wwPDB X-ray Structure Validation Summary Report (i)

Aug 21, 2023 – 11:27 PM EDT

PDB ID	:	2Q4X
Title	:	Ensemble refinement of the protein crystal structure of gene product from Arabidopsis thaliana At3g16990
Authors	:	Levin, E.J.; Kondrashov, D.A.; Wesenberg, G.E.; Phillips Jr., G.N.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on	:	2007-05-31
Resolution	:	2.10 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

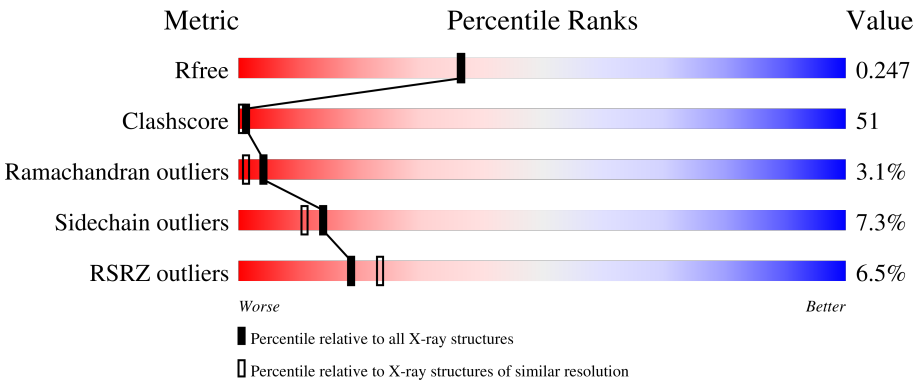
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	1-A	221	5%; 43%; 49%; 5%; •
1	1-B	221	8%; 38%; 54%; •; 5%
1	2-A	221	5%; 47%; 48%; •; •
1	2-B	221	8%; 34%; 52%; 10%; 5%
1	3-A	221	5%; 44%; 48%; •; •; •

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Mol	Chain	Length	Quality of chain
1	3-B	221	8% 38% 50% 6% 5%
1	4-A	221	5% 42% 50% 5%
1	4-B	221	8% 43% 46% 6% 5%
1	5-A	221	5% 38% 52% 6%
1	5-B	221	8% 29% 60% 7% 5%
1	6-A	221	5% 40% 48% 9%
1	6-B	221	8% 30% 55% 10% 5%
1	7-A	221	5% 38% 51% 7%
1	7-B	221	8% 34% 52% 10% 5%
1	8-A	221	5% 47% 44% 6%
1	8-B	221	8% 27% 56% 12% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	1-B	1401	-	-	X	-
2	SO4	5-B	1404	-	-	X	-
2	SO4	7-A	1401	-	-	X	-
2	SO4	7-B	1404	-	-	X	-
3	HMH	1-A	1300	-	X	-	-
3	HMH	1-B	1301	-	X	-	-
3	HMH	2-A	1300	-	X	-	-
3	HMH	2-B	1301	-	X	-	-
3	HMH	3-A	1300	-	X	-	-
3	HMH	3-B	1301	-	X	-	-
3	HMH	4-A	1300	-	X	-	-
3	HMH	4-B	1301	-	X	-	-
3	HMH	5-A	1300	-	X	X	-
3	HMH	5-B	1301	-	X	-	-
3	HMH	6-A	1300	-	X	-	-
3	HMH	6-B	1301	-	X	-	-
3	HMH	7-A	1300	-	X	-	-
3	HMH	7-B	1301	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	HMH	8-A	1300	-	X	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 30952 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.

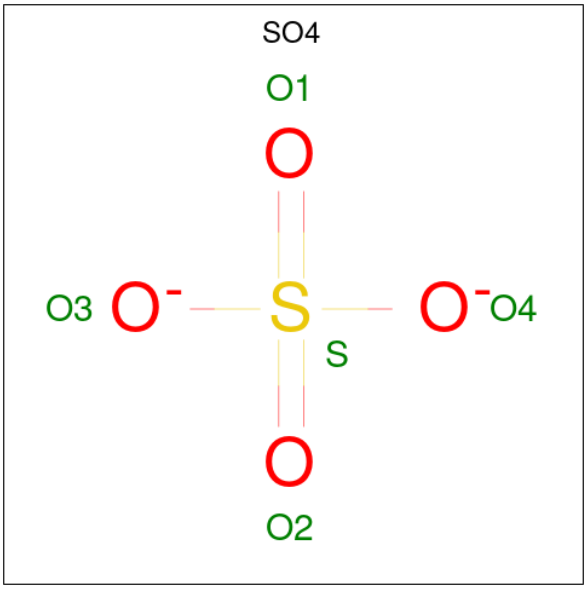
- Molecule 1 is a protein called Seed maturation protein PM36 homolog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	1-A	215	1714	1087	291	327	5	4	0	0	0
1	2-A	215	1714	1087	291	327	5	4	0	0	0
1	3-A	215	1714	1087	291	327	5	4	0	0	0
1	4-A	215	1714	1087	291	327	5	4	0	0	0
1	5-A	215	1714	1087	291	327	5	4	0	0	0
1	6-A	215	1714	1087	291	327	5	4	0	0	0
1	7-A	215	1714	1087	291	327	5	4	0	0	0
1	8-A	215	1714	1087	291	327	5	4	0	0	0
1	1-B	211	1688	1072	289	318	5	4	0	0	0
1	2-B	211	1688	1072	289	318	5	4	0	0	0
1	3-B	211	1688	1072	289	318	5	4	0	0	0
1	4-B	211	1688	1072	289	318	5	4	0	0	0
1	5-B	211	1688	1072	289	318	5	4	0	0	0
1	6-B	211	1688	1072	289	318	5	4	0	0	0
1	7-B	211	1688	1072	289	318	5	4	0	0	0
1	8-B	211	1688	1072	289	318	5	4	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q9ASY9
A	21	ALA	SER	engineered mutation	UNP Q9ASY9
A	75	MSE	MET	modified residue	UNP Q9ASY9
A	123	MSE	MET	modified residue	UNP Q9ASY9
A	133	MSE	MET	modified residue	UNP Q9ASY9
A	216	MSE	MET	modified residue	UNP Q9ASY9
B	1	MSE	MET	modified residue	UNP Q9ASY9
B	21	ALA	SER	engineered mutation	UNP Q9ASY9
B	75	MSE	MET	modified residue	UNP Q9ASY9
B	123	MSE	MET	modified residue	UNP Q9ASY9
B	133	MSE	MET	modified residue	UNP Q9ASY9
B	216	MSE	MET	modified residue	UNP Q9ASY9

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
2	1-A	1	5	4	1		0	0
2	2-A	1	5	4	1		0	0
2	3-A	1	5	4	1		0	0
2	4-A	1	5	4	1		0	0
2	5-A	1	5	4	1		0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	6-A	1	5	4	1	0	0
2	7-A	1	5	4	1	0	0
2	8-A	1	5	4	1	0	0
2	1-B	1	5	4	1	0	0
2	2-B	1	5	4	1	0	0
2	3-B	1	5	4	1	0	0
2	4-B	1	5	4	1	0	0
2	5-B	1	5	4	1	0	0
2	6-B	1	5	4	1	0	0
2	7-B	1	5	4	1	0	0
2	8-B	1	5	4	1	0	0
2	1-B	1	5	4	1	0	0
2	2-B	1	5	4	1	0	0
2	3-B	1	5	4	1	0	0
2	4-B	1	5	4	1	0	0
2	5-B	1	5	4	1	0	0
2	6-B	1	5	4	1	0	0
2	7-B	1	5	4	1	0	0
2	8-B	1	5	4	1	0	0
2	1-B	1	5	4	1	0	0
2	2-B	1	5	4	1	0	0

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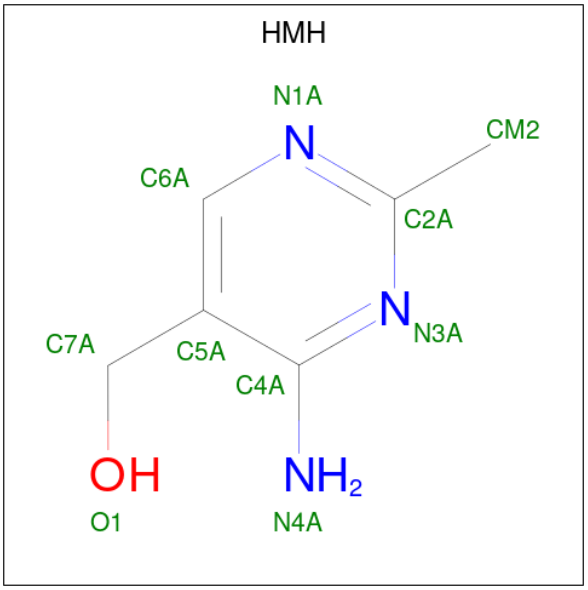
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	O	S			
2	3-B	1	5	4	1		0	0
			Total	O	S			
2	4-B	1	5	4	1		0	0
			Total	O	S			
2	5-B	1	5	4	1		0	0
			Total	O	S			
2	6-B	1	5	4	1		0	0
			Total	O	S			
2	7-B	1	5	4	1		0	0
			Total	O	S			
2	8-B	1	5	4	1		0	0

- Molecule 3 is 4-AMINO-5-HYDROXYMETHYL-2-METHYLPYRIMIDINE (three-letter code: HMH) (formula: $C_6H_9N_3O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	1-A	1	10	6	3	1	0	0
			Total	C	N	O		
3	2-A	1	10	6	3	1	0	0
			Total	C	N	O		
3	3-A	1	10	6	3	1	0	0
			Total	C	N	O		
3	4-A	1	10	6	3	1	0	0
			Total	C	N	O		
3	5-A	1	10	6	3	1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	6-A	1	10	6	3	1	0	0
3	7-A	1	10	6	3	1	0	0
3	8-A	1	10	6	3	1	0	0
3	1-B	1	10	6	3	1	0	0
3	2-B	1	10	6	3	1	0	0
3	3-B	1	10	6	3	1	0	0
3	4-B	1	10	6	3	1	0	0
3	5-B	1	10	6	3	1	0	0
3	6-B	1	10	6	3	1	0	0
3	7-B	1	10	6	3	1	0	0
3	8-B	1	10	6	3	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	1-A	213	213	213	0	0
4	2-A	214	214	214	0	0
4	3-A	214	214	214	0	0
4	4-A	214	214	214	0	0
4	5-A	213	213	213	0	0
4	6-A	214	214	214	0	0
4	7-A	214	214	214	0	0
4	8-A	214	214	214	0	0

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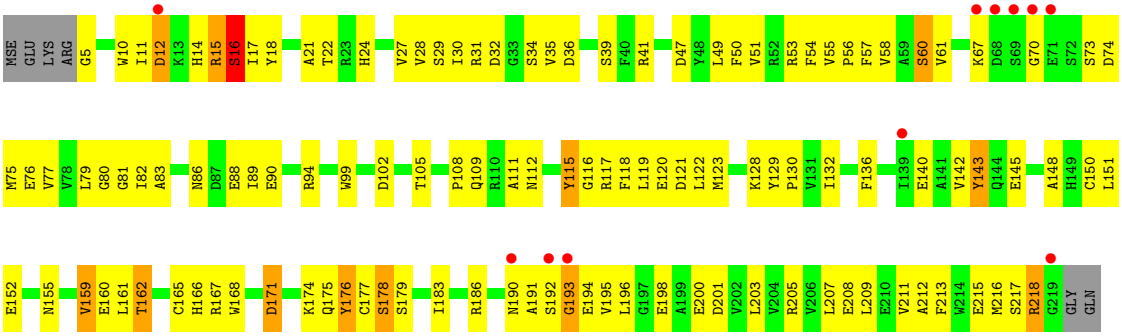
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	1-B	214	214	214	0	0
			Total	O		
4	2-B	213	213	213	0	0
			Total	O		
4	3-B	213	213	213	0	0
			Total	O		
4	4-B	213	213	213	0	0
			Total	O		
4	5-B	214	214	214	0	0
			Total	O		
4	6-B	213	213	213	0	0
			Total	O		
4	7-B	213	213	213	0	0
			Total	O		
4	8-B	213	213	213	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

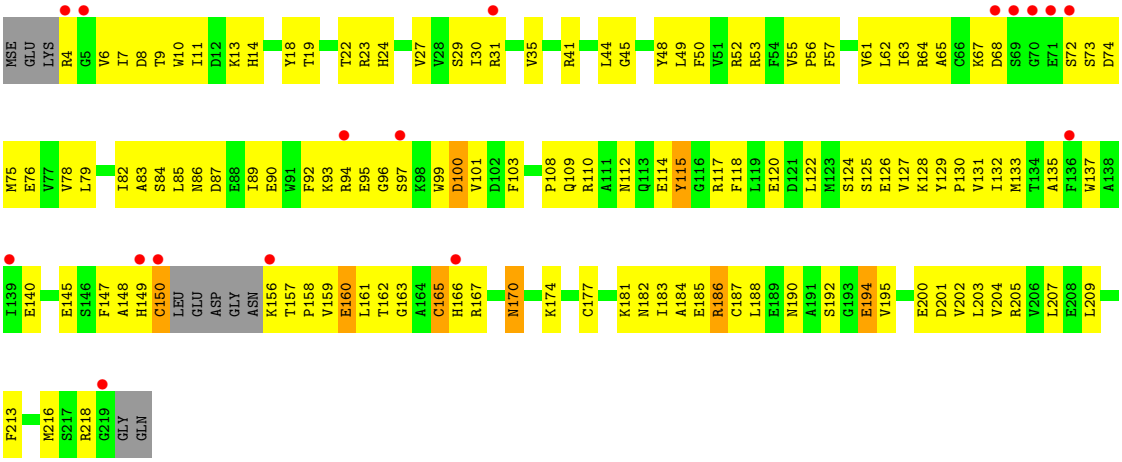
• Molecule 1: Seed maturation protein PM36 homolog

Chain 1-A:



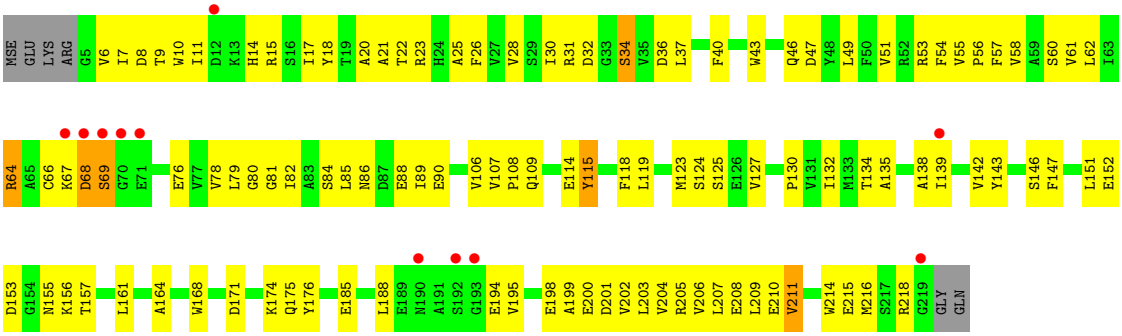
• Molecule 1: Seed maturation protein PM36 homolog

Chain 1-B:



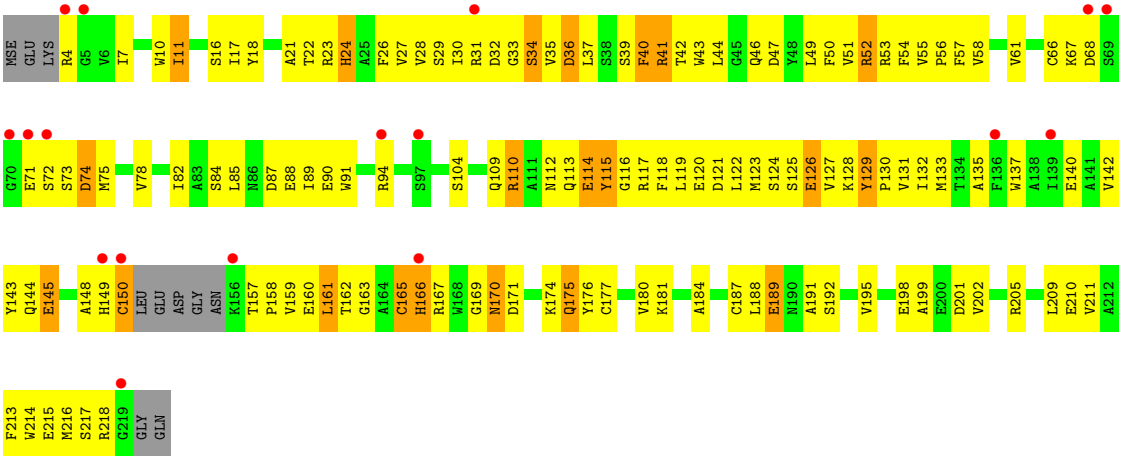
• Molecule 1: Seed maturation protein PM36 homolog

Chain 2-A:



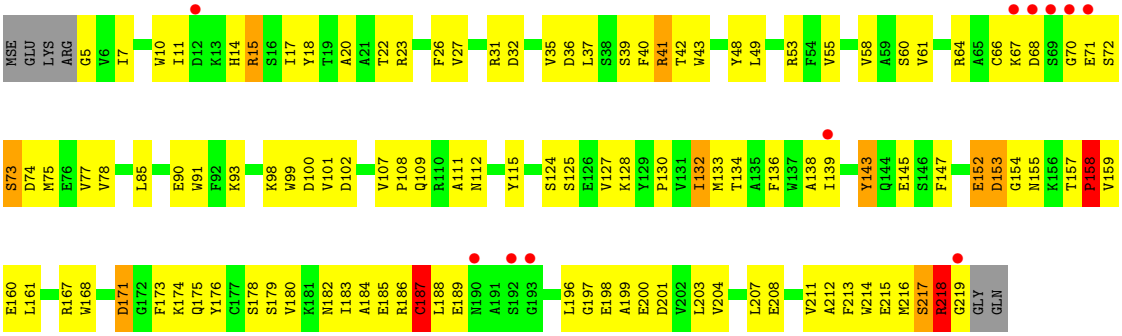
• Molecule 1: Seed maturation protein PM36 homolog

Chain 2-B:



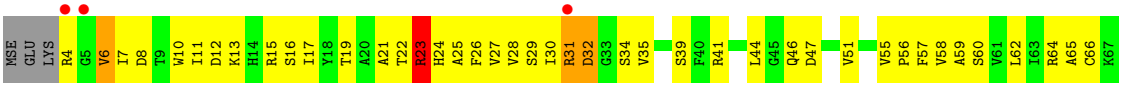
• Molecule 1: Seed maturation protein PM36 homolog

Chain 3-A:



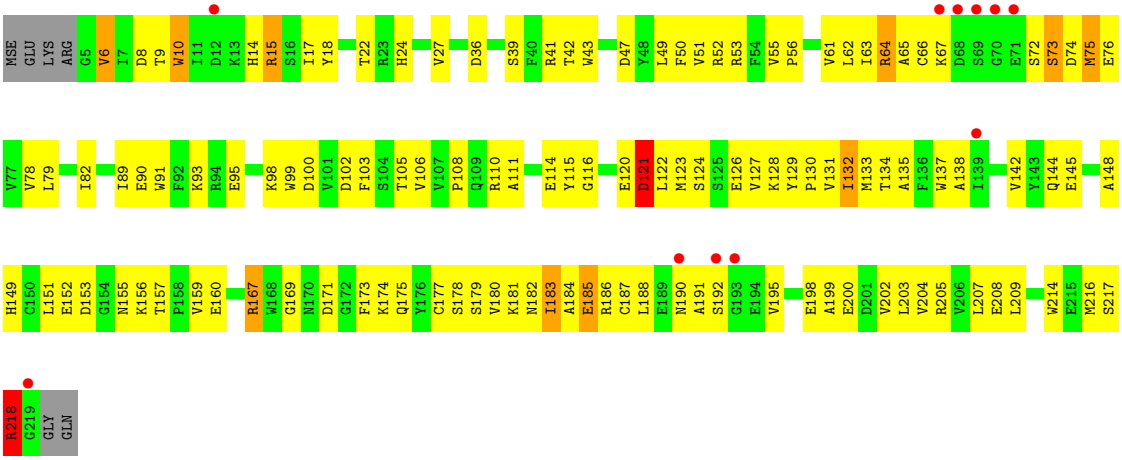
• Molecule 1: Seed maturation protein PM36 homolog

Chain 3-B:



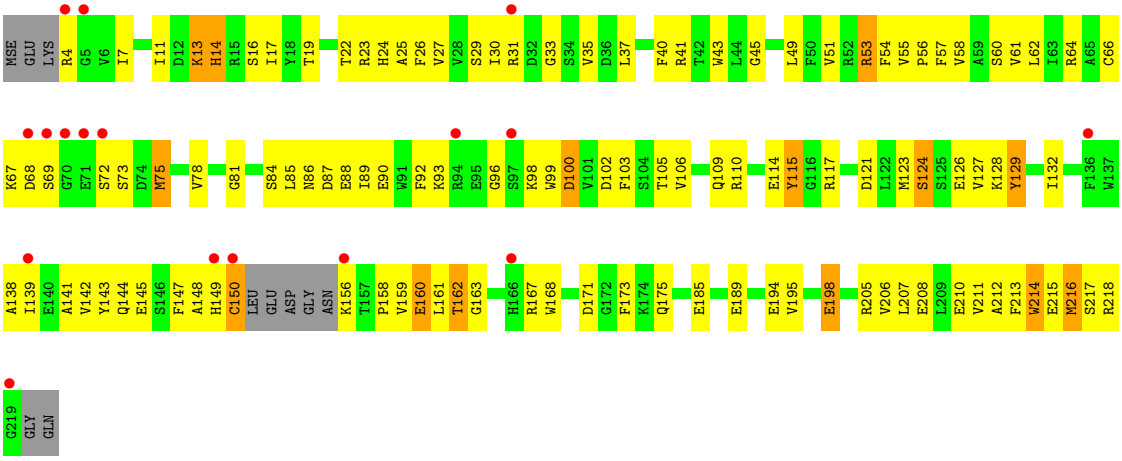
• Molecule 1: Seed maturation protein PM36 homolog

Chain 4-A:



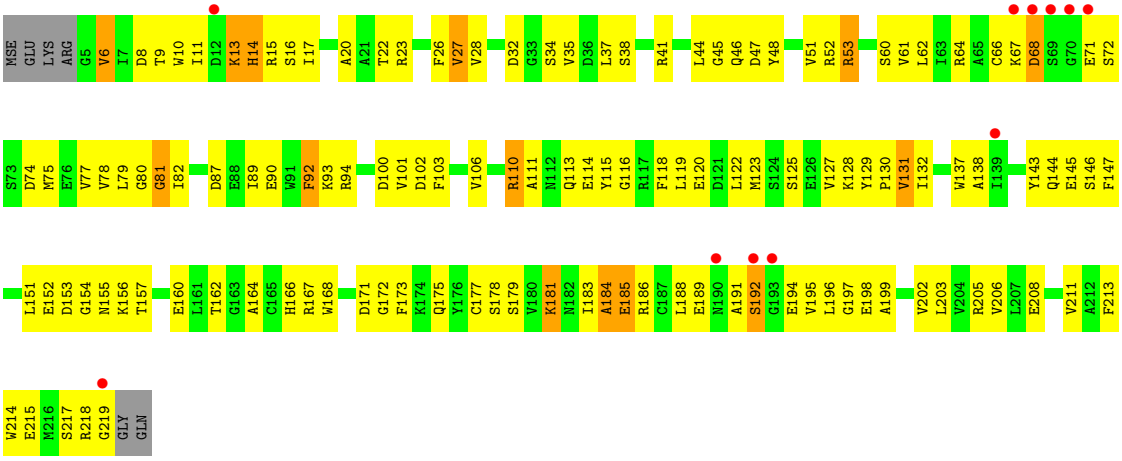
• Molecule 1: Seed maturation protein PM36 homolog

Chain 4-B:



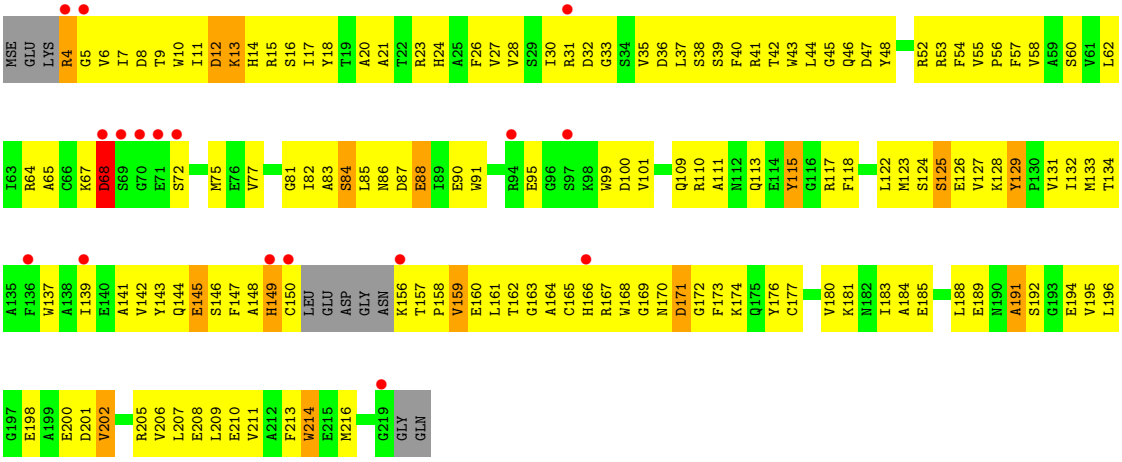
• Molecule 1: Seed maturation protein PM36 homolog

Chain 5-A:



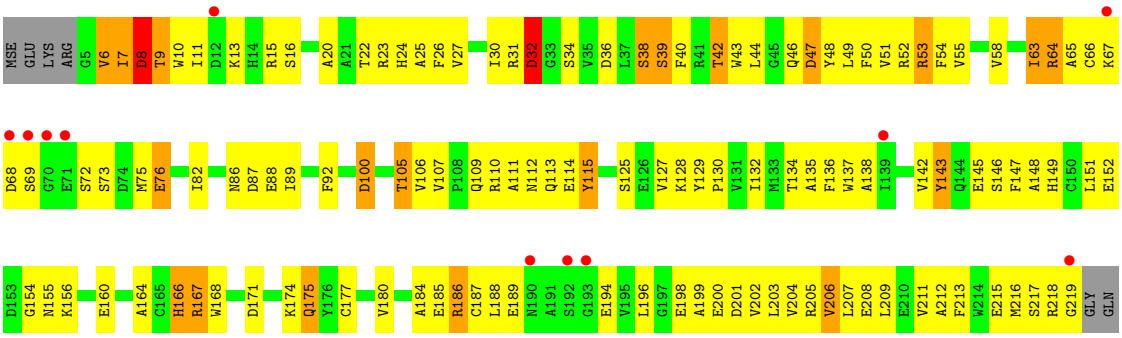
• Molecule 1: Seed maturation protein PM36 homolog

Chain 5-B:



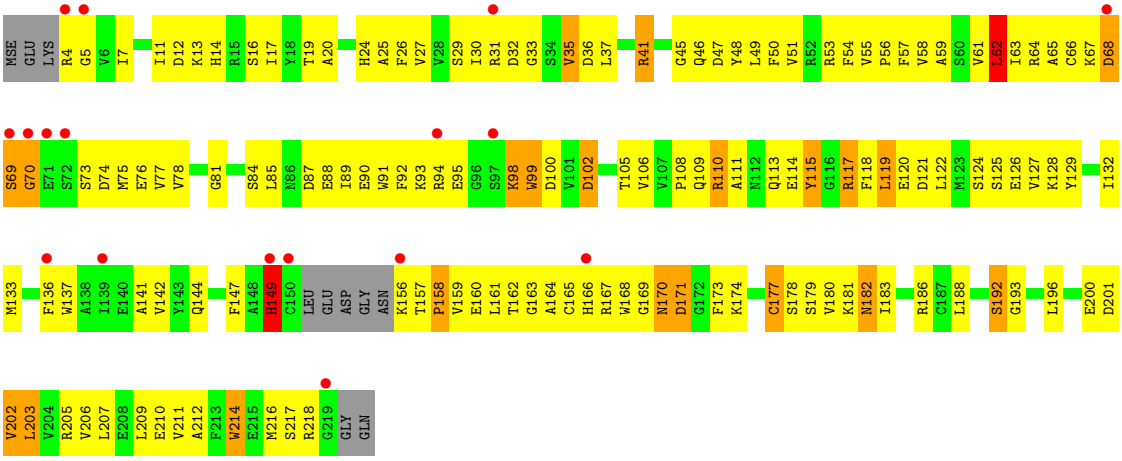
• Molecule 1: Seed maturation protein PM36 homolog

Chain 6-A:



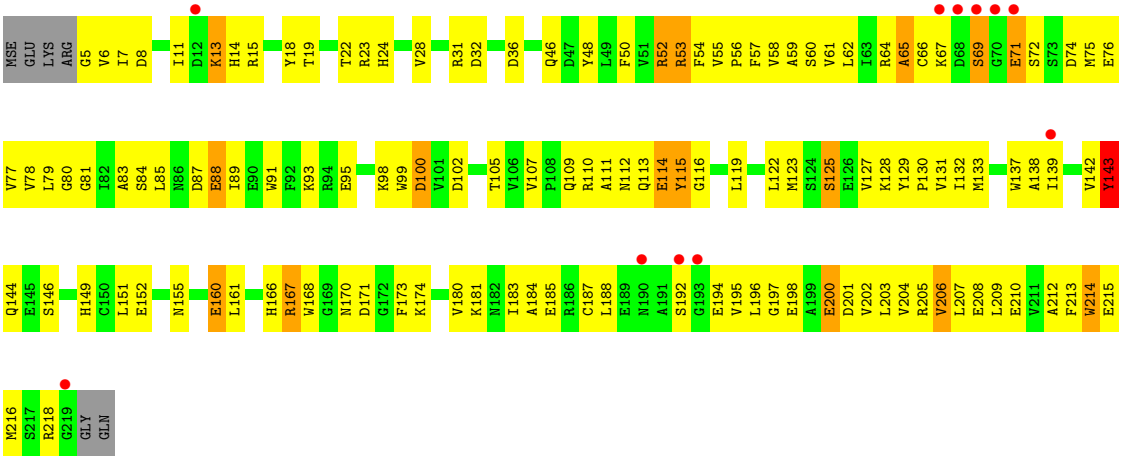
• Molecule 1: Seed maturation protein PM36 homolog

Chain 6-B:



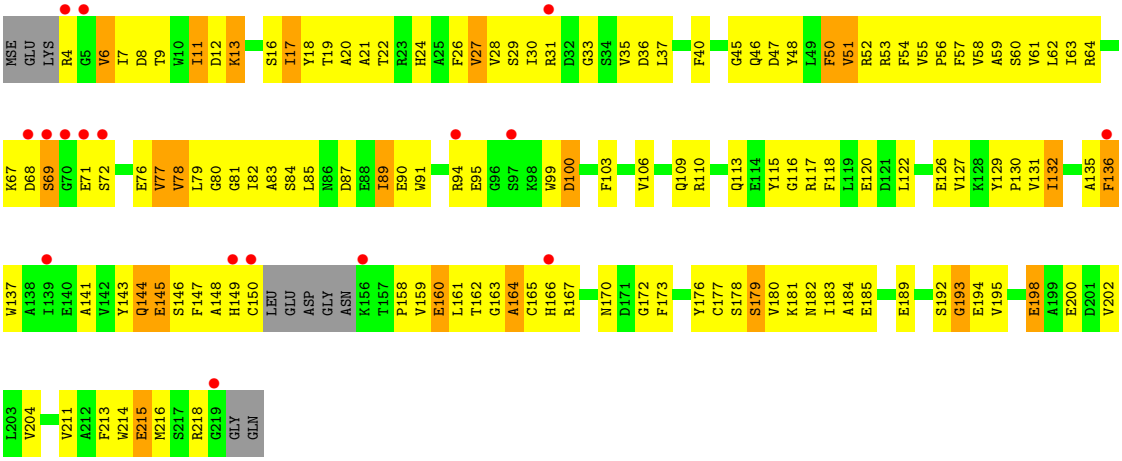
- Molecule 1: Seed maturation protein PM36 homolog

Chain 7-A:



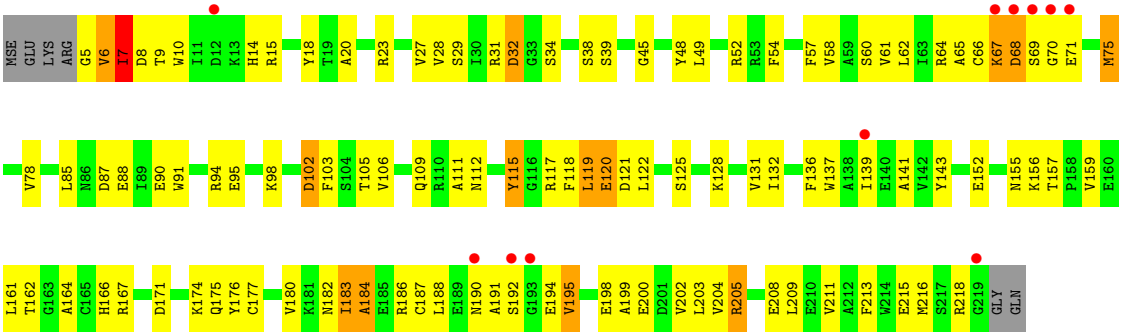
- Molecule 1: Seed maturation protein PM36 homolog

Chain 7-B:



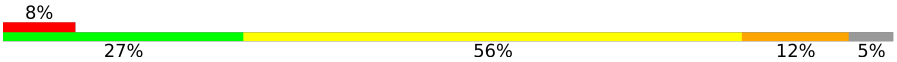
• Molecule 1: Seed maturation protein PM36 homolog

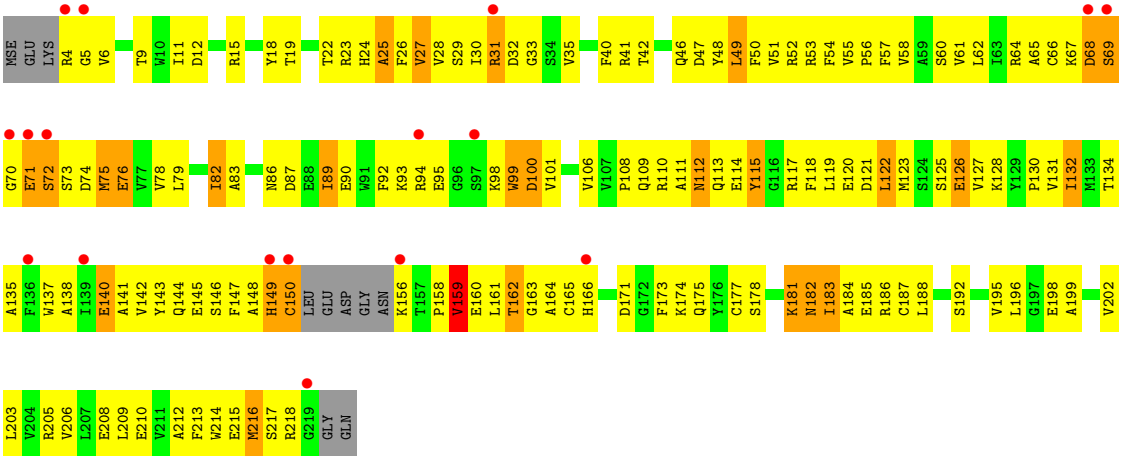
Chain 8-A:



• Molecule 1: Seed maturation protein PM36 homolog

Chain 8-B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	62.70Å 62.70Å 287.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.04 – 2.10 28.04 – 2.10	Depositor EDS
% Data completeness (in resolution range)	86.4 (28.04-2.10) 86.5 (28.04-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.46 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.136 , 0.231 0.154 , 0.247	Depositor DCC
R_{free} test set	1519 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	28.5	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 85.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	30952	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: HMH, SO4

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	1-A	0.86	0/1749	0.85	0/2362
1	1-B	0.90	0/1722	0.85	1/2323 (0.0%)
1	2-A	0.91	1/1749 (0.1%)	0.90	0/2362
1	2-B	0.91	0/1722	0.89	2/2323 (0.1%)
1	3-A	0.86	0/1749	0.84	1/2362 (0.0%)
1	3-B	0.90	0/1722	0.87	1/2323 (0.0%)
1	4-A	0.87	0/1749	0.88	1/2362 (0.0%)
1	4-B	0.90	0/1722	0.85	0/2323
1	5-A	1.00	1/1749 (0.1%)	1.00	3/2362 (0.1%)
1	5-B	1.01	1/1722 (0.1%)	0.98	0/2323
1	6-A	0.94	0/1749	0.93	3/2362 (0.1%)
1	6-B	0.98	0/1722	0.96	5/2323 (0.2%)
1	7-A	1.02	3/1749 (0.2%)	1.00	4/2362 (0.2%)
1	7-B	1.06	2/1722 (0.1%)	0.97	3/2323 (0.1%)
1	8-A	0.93	0/1749	0.95	2/2362 (0.1%)
1	8-B	0.99	1/1722 (0.1%)	0.95	3/2323 (0.1%)
All	All	0.94	9/27768 (0.0%)	0.92	29/37480 (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
1	2-A	0	1
1	2-B	0	1
1	3-B	0	1
1	4-B	0	1
1	5-B	0	1
1	6-A	0	1
All	All	0	6

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	7-B	215	GLU	CD-OE1	14.97	1.42	1.25
1	7-A	88	GLU	CG-CD	7.26	1.62	1.51
1	5-B	88	GLU	CB-CG	6.82	1.65	1.52
1	7-A	187	CYS	CB-SG	-6.58	1.71	1.82
1	2-A	114	GLU	CG-CD	6.48	1.61	1.51

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	8-A	117	ARG	NE-CZ-NH2	-8.87	115.86	120.30
1	7-B	215	GLU	OE1-CD-OE2	8.75	133.80	123.30
1	7-B	215	GLU	CG-CD-OE2	-8.34	101.62	118.30
1	8-A	117	ARG	NE-CZ-NH1	7.75	124.17	120.30
1	2-B	74	ASP	CB-CG-OD1	7.23	124.80	118.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2-A	176	TYR	Sidechain
1	2-B	129	TYR	Sidechain
1	3-B	129	TYR	Sidechain
1	4-B	129	TYR	Sidechain
1	5-B	129	TYR	Sidechain

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	1-A	1714	0	1642	127	0
1	1-B	1688	0	1624	152	0
1	2-A	1714	0	1642	144	0
1	2-B	1688	0	1624	209	0
1	3-A	1714	0	1642	130	0
1	3-B	1688	0	1624	152	0
1	4-A	1714	0	1642	146	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	4-B	1688	0	1624	166	0
1	5-A	1714	0	1642	154	0
1	5-B	1688	0	1624	222	0
1	6-A	1714	0	1642	184	0
1	6-B	1688	0	1624	212	0
1	7-A	1714	0	1642	172	0
1	7-B	1688	0	1624	200	0
1	8-A	1714	0	1642	139	0
1	8-B	1688	0	1624	216	0
2	1-A	5	0	0	0	0
2	1-B	15	0	0	3	0
2	2-A	5	0	0	0	0
2	2-B	15	0	0	0	0
2	3-A	5	0	0	0	0
2	3-B	15	0	0	1	0
2	4-A	5	0	0	1	0
2	4-B	15	0	0	1	0
2	5-A	5	0	0	0	0
2	5-B	15	0	0	3	0
2	6-A	5	0	0	1	0
2	6-B	15	0	0	0	0
2	7-A	5	0	0	2	0
2	7-B	15	0	0	4	0
2	8-A	5	0	0	1	0
2	8-B	15	0	0	1	0
3	1-A	10	0	8	1	0
3	1-B	10	0	9	0	0
3	2-A	10	0	8	1	0
3	2-B	10	0	9	1	0
3	3-A	10	0	8	1	0
3	3-B	10	0	9	2	0
3	4-A	10	0	8	0	0
3	4-B	10	0	8	1	0
3	5-A	10	0	9	5	0
3	5-B	10	0	9	1	0
3	6-A	10	0	9	1	0
3	6-B	10	0	8	2	0
3	7-A	10	0	8	0	0
3	7-B	10	0	9	2	0
3	8-A	10	0	8	1	0
3	8-B	10	0	9	3	0
4	1-A	213	0	0	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	1-B	214	0	0	45	0
4	2-A	214	0	0	23	0
4	2-B	213	0	0	61	0
4	3-A	214	0	0	29	0
4	3-B	213	0	0	45	0
4	4-A	214	0	0	27	0
4	4-B	213	0	0	34	0
4	5-A	213	0	0	37	0
4	5-B	214	0	0	81	0
4	6-A	214	0	0	51	0
4	6-B	213	0	0	52	0
4	7-A	214	0	0	41	0
4	7-B	213	0	0	57	0
4	8-A	214	0	0	43	0
4	8-B	213	0	0	60	0
All	All	30952	0	26264	2728	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 51.

The worst 5 of 2728 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:ARG:NH2	1:B:100:ASP:HB2	1.45	1.30
1:A:27:VAL:HG23	4:A:1410:HOH:O	1.30	1.27
1:B:150:CYS:SG	4:B:1542:HOH:O	1.95	1.25
1:B:72:SER:HA	4:B:1596:HOH:O	1.40	1.22
1:B:149:HIS:HB2	4:B:1463:HOH:O	1.35	1.22

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	1-A	213/221 (96%)	192 (90%)	15 (7%)	6 (3%)	5	1
1	1-B	207/221 (94%)	190 (92%)	14 (7%)	3 (1%)	11	6
1	2-A	213/221 (96%)	203 (95%)	8 (4%)	2 (1%)	17	12
1	2-B	207/221 (94%)	179 (86%)	20 (10%)	8 (4%)	3	1
1	3-A	213/221 (96%)	181 (85%)	26 (12%)	6 (3%)	5	1
1	3-B	207/221 (94%)	175 (84%)	23 (11%)	9 (4%)	2	0
1	4-A	213/221 (96%)	186 (87%)	19 (9%)	8 (4%)	3	1
1	4-B	207/221 (94%)	184 (89%)	21 (10%)	2 (1%)	15	11
1	5-A	213/221 (96%)	191 (90%)	16 (8%)	6 (3%)	5	1
1	5-B	207/221 (94%)	184 (89%)	18 (9%)	5 (2%)	6	2
1	6-A	213/221 (96%)	190 (89%)	15 (7%)	8 (4%)	3	1
1	6-B	207/221 (94%)	181 (87%)	17 (8%)	9 (4%)	2	0
1	7-A	213/221 (96%)	188 (88%)	21 (10%)	4 (2%)	8	3
1	7-B	207/221 (94%)	165 (80%)	28 (14%)	14 (7%)	1	0
1	8-A	213/221 (96%)	188 (88%)	19 (9%)	6 (3%)	5	1
1	8-B	207/221 (94%)	179 (86%)	20 (10%)	8 (4%)	3	1
All	All	3360/3536 (95%)	2956 (88%)	300 (9%)	104 (3%)	4	1

5 of 104 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1-A	190	ASN
1	1-A	193	GLY
1	2-B	170	ASN
1	3-B	124	SER
1	4-A	73	SER

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	1-A	184/184 (100%)	169 (92%)	15 (8%)	11	8
1	1-B	181/184 (98%)	171 (94%)	10 (6%)	21	19
1	2-A	184/184 (100%)	179 (97%)	5 (3%)	44	48
1	2-B	181/184 (98%)	165 (91%)	16 (9%)	10	6
1	3-A	184/184 (100%)	170 (92%)	14 (8%)	13	10
1	3-B	181/184 (98%)	166 (92%)	15 (8%)	11	7
1	4-A	184/184 (100%)	172 (94%)	12 (6%)	17	14
1	4-B	181/184 (98%)	168 (93%)	13 (7%)	14	11
1	5-A	184/184 (100%)	170 (92%)	14 (8%)	13	10
1	5-B	181/184 (98%)	166 (92%)	15 (8%)	11	7
1	6-A	184/184 (100%)	169 (92%)	15 (8%)	11	8
1	6-B	181/184 (98%)	167 (92%)	14 (8%)	13	9
1	7-A	184/184 (100%)	173 (94%)	11 (6%)	19	16
1	7-B	181/184 (98%)	173 (96%)	8 (4%)	28	28
1	8-A	184/184 (100%)	169 (92%)	15 (8%)	11	8
1	8-B	181/184 (98%)	160 (88%)	21 (12%)	5	3
All	All	2920/2944 (99%)	2707 (93%)	213 (7%)	14	11

5 of 213 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	5-B	12	ASP
1	6-A	186	ARG
1	8-B	82	ILE
1	5-B	82	ILE
1	6-A	32	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	8-A	113	GLN
1	8-A	155	ASN
1	8-B	112	ASN
1	3-B	166	HIS
1	3-B	24	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

48 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	SO4	2-A	1401	-	4,4,4	0.37	0	6,6,6	0.41	0
3	HMH	7-B	1301	-	10,10,10	1.94	4 (40%)	12,13,13	2.68	8 (66%)
2	SO4	4-B	1404	-	4,4,4	0.39	0	6,6,6	0.28	0
3	HMH	4-A	1300	-	10,10,10	2.35	7 (70%)	12,13,13	3.14	8 (66%)
2	SO4	5-B	1404	-	4,4,4	0.42	0	6,6,6	0.19	0
2	SO4	6-B	1403	-	4,4,4	0.30	0	6,6,6	0.13	0
2	SO4	8-A	1401	-	4,4,4	0.39	0	6,6,6	0.40	0
2	SO4	2-B	1402	-	4,4,4	0.43	0	6,6,6	0.20	0
2	SO4	7-B	1403	-	4,4,4	0.43	0	6,6,6	0.27	0
2	SO4	8-B	1402	-	4,4,4	0.39	0	6,6,6	0.17	0
2	SO4	5-B	1403	-	4,4,4	0.30	0	6,6,6	0.28	0
2	SO4	1-B	1404	-	4,4,4	0.38	0	6,6,6	0.31	0
3	HMH	8-B	1301	-	10,10,10	1.77	3 (30%)	12,13,13	2.36	7 (58%)
3	HMH	3-B	1301	-	10,10,10	1.66	3 (30%)	12,13,13	2.67	8 (66%)
3	HMH	3-A	1300	-	10,10,10	2.45	4 (40%)	12,13,13	3.21	8 (66%)
2	SO4	1-A	1403	-	4,4,4	0.33	0	6,6,6	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	SO4	6-A	1401	-	4,4,4	0.27	0	6,6,6	0.55	0
2	SO4	2-B	1404	-	4,4,4	0.36	0	6,6,6	0.22	0
2	SO4	7-A	1401	-	4,4,4	0.50	0	6,6,6	0.54	0
3	HMH	1-B	1301	-	10,10,10	1.75	3 (30%)	12,13,13	2.56	8 (66%)
3	HMH	6-B	1301	-	10,10,10	1.93	4 (40%)	12,13,13	2.74	8 (66%)
2	SO4	1-B	1401	-	4,4,4	0.33	0	6,6,6	0.35	0
2	SO4	3-B	1404	-	4,4,4	0.39	0	6,6,6	0.31	0
2	SO4	5-B	1402	-	4,4,4	0.37	0	6,6,6	0.18	0
2	SO4	4-A	1401	-	4,4,4	0.56	0	6,6,6	0.58	0
2	SO4	4-B	1403	-	4,4,4	0.30	0	6,6,6	0.22	0
3	HMH	1-A	1300	-	10,10,10	2.37	6 (60%)	12,13,13	3.22	8 (66%)
2	SO4	8-B	1404	-	4,4,4	0.40	0	6,6,6	0.20	0
3	HMH	5-A	1300	-	10,10,10	2.65	4 (40%)	12,13,13	3.08	7 (58%)
3	HMH	2-A	1300	-	10,10,10	2.30	5 (50%)	12,13,13	3.11	9 (75%)
2	SO4	3-A	1401	-	4,4,4	0.24	0	6,6,6	0.51	0
2	SO4	7-B	1402	-	4,4,4	0.32	0	6,6,6	0.19	0
2	SO4	6-B	1404	-	4,4,4	0.43	0	6,6,6	0.21	0
3	HMH	2-B	1301	-	10,10,10	1.92	3 (30%)	12,13,13	2.35	8 (66%)
3	HMH	6-A	1300	-	10,10,10	2.57	3 (30%)	12,13,13	2.66	8 (66%)
2	SO4	7-B	1404	-	4,4,4	0.22	0	6,6,6	0.37	0
2	SO4	4-B	1402	-	4,4,4	0.28	0	6,6,6	0.29	0
3	HMH	8-A	1300	-	10,10,10	2.47	6 (60%)	12,13,13	3.10	8 (66%)
2	SO4	1-B	1402	-	4,4,4	0.32	0	6,6,6	0.21	0
2	SO4	2-B	1403	-	4,4,4	0.43	0	6,6,6	0.08	0
3	HMH	4-B	1301	-	10,10,10	1.46	3 (30%)	12,13,13	2.57	8 (66%)
2	SO4	3-B	1402	-	4,4,4	0.30	0	6,6,6	0.17	0
3	HMH	5-B	1301	-	10,10,10	2.24	4 (40%)	12,13,13	2.72	7 (58%)
3	HMH	7-A	1300	-	10,10,10	2.40	4 (40%)	12,13,13	3.02	9 (75%)
2	SO4	6-B	1402	-	4,4,4	0.34	0	6,6,6	0.19	0
2	SO4	5-A	1401	-	4,4,4	0.42	0	6,6,6	0.38	0
2	SO4	8-B	1403	-	4,4,4	0.34	0	6,6,6	0.21	0
2	SO4	3-B	1403	-	4,4,4	0.44	0	6,6,6	0.28	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
3	HMH	7-B	1301	-	-	0/2/2/2	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HMH	5-A	1300	-	-	0/2/2/2	0/1/1/1
3	HMH	4-A	1300	-	-	0/2/2/2	0/1/1/1
3	HMH	8-B	1301	-	-	0/2/2/2	0/1/1/1
3	HMH	2-A	1300	-	-	0/2/2/2	0/1/1/1
3	HMH	8-A	1300	-	-	0/2/2/2	0/1/1/1
3	HMH	3-B	1301	-	-	0/2/2/2	0/1/1/1
3	HMH	3-A	1300	-	-	0/2/2/2	0/1/1/1
3	HMH	4-B	1301	-	-	0/2/2/2	0/1/1/1
3	HMH	5-B	1301	-	-	0/2/2/2	0/1/1/1
3	HMH	7-A	1300	-	-	0/2/2/2	0/1/1/1
3	HMH	2-B	1301	-	-	0/2/2/2	0/1/1/1
3	HMH	6-A	1300	-	-	0/2/2/2	0/1/1/1
3	HMH	6-B	1301	-	-	0/2/2/2	0/1/1/1
3	HMH	1-B	1301	-	-	0/2/2/2	0/1/1/1
3	HMH	1-A	1300	-	-	0/2/2/2	0/1/1/1

The worst 5 of 66 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	6-A	1300	HMH	C4A-N3A	5.16	1.42	1.35
3	5-A	1300	HMH	C6A-N1A	4.35	1.43	1.34
3	3-A	1300	HMH	C4A-N3A	4.23	1.41	1.35
3	7-A	1300	HMH	C4A-N3A	4.22	1.41	1.35
3	5-A	1300	HMH	C6A-C5A	4.20	1.46	1.37

The worst 5 of 127 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	5-A	1300	HMH	CM2-C2A-N1A	5.70	123.41	117.14
3	3-A	1300	HMH	C7A-C5A-C6A	5.60	128.49	119.37
3	7-A	1300	HMH	N4A-C4A-N3A	5.41	124.68	117.03
3	2-A	1300	HMH	N4A-C4A-N3A	5.35	124.59	117.03
3	1-A	1300	HMH	C7A-C5A-C6A	5.27	127.94	119.37

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

25 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	7-B	1301	HMH	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	4-B	1404	SO4	1	0
2	5-B	1404	SO4	2	0
2	8-A	1401	SO4	1	0
2	1-B	1404	SO4	1	0
3	8-B	1301	HMH	3	0
3	3-B	1301	HMH	2	0
3	3-A	1300	HMH	1	0
2	6-A	1401	SO4	1	0
2	7-A	1401	SO4	2	0
3	6-B	1301	HMH	2	0
2	1-B	1401	SO4	2	0
2	3-B	1404	SO4	1	0
2	5-B	1402	SO4	1	0
2	4-A	1401	SO4	1	0
3	1-A	1300	HMH	1	0
3	5-A	1300	HMH	5	0
3	2-A	1300	HMH	1	0
3	2-B	1301	HMH	1	0
3	6-A	1300	HMH	1	0
2	7-B	1404	SO4	4	0
3	8-A	1300	HMH	1	0
3	4-B	1301	HMH	1	0
3	5-B	1301	HMH	1	0
2	8-B	1403	SO4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (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	1-A	211/221 (95%)	-0.11	11 (5%)	27	32	11, 21, 34, 59	211 (100%)
1	1-B	207/221 (93%)	0.14	17 (8%)	11	15	6, 22, 44, 59	207 (100%)
1	2-A	211/221 (95%)	-0.11	11 (5%)	27	32	11, 21, 34, 59	211 (100%)
1	2-B	207/221 (93%)	0.14	17 (8%)	11	15	6, 22, 44, 59	207 (100%)
1	3-A	211/221 (95%)	-0.11	11 (5%)	27	32	11, 21, 34, 59	211 (100%)
1	3-B	207/221 (93%)	0.14	17 (8%)	11	15	6, 22, 44, 59	207 (100%)
1	4-A	211/221 (95%)	-0.11	11 (5%)	27	32	11, 21, 34, 59	211 (100%)
1	4-B	207/221 (93%)	0.14	17 (8%)	11	15	6, 22, 44, 59	207 (100%)
1	5-A	211/221 (95%)	-0.11	11 (5%)	27	32	11, 21, 34, 59	211 (100%)
1	5-B	207/221 (93%)	0.14	17 (8%)	11	15	6, 22, 44, 59	207 (100%)
1	6-A	211/221 (95%)	-0.11	11 (5%)	27	32	11, 21, 34, 59	211 (100%)
1	6-B	207/221 (93%)	0.14	17 (8%)	11	15	6, 22, 44, 59	207 (100%)
1	7-A	211/221 (95%)	-0.11	11 (5%)	27	32	11, 21, 34, 59	211 (100%)
1	7-B	207/221 (93%)	0.14	17 (8%)	11	15	6, 22, 44, 59	207 (100%)
1	8-A	211/221 (95%)	-0.11	11 (5%)	27	32	11, 21, 34, 59	211 (100%)
1	8-B	207/221 (93%)	0.14	17 (8%)	11	15	6, 22, 44, 59	207 (100%)
All	All	3344/3536 (94%)	0.01	224 (6%)	18	22	6, 22, 41, 59	3344 (100%)

The worst 5 of 224 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	1-B	70	GLY	7.4
1	2-B	70	GLY	7.4
1	3-B	70	GLY	7.4
1	4-B	70	GLY	7.4
1	5-B	70	GLY	7.4

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 monosaccharides 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
3	HMH	1-A	1300	10/10	0.93	0.23	19,24,25,26	10
3	HMH	2-A	1300	10/10	0.93	0.23	17,23,25,26	10
3	HMH	3-A	1300	10/10	0.93	0.23	21,24,26,28	10
3	HMH	4-A	1300	10/10	0.93	0.23	17,23,25,25	10
3	HMH	5-A	1300	10/10	0.93	0.23	21,25,27,29	10
3	HMH	6-A	1300	10/10	0.93	0.23	14,23,26,27	10
3	HMH	7-A	1300	10/10	0.93	0.23	16,21,23,31	10
3	HMH	8-A	1300	10/10	0.93	0.23	21,24,26,26	10
2	SO4	1-B	1404	5/5	0.94	0.19	66,67,68,69	5
2	SO4	2-B	1404	5/5	0.94	0.19	65,67,68,68	5
2	SO4	3-B	1404	5/5	0.94	0.19	68,68,68,69	5
2	SO4	4-B	1404	5/5	0.94	0.19	66,67,68,69	5
2	SO4	5-B	1404	5/5	0.94	0.19	66,67,68,68	5
2	SO4	6-B	1404	5/5	0.94	0.19	67,67,68,69	5
2	SO4	7-B	1404	5/5	0.94	0.19	63,64,67,67	5
2	SO4	8-B	1404	5/5	0.94	0.19	64,66,67,68	5
3	HMH	1-B	1301	10/10	0.94	0.22	15,19,23,33	10
3	HMH	2-B	1301	10/10	0.94	0.22	15,17,21,34	10
3	HMH	3-B	1301	10/10	0.94	0.22	23,25,29,32	10
3	HMH	4-B	1301	10/10	0.94	0.22	19,21,25,26	10
3	HMH	5-B	1301	10/10	0.94	0.22	17,19,21,24	10
3	HMH	6-B	1301	10/10	0.94	0.22	19,24,26,26	10
3	HMH	7-B	1301	10/10	0.94	0.22	21,25,28,31	10
3	HMH	8-B	1301	10/10	0.94	0.22	3,20,23,24	10
2	SO4	1-A	1403	5/5	0.96	0.15	62,62,62,63	5
2	SO4	5-B	1403	5/5	0.97	0.16	58,61,61,61	5
2	SO4	6-B	1403	5/5	0.97	0.16	57,57,58,58	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	7-B	1403	5/5	0.97	0.16	61,62,63,63	5
2	SO4	8-B	1403	5/5	0.97	0.16	61,61,62,63	5
2	SO4	2-B	1403	5/5	0.97	0.16	58,58,59,59	5
2	SO4	3-B	1403	5/5	0.97	0.16	60,60,61,61	5
2	SO4	4-B	1403	5/5	0.97	0.16	61,62,62,63	5
2	SO4	8-B	1402	5/5	1.00	0.08	21,22,23,25	5
2	SO4	2-A	1401	5/5	1.00	0.14	27,30,30,31	5
2	SO4	3-A	1401	5/5	1.00	0.14	28,30,31,32	5
2	SO4	4-A	1401	5/5	1.00	0.14	29,35,36,36	5
2	SO4	5-A	1401	5/5	1.00	0.14	24,25,27,27	5
2	SO4	6-A	1401	5/5	1.00	0.14	26,28,30,31	5
2	SO4	7-A	1401	5/5	1.00	0.14	26,28,29,29	5
2	SO4	8-A	1401	5/5	1.00	0.14	25,25,26,28	5
2	SO4	1-B	1401	5/5	1.00	0.12	29,29,30,31	5
2	SO4	1-B	1402	5/5	1.00	0.08	21,21,22,23	5
2	SO4	2-B	1402	5/5	1.00	0.08	23,24,26,26	5
2	SO4	3-B	1402	5/5	1.00	0.08	22,22,23,24	5
2	SO4	4-B	1402	5/5	1.00	0.08	24,24,26,26	5
2	SO4	5-B	1402	5/5	1.00	0.08	21,25,26,27	5
2	SO4	6-B	1402	5/5	1.00	0.08	22,22,25,25	5
2	SO4	7-B	1402	5/5	1.00	0.08	22,23,25,25	5

6.5 Other polymers (i)

There are no such residues in this entry.