
1	D	509/496 (103%)	467 (92%)	42 (8%)	13	36
2	B	314/357 (88%)	286 (91%)	28 (9%)	11	32
2	E	315/357 (88%)	291 (92%)	24 (8%)	15	40
3	C	259/275 (94%)	240 (93%)	19 (7%)	16	42
3	F	259/275 (94%)	243 (94%)	16 (6%)	21	52
4	G	2/2 (100%)	2 (100%)	0	100	100
4	H	2/2 (100%)	2 (100%)	0	100	100
All	All	2169/2260 (96%)	1990 (92%)	179 (8%)	13	36

5 of 179 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	41	LYS
1	D	80	VAL
3	F	49	ARG
3	C	55	CYS
3	C	160	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	305	ASN
1	D	168	GLN
3	F	162	GLN
1	D	22	ASN
1	D	211	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

10 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$
4	DAL	G	1	4	4,4,5	0.93	0	1,4,6	1.10	0
4	ACB	G	3	4	5,8,9	1.98	1 (20%)	3,10,12	4.10	1 (33%)
4	1ZN	G	5	4	22,23,24	2.57	5 (22%)	24,29,31	1.57	5 (20%)
4	FGA	G	6	4	3,8,9	1.88	1 (33%)	2,9,11	0.81	0
4	MAA	G	7	3,4	5,5,6	1.23	0	1,5,7	0.76	0
4	DAL	H	1	4	4,4,5	1.67	1 (25%)	1,4,6	1.05	0
4	ACB	H	3	4	5,8,9	1.99	1 (20%)	3,10,12	3.12	1 (33%)
4	1ZN	H	5	4	22,23,24	2.52	5 (22%)	24,29,31	1.73	4 (16%)
4	FGA	H	6	4	3,8,9	1.97	1 (33%)	2,9,11	0.95	0
4	MAA	H	7	3,4	5,5,6	1.23	1 (20%)	1,5,7	0.45	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
4	DAL	G	1	4	-	0/0/2/4	0/0/0/0
4	ACB	G	3	4	-	0/6/10/12	0/0/0/0
4	1ZN	G	5	4	-	0/22/25/27	0/1/1/1
4	FGA	G	6	4	-	0/4/8/9	0/0/0/0
4	MAA	G	7	3,4	-	0/1/4/6	0/0/0/0
4	DAL	H	1	4	-	0/0/2/4	0/0/0/0
4	ACB	H	3	4	-	0/6/10/12	0/0/0/0
4	1ZN	H	5	4	-	0/22/25/27	0/1/1/1
4	FGA	H	6	4	-	0/4/8/9	0/0/0/0
4	MAA	H	7	3,4	-	0/1/4/6	0/0/0/0

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	3	ACB	OD2-CG	-4.43	1.23	1.42
4	G	3	ACB	OD2-CG	-4.30	1.24	1.42
4	H	5	1ZN	C3-C4	-3.98	1.41	1.51
4	G	5	1ZN	C3-C4	-3.59	1.42	1.51
4	H	6	FGA	OE2-CD	-3.36	1.24	1.42

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	5	1ZN	C3-C2-C10	-4.72	104.09	115.42
4	G	5	1ZN	C17-C16-C15	-4.23	116.91	123.70
4	H	5	1ZN	C17-C16-C15	-3.62	117.89	123.70
4	G	5	1ZN	C3-C2-C10	-2.99	108.24	115.42
4	H	5	1ZN	C2-C10-C12	-2.76	105.50	110.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	1	DAL	2	0
4	G	7	MAA	2	0
4	H	1	DAL	1	0
4	H	7	MAA	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 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	568/584 (97%)	-0.11	7 (1%) 79 72	37, 58, 89, 117	0
1	D	568/584 (97%)	-0.06	6 (1%) 80 74	35, 54, 83, 105	0
2	B	346/413 (83%)	-0.22	1 (0%) 93 92	33, 50, 79, 107	0
2	E	348/413 (84%)	-0.21	1 (0%) 93 92	31, 50, 80, 99	1 (0%)
3	C	293/311 (94%)	-0.34	0 100 100	33, 48, 65, 92	0
3	F	294/311 (94%)	-0.31	1 (0%) 93 92	30, 45, 66, 119	1 (0%)
4	G	2/7 (28%)	0.97	0 100 100	82, 82, 82, 97	0
4	H	2/7 (28%)	0.84	0 100 100	86, 86, 86, 98	0
All	All	2421/2630 (92%)	-0.18	16 (0%) 87 83	30, 52, 82, 119	2 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	317	CYS	3.1
1	D	364	HIS	3.1
1	D	589	ALA	3.0
1	D	363	GLU	2.8
2	E	226	CYS	2.8

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(\AA^2)	Q<0.9
4	ACB	G	3	9/10	0.95	0.29	-	71,78,81,85	0
4	DAL	G	1	5/6	0.95	0.29	-	65,72,75,78	0
4	FGA	H	6	9/10	0.90	0.23	-	71,73,81,85	0
4	DAL	H	1	5/6	0.93	0.26	-	77,78,87,87	0
4	MAA	G	7	6/7	0.92	0.17	-	58,61,63,65	0
4	MAA	H	7	6/7	0.94	0.14	-	65,66,66,71	0
4	1ZN	G	5	23/24	0.95	0.25	-	54,61,69,72	0
4	1ZN	H	5	23/24	0.94	0.29	-	55,59,74,82	0
4	ACB	H	3	9/10	0.91	0.18	-	65,81,85,87	0
4	FGA	G	6	9/10	0.91	0.25	-	59,64,66,68	0

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. 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(\AA^2)	Q<0.9
5	CA	B	602	1/1	0.91	0.14	-0.51	56,56,56,56	0
5	CA	E	702	1/1	0.92	0.14	-1.04	68,68,68,68	0
6	MN	C	502	1/1	0.98	0.11	-1.22	43,43,43,43	0
6	MN	F	601	1/1	0.96	0.11	-1.39	41,41,41,41	0
6	MN	F	602	1/1	0.91	0.09	-2.26	53,53,53,53	0
5	CA	B	601	1/1	0.94	0.08	-2.46	49,49,49,49	0
6	MN	C	501	1/1	0.99	0.07	-3.39	52,52,52,52	0
5	CA	E	701	1/1	0.94	0.08	-3.54	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.