



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 01:43 AM UTC

PDB ID : 2ONK / pdb_00002onk
Title : ABC transporter ModBC in complex with its binding protein ModA
Authors : Hollenstein, K.; Frei, D.C.; Locher, K.P.
Deposited on : 2007-01-24
Resolution : 3.10 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

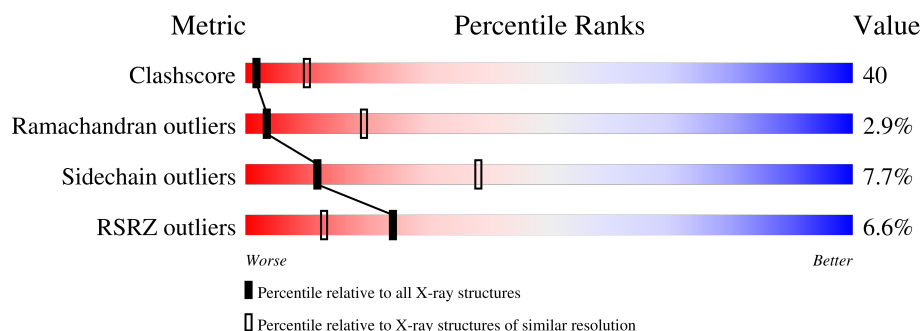
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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.



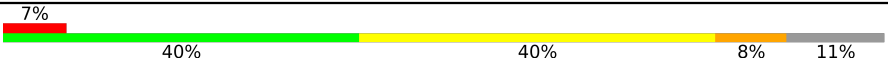
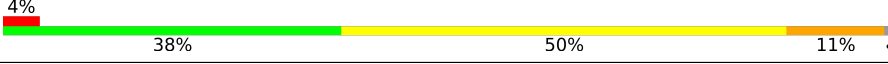
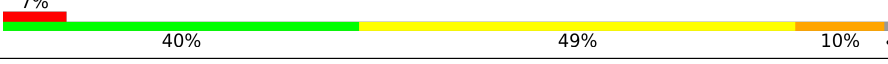
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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 $\leq 5\%$. 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	240	6% 39% 52% 9%
1	B	240	8% 36% 55% 9%
1	F	240	6% 36% 53% 10%
1	G	240	12% 35% 56% 9%
2	C	284	4% 42% 39% 8% 11%
2	D	284	2% 42% 37% 9% 11%

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Mol	Chain	Length	Quality of chain
2	H	284	
2	I	284	
3	E	314	
3	J	314	

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
4	PO4	B	802	-	X	-	-
4	PO4	F	803	-	X	-	-
4	PO4	G	804	-	X	-	-
6	WO4	E	701	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20218 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 Molybdate/tungstate ABC transporter, ATP-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	0	0	0
			1902	1212	349	334	7			
1	B	240	Total	C	N	O	S	0	0	0
			1902	1212	349	334	7			
1	F	240	Total	C	N	O	S	0	0	0
			1902	1212	349	334	7			
1	G	240	Total	C	N	O	S	0	0	0
			1902	1212	349	334	7			

- Molecule 2 is a protein called Molybdate/tungstate ABC transporter, permease protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	252	Total	C	N	O	S	0	0	0
			1901	1279	297	320	5			
2	D	252	Total	C	N	O	S	0	0	0
			1901	1279	297	320	5			
2	H	252	Total	C	N	O	S	0	0	0
			1901	1279	297	320	5			
2	I	252	Total	C	N	O	S	0	0	0
			1901	1279	297	320	5			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-22	MET	-	cloning artifact	UNP O30143
C	-21	GLY	-	cloning artifact	UNP O30143
C	-20	HIS	-	expression tag	UNP O30143
C	-19	HIS	-	expression tag	UNP O30143
C	-18	HIS	-	expression tag	UNP O30143
C	-17	HIS	-	expression tag	UNP O30143
C	-16	HIS	-	expression tag	UNP O30143
C	-15	HIS	-	expression tag	UNP O30143

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	HIS	-	expression tag	UNP O30143
C	-13	HIS	-	expression tag	UNP O30143
C	-12	HIS	-	expression tag	UNP O30143
C	-11	HIS	-	expression tag	UNP O30143
C	-10	SER	-	cloning artifact	UNP O30143
C	-9	SER	-	cloning artifact	UNP O30143
C	-8	GLY	-	cloning artifact	UNP O30143
C	-7	GLU	-	cloning artifact	UNP O30143
C	-6	ASN	-	cloning artifact	UNP O30143
C	-5	LEU	-	cloning artifact	UNP O30143
C	-4	TYR	-	cloning artifact	UNP O30143
C	-3	PHE	-	cloning artifact	UNP O30143
C	-2	GLN	-	cloning artifact	UNP O30143
C	-1	GLY	-	cloning artifact	UNP O30143
C	0	HIS	-	cloning artifact	UNP O30143
D	-22	MET	-	cloning artifact	UNP O30143
D	-21	GLY	-	cloning artifact	UNP O30143
D	-20	HIS	-	expression tag	UNP O30143
D	-19	HIS	-	expression tag	UNP O30143
D	-18	HIS	-	expression tag	UNP O30143
D	-17	HIS	-	expression tag	UNP O30143
D	-16	HIS	-	expression tag	UNP O30143
D	-15	HIS	-	expression tag	UNP O30143
D	-14	HIS	-	expression tag	UNP O30143
D	-13	HIS	-	expression tag	UNP O30143
D	-12	HIS	-	expression tag	UNP O30143
D	-11	HIS	-	expression tag	UNP O30143
D	-10	SER	-	cloning artifact	UNP O30143
D	-9	SER	-	cloning artifact	UNP O30143
D	-8	GLY	-	cloning artifact	UNP O30143
D	-7	GLU	-	cloning artifact	UNP O30143
D	-6	ASN	-	cloning artifact	UNP O30143
D	-5	LEU	-	cloning artifact	UNP O30143
D	-4	TYR	-	cloning artifact	UNP O30143
D	-3	PHE	-	cloning artifact	UNP O30143
D	-2	GLN	-	cloning artifact	UNP O30143
D	-1	GLY	-	cloning artifact	UNP O30143
D	0	HIS	-	cloning artifact	UNP O30143
H	-22	MET	-	cloning artifact	UNP O30143
H	-21	GLY	-	cloning artifact	UNP O30143
H	-20	HIS	-	expression tag	UNP O30143
H	-19	HIS	-	expression tag	UNP O30143

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-18	HIS	-	expression tag	UNP O30143
H	-17	HIS	-	expression tag	UNP O30143
H	-16	HIS	-	expression tag	UNP O30143
H	-15	HIS	-	expression tag	UNP O30143
H	-14	HIS	-	expression tag	UNP O30143
H	-13	HIS	-	expression tag	UNP O30143
H	-12	HIS	-	expression tag	UNP O30143
H	-11	HIS	-	expression tag	UNP O30143
H	-10	SER	-	cloning artifact	UNP O30143
H	-9	SER	-	cloning artifact	UNP O30143
H	-8	GLY	-	cloning artifact	UNP O30143
H	-7	GLU	-	cloning artifact	UNP O30143
H	-6	ASN	-	cloning artifact	UNP O30143
H	-5	LEU	-	cloning artifact	UNP O30143
H	-4	TYR	-	cloning artifact	UNP O30143
H	-3	PHE	-	cloning artifact	UNP O30143
H	-2	GLN	-	cloning artifact	UNP O30143
H	-1	GLY	-	cloning artifact	UNP O30143
H	0	HIS	-	cloning artifact	UNP O30143
I	-22	MET	-	cloning artifact	UNP O30143
I	-21	GLY	-	cloning artifact	UNP O30143
I	-20	HIS	-	expression tag	UNP O30143
I	-19	HIS	-	expression tag	UNP O30143
I	-18	HIS	-	expression tag	UNP O30143
I	-17	HIS	-	expression tag	UNP O30143
I	-16	HIS	-	expression tag	UNP O30143
I	-15	HIS	-	expression tag	UNP O30143
I	-14	HIS	-	expression tag	UNP O30143
I	-13	HIS	-	expression tag	UNP O30143
I	-12	HIS	-	expression tag	UNP O30143
I	-11	HIS	-	expression tag	UNP O30143
I	-10	SER	-	cloning artifact	UNP O30143
I	-9	SER	-	cloning artifact	UNP O30143
I	-8	GLY	-	cloning artifact	UNP O30143
I	-7	GLU	-	cloning artifact	UNP O30143
I	-6	ASN	-	cloning artifact	UNP O30143
I	-5	LEU	-	cloning artifact	UNP O30143
I	-4	TYR	-	cloning artifact	UNP O30143
I	-3	PHE	-	cloning artifact	UNP O30143
I	-2	GLN	-	cloning artifact	UNP O30143
I	-1	GLY	-	cloning artifact	UNP O30143
I	0	HIS	-	cloning artifact	UNP O30143

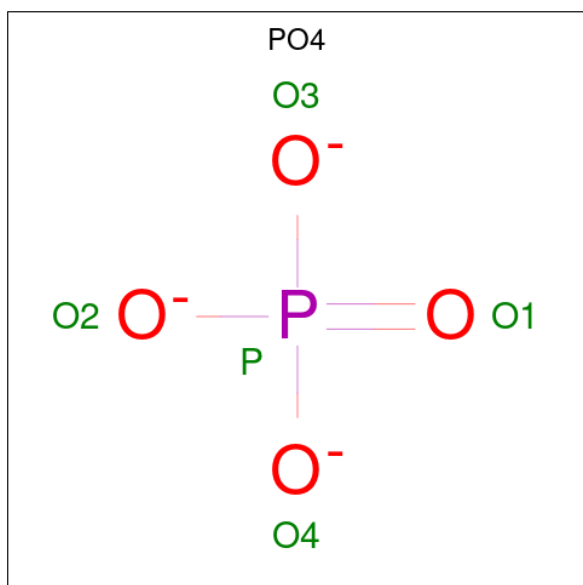
- Molecule 3 is a protein called Molybdate/tungstate binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	311	Total	C	N	O	S	0	0	0
			2489	1590	414	474	11			
3	J	310	Total	C	N	O	S	0	0	0
			2481	1585	415	469	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	29	GLY	-	cloning artifact	UNP O30142
E	30	HIS	-	cloning artifact	UNP O30142
E	31	MET	-	cloning artifact	UNP O30142
J	29	GLY	-	cloning artifact	UNP O30142
J	30	HIS	-	cloning artifact	UNP O30142
J	31	MET	-	cloning artifact	UNP O30142

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).

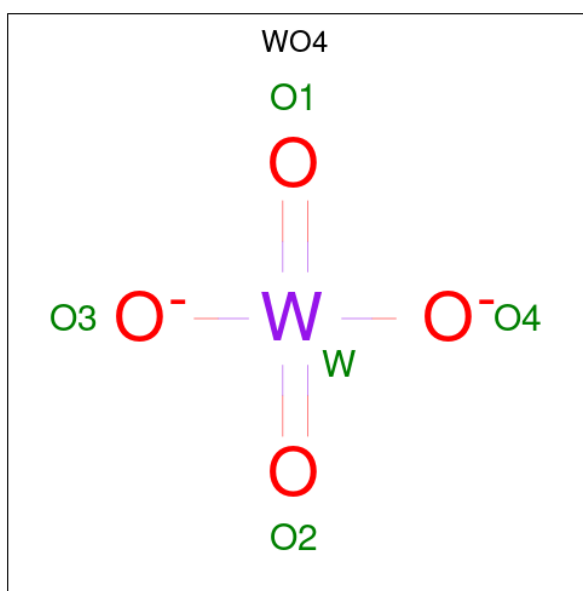


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		
4	F	1	Total	O	P	0	0
			5	4	1		
4	G	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	B	1	Total	Mg	0	0
			1	1		
5	F	1	Total	Mg	0	0
			1	1		
5	G	1	Total	Mg	0	0
			1	1		
5	E	1	Total	Mg	0	0
			1	1		
5	J	1	Total	Mg	0	0
			1	1		

- Molecule 6 is TUNGSTATE(VI)ION (CCD ID: WO4) (formula: O₄W).

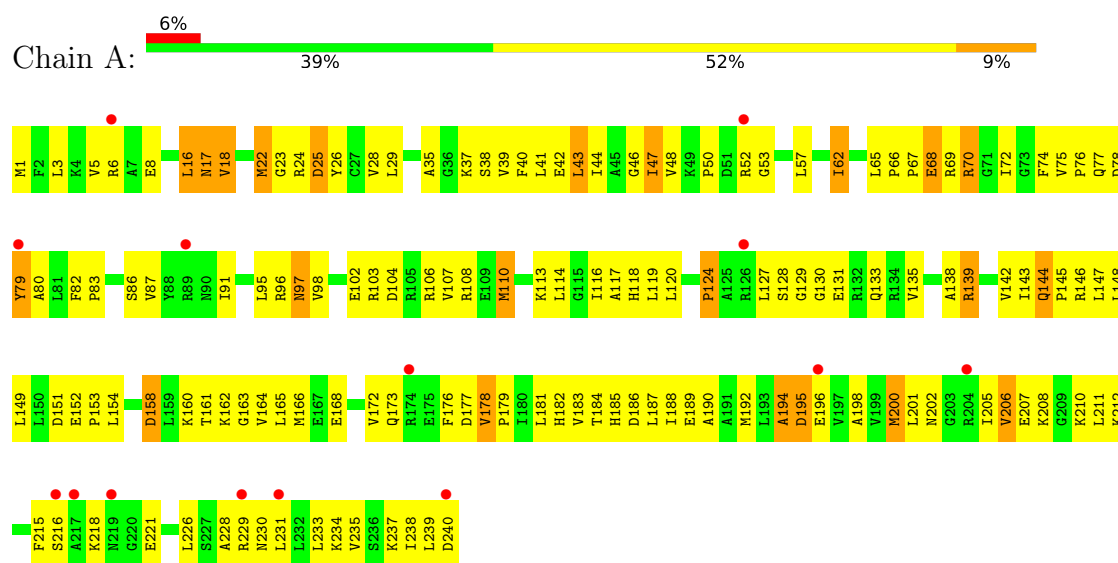


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	O	W	0	0
			5	4	1		
6	J	1	Total	O	W	0	0
			5	4	1		

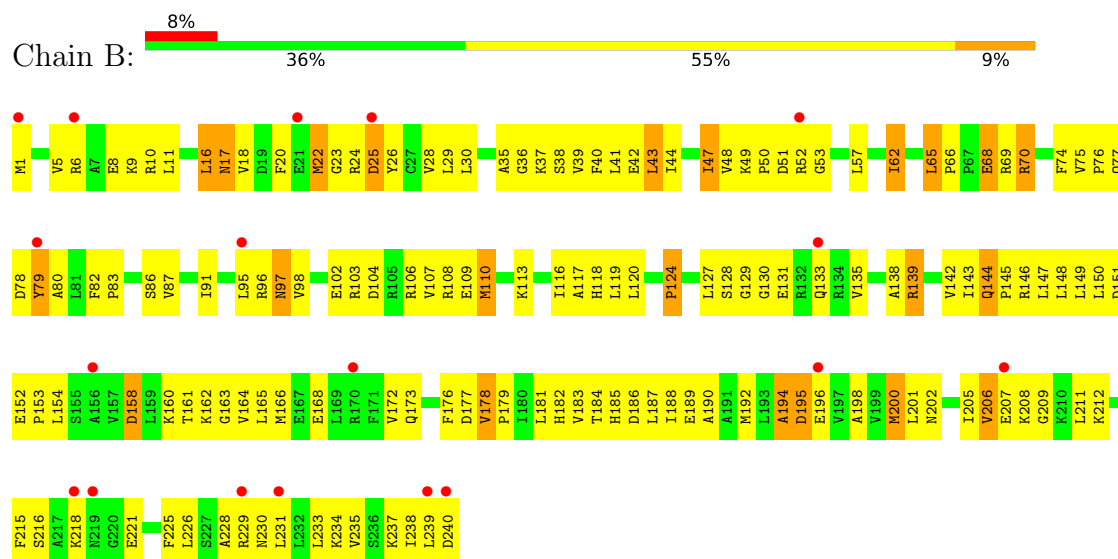
3 Residue-property plots

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.

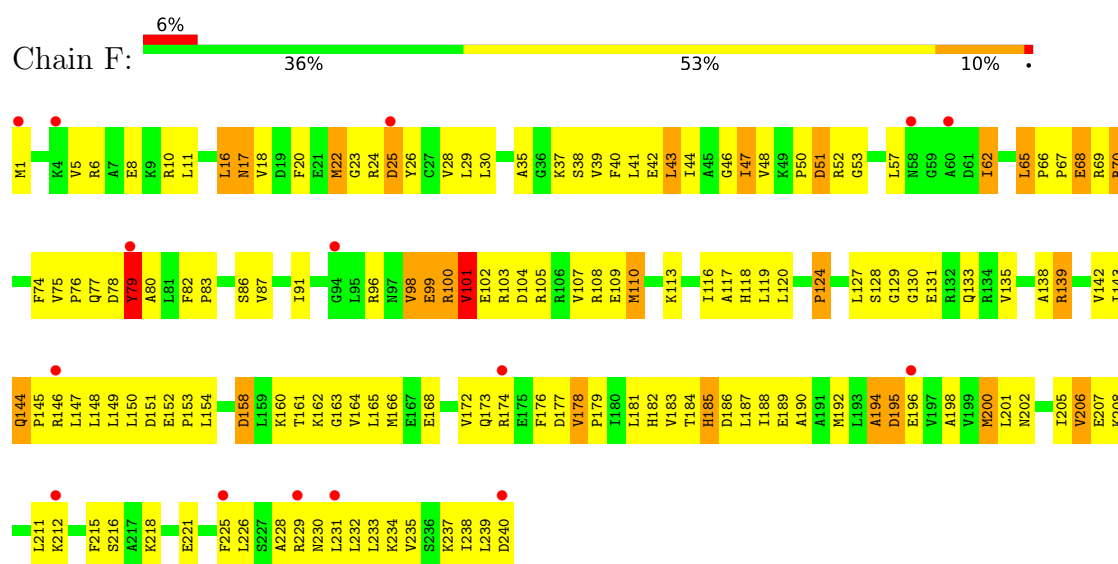
- Molecule 1: Molybdate/tungstate ABC transporter, ATP-binding protein



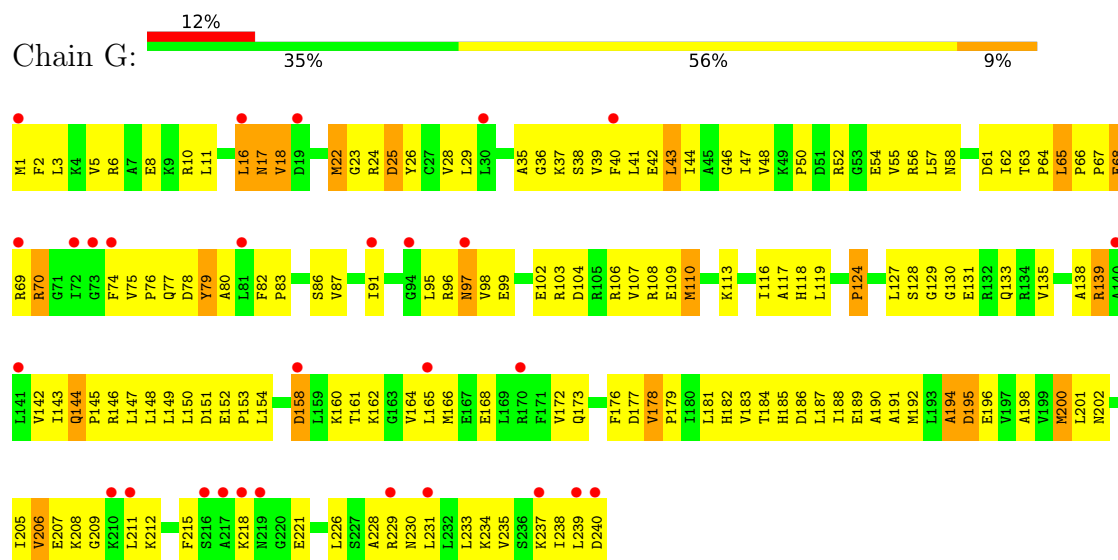
- Molecule 1: Molybdate/tungstate ABC transporter, ATP-binding protein



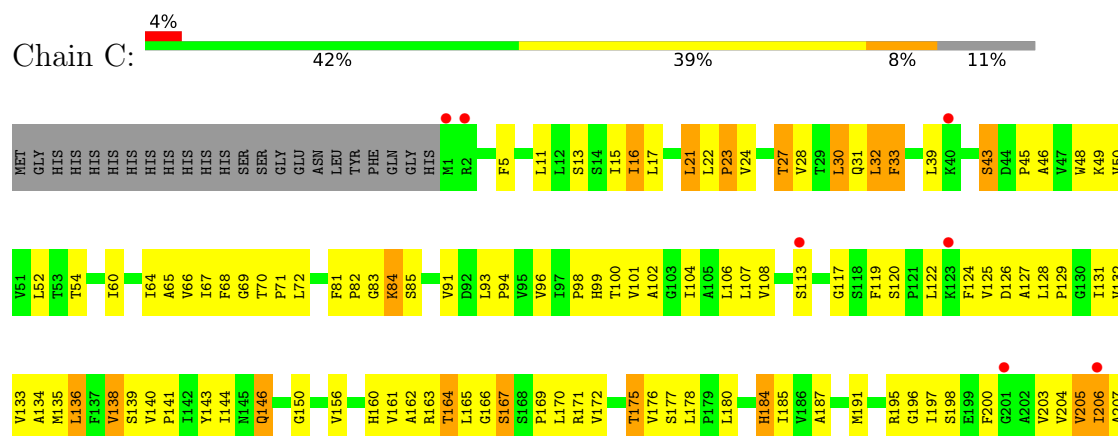
- Molecule 1: Molybdate/tungstate ABC transporter, ATP-binding protein

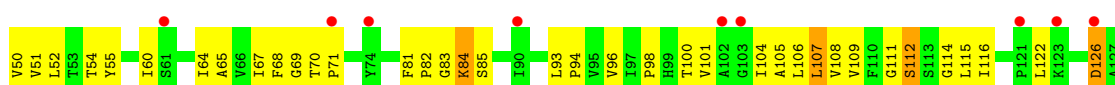


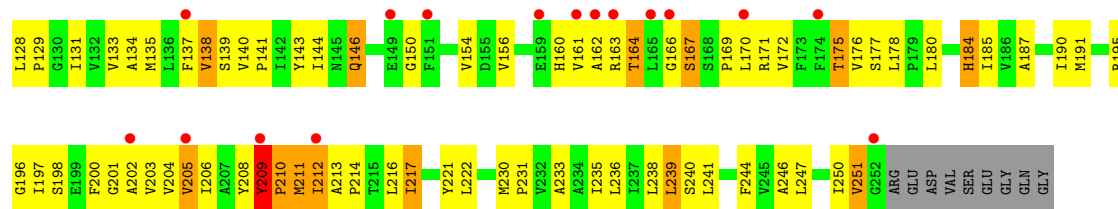
- Molecule 1: Molybdate/tungstate ABC transporter, ATP-binding protein



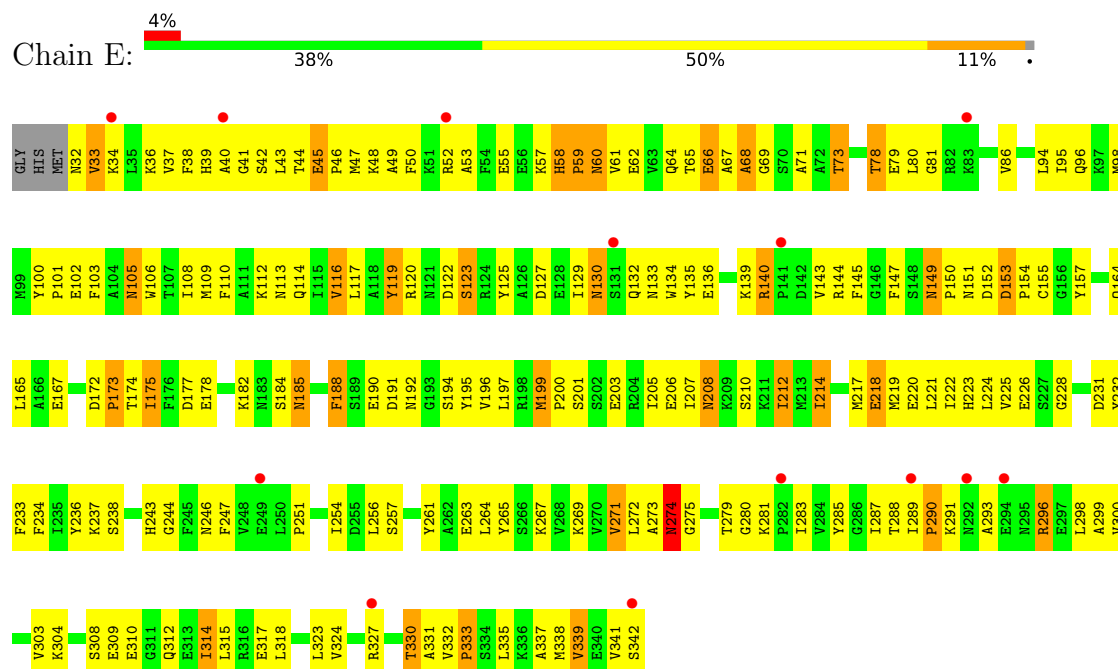
- Molecule 2: Molybdate/tungstate ABC transporter, permease protein



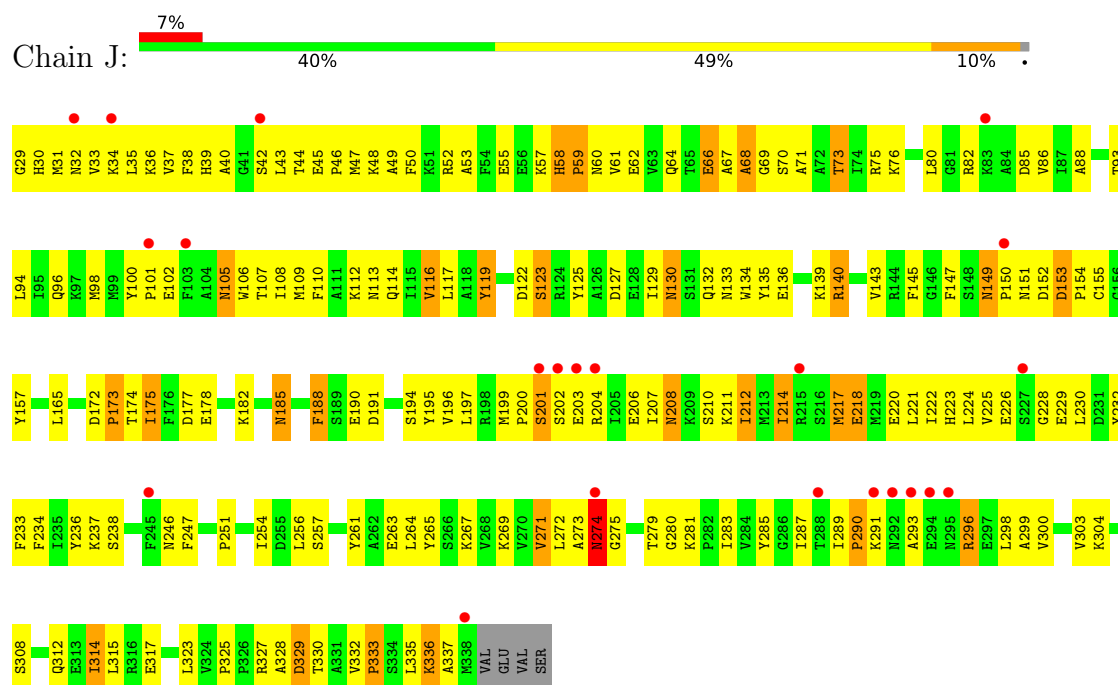




• Molecule 3: Molybdate/tungstate binding protein



• Molecule 3: Molybdate/tungstate binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.03Å 171.20Å 158.47Å 90.00° 98.79° 90.00°	Depositor
Resolution (Å)	30.00 – 3.10 30.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.10) 99.9 (30.00-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 3.11Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.256 , 0.283 0.244 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	92.1	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 86.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	20218	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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: MG, WO4, PO4

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	0.55	0/1930	1.15	16/2596 (0.6%)
1	B	0.50	0/1930	1.14	15/2596 (0.6%)
1	F	0.54	0/1930	1.16	17/2596 (0.7%)
1	G	0.52	0/1930	1.12	14/2596 (0.5%)
2	C	0.59	0/1945	1.03	11/2662 (0.4%)
2	D	0.63	1/1945 (0.1%)	1.03	10/2662 (0.4%)
2	H	0.55	0/1945	1.03	12/2662 (0.5%)
2	I	0.60	1/1945 (0.1%)	1.03	10/2662 (0.4%)
3	E	0.56	0/2540	1.08	17/3435 (0.5%)
3	J	0.55	0/2533	1.06	14/3425 (0.4%)
All	All	0.56	2/20573 (0.0%)	1.08	136/27892 (0.5%)

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	D	0	1
2	I	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	211	MET	SD-CE	8.27	2.00	1.79
2	D	211	MET	SD-CE	6.71	1.96	1.79

The worst 5 of 136 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	209	TYR	CA-C-N	-11.10	105.96	119.84
2	C	209	TYR	C-N-CA	-11.10	105.96	119.84
2	H	209	TYR	CA-C-N	-11.09	105.98	119.84
2	H	209	TYR	C-N-CA	-11.09	105.98	119.84
1	G	195	ASP	N-CA-C	-10.32	100.80	113.50

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	209	TYR	Sidechain
2	I	209	TYR	Sidechain

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	1902	0	2002	183	1
1	B	1902	0	2002	170	0
1	F	1902	0	2002	193	1
1	G	1902	0	2002	193	0
2	C	1901	0	2044	177	0
2	D	1901	0	2044	162	0
2	H	1901	0	2044	179	0
2	I	1901	0	2044	174	0
3	E	2489	0	2487	214	0
3	J	2481	0	2477	205	0
4	A	5	0	0	1	0
4	B	5	0	0	1	0
4	F	5	0	0	1	0
4	G	5	0	0	1	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	J	1	0	0	0	0
6	E	5	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	J	5	0	0	1	0
All	All	20218	0	21148	1660	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 40.

The worst 5 of 1660 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:G:166:MET:HE1	1:G:189:GLU:HA	1.22	1.16
1:F:166:MET:HE1	1:F:189:GLU:HA	1.23	1.15
1:B:187:LEU:HB3	1:B:229:ARG:NH1	1.62	1.15
1:A:187:LEU:HB3	1:A:229:ARG:NH1	1.62	1.15
1:G:187:LEU:HB3	1:G:229:ARG:NH1	1.62	1.14

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)
1:A:210:LYS:NZ	1:F:174:ARG:O[1_546]	2.14	0.06

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	238/240 (99%)	203 (85%)	31 (13%)	4 (2%)	7	30
1	B	238/240 (99%)	202 (85%)	32 (13%)	4 (2%)	7	30
1	F	238/240 (99%)	202 (85%)	29 (12%)	7 (3%)	3	19
1	G	238/240 (99%)	194 (82%)	40 (17%)	4 (2%)	7	30
2	C	250/284 (88%)	193 (77%)	50 (20%)	7 (3%)	4	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	250/284 (88%)	192 (77%)	48 (19%)	10 (4%)	2	13
2	H	250/284 (88%)	194 (78%)	49 (20%)	7 (3%)	4	20
2	I	250/284 (88%)	192 (77%)	49 (20%)	9 (4%)	2	16
3	E	309/314 (98%)	254 (82%)	44 (14%)	11 (4%)	2	16
3	J	308/314 (98%)	254 (82%)	43 (14%)	11 (4%)	2	16
All	All	2569/2724 (94%)	2080 (81%)	415 (16%)	74 (3%)	3	19

5 of 74 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	100	ARG
2	C	84	LYS
2	D	84	LYS
2	D	115	LEU
2	H	84	LYS

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	202/202 (100%)	188 (93%)	14 (7%)	14	41
1	B	202/202 (100%)	188 (93%)	14 (7%)	14	41
1	F	202/202 (100%)	187 (93%)	15 (7%)	13	40
1	G	202/202 (100%)	189 (94%)	13 (6%)	16	44
2	C	206/233 (88%)	188 (91%)	18 (9%)	9	34
2	D	206/233 (88%)	188 (91%)	18 (9%)	9	34
2	H	206/233 (88%)	188 (91%)	18 (9%)	9	34
2	I	206/233 (88%)	188 (91%)	18 (9%)	9	34
3	E	273/275 (99%)	253 (93%)	20 (7%)	13	40
3	J	271/275 (98%)	252 (93%)	19 (7%)	14	41
All	All	2176/2290 (95%)	2009 (92%)	167 (8%)	12	38

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	43	SER
3	E	274	ASN
2	I	156	VAL
3	E	105	ASN
3	J	116	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	223	HIS
3	J	185	ASN
3	E	274	ASN
3	J	130	ASN
3	J	208	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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
4	PO4	F	803	5	4,4,4	2.99	4 (100%)	6,6,6	0.50	0
4	PO4	A	801	5	4,4,4	3.11	3 (75%)	6,6,6	0.52	0
4	PO4	G	804	5	4,4,4	3.05	4 (100%)	6,6,6	0.51	0
6	WO4	E	701	3	2,4,4	11.41	2 (100%)	-		
6	WO4	J	702	3	2,4,4	11.46	2 (100%)	-		
4	PO4	B	802	5	4,4,4	2.90	4 (100%)	6,6,6	0.42	0

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	701	WO4	W-O2	12.03	2.03	1.77
6	J	702	WO4	W-O2	12.03	2.03	1.77
6	J	702	WO4	W-O1	10.87	2.00	1.77
6	E	701	WO4	W-O1	10.76	2.00	1.77
4	A	801	PO4	P-O1	4.65	1.61	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	803	PO4	1	0
4	A	801	PO4	1	0
4	G	804	PO4	1	0
6	E	701	WO4	3	0
6	J	702	WO4	1	0
4	B	802	PO4	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 ⓘ

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	240/240 (100%)	0.34	14 (5%)	29	16	32, 73, 148, 178	0
1	B	240/240 (100%)	0.64	18 (7%)	20	11	60, 115, 183, 200	0
1	F	240/240 (100%)	0.60	15 (6%)	26	14	38, 96, 168, 197	0
1	G	240/240 (100%)	0.88	29 (12%)	8	5	62, 134, 188, 200	0
2	C	252/284 (88%)	0.21	10 (3%)	42	23	33, 66, 134, 200	0
2	D	252/284 (88%)	0.32	6 (2%)	59	38	39, 76, 146, 200	0
2	H	252/284 (88%)	0.73	19 (7%)	20	11	40, 93, 175, 199	0
2	I	252/284 (88%)	0.73	26 (10%)	12	6	52, 102, 169, 200	0
3	E	311/314 (99%)	0.45	13 (4%)	40	22	36, 81, 148, 188	0
3	J	310/314 (98%)	0.64	22 (7%)	22	12	32, 87, 156, 198	0
All	All	2589/2724 (95%)	0.55	172 (6%)	24	13	32, 91, 169, 200	0

The worst 5 of 172 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	209	TYR	4.9
1	B	240	ASP	4.8
1	F	174	ARG	4.8
2	I	209	TYR	4.7
1	A	219	ASN	4.6

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MG	F	703	1/1	0.67	0.24	89,89,89,89	0
5	MG	B	702	1/1	0.72	0.23	87,87,87,87	0
5	MG	E	705	1/1	0.78	0.18	86,86,86,86	0
5	MG	A	701	1/1	0.84	0.15	75,75,75,75	0
4	PO4	G	804	5/5	0.90	0.08	99,99,99,99	0
5	MG	G	704	1/1	0.93	0.12	83,83,83,83	0
4	PO4	B	802	5/5	0.94	0.11	84,84,84,84	0
5	MG	J	706	1/1	0.94	0.12	42,42,42,42	0
4	PO4	F	803	5/5	0.96	0.07	60,60,60,60	0
4	PO4	A	801	5/5	0.96	0.07	60,60,60,60	0
6	WO4	E	701	5/5	0.99	0.08	49,49,49,49	0
6	WO4	J	702	5/5	0.99	0.07	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.