



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 5A2V / pdb_00005a2v
Title : Crystal structure of mtPAP in Apo form
Authors : Lapkouski, M.; Hallberg, B.M.
Deposited on : 2015-05-26
Resolution : 1.82 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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
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

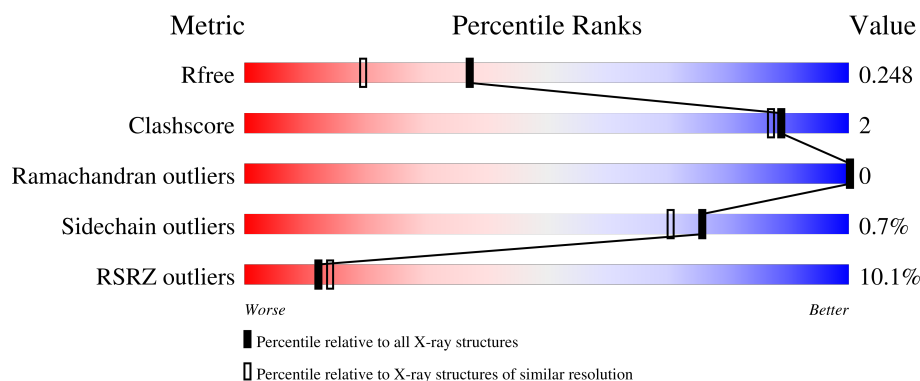
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.82 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}	180053	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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	555	9% 81% • 15%
1	B	555	8% 81% • 15%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8229 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 MITOCHONDRIAL PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	470	Total	C	N	O	S	0	9	0
			3751	2418	614	693	26			
1	B	472	Total	C	N	O	S	0	18	0
			3805	2456	622	701	26			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	MET	-	expression tag	UNP F1NBW0
A	15	HIS	-	expression tag	UNP F1NBW0
A	16	HIS	-	expression tag	UNP F1NBW0
A	17	HIS	-	expression tag	UNP F1NBW0
A	18	HIS	-	expression tag	UNP F1NBW0
A	19	HIS	-	expression tag	UNP F1NBW0
A	20	HIS	-	expression tag	UNP F1NBW0
A	21	SER	-	expression tag	UNP F1NBW0
A	22	SER	-	expression tag	UNP F1NBW0
A	23	GLY	-	expression tag	UNP F1NBW0
A	24	VAL	-	expression tag	UNP F1NBW0
A	25	ASP	-	expression tag	UNP F1NBW0
A	26	LEU	-	expression tag	UNP F1NBW0
A	27	GLY	-	expression tag	UNP F1NBW0
A	28	THR	-	expression tag	UNP F1NBW0
A	29	GLU	-	expression tag	UNP F1NBW0
A	30	ASN	-	expression tag	UNP F1NBW0
A	31	LEU	-	expression tag	UNP F1NBW0
A	32	TYR	-	expression tag	UNP F1NBW0
A	33	PHE	-	expression tag	UNP F1NBW0
A	34	GLN	-	expression tag	UNP F1NBW0
A	35	SER	-	expression tag	UNP F1NBW0
A	36	MET	-	expression tag	UNP F1NBW0
B	14	MET	-	expression tag	UNP F1NBW0
B	15	HIS	-	expression tag	UNP F1NBW0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	16	HIS	-	expression tag	UNP F1NBW0
B	17	HIS	-	expression tag	UNP F1NBW0
B	18	HIS	-	expression tag	UNP F1NBW0
B	19	HIS	-	expression tag	UNP F1NBW0
B	20	HIS	-	expression tag	UNP F1NBW0
B	21	SER	-	expression tag	UNP F1NBW0
B	22	SER	-	expression tag	UNP F1NBW0
B	23	GLY	-	expression tag	UNP F1NBW0
B	24	VAL	-	expression tag	UNP F1NBW0
B	25	ASP	-	expression tag	UNP F1NBW0
B	26	LEU	-	expression tag	UNP F1NBW0
B	27	GLY	-	expression tag	UNP F1NBW0
B	28	THR	-	expression tag	UNP F1NBW0
B	29	GLU	-	expression tag	UNP F1NBW0
B	30	ASN	-	expression tag	UNP F1NBW0
B	31	LEU	-	expression tag	UNP F1NBW0
B	32	TYR	-	expression tag	UNP F1NBW0
B	33	PHE	-	expression tag	UNP F1NBW0
B	34	GLN	-	expression tag	UNP F1NBW0
B	35	SER	-	expression tag	UNP F1NBW0
B	36	MET	-	expression tag	UNP F1NBW0

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cl 1 1	0	0
2	B	3	Total Cl 3 3	0	0

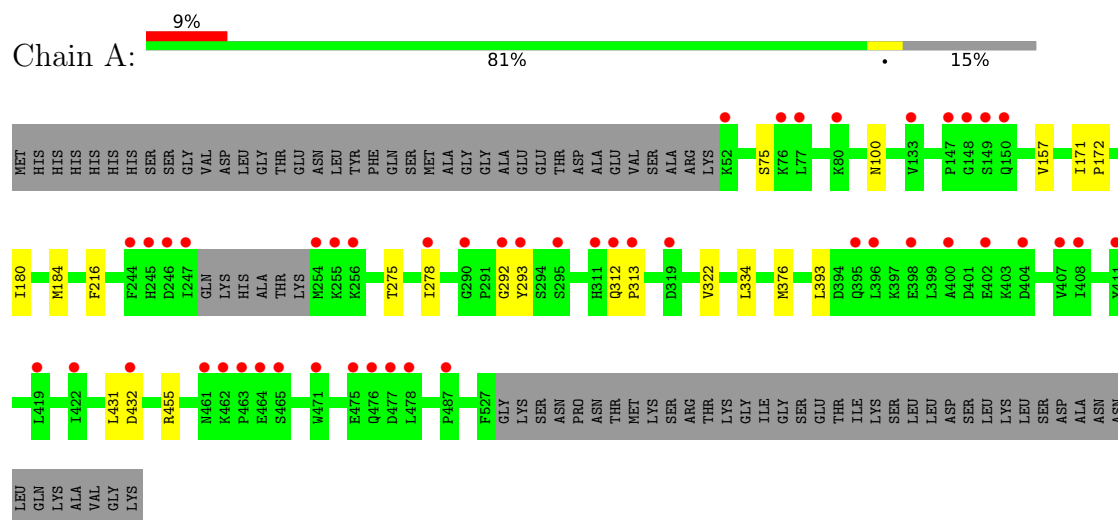
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	343	Total O 343 343	0	0
3	B	326	Total O 326 326	0	0

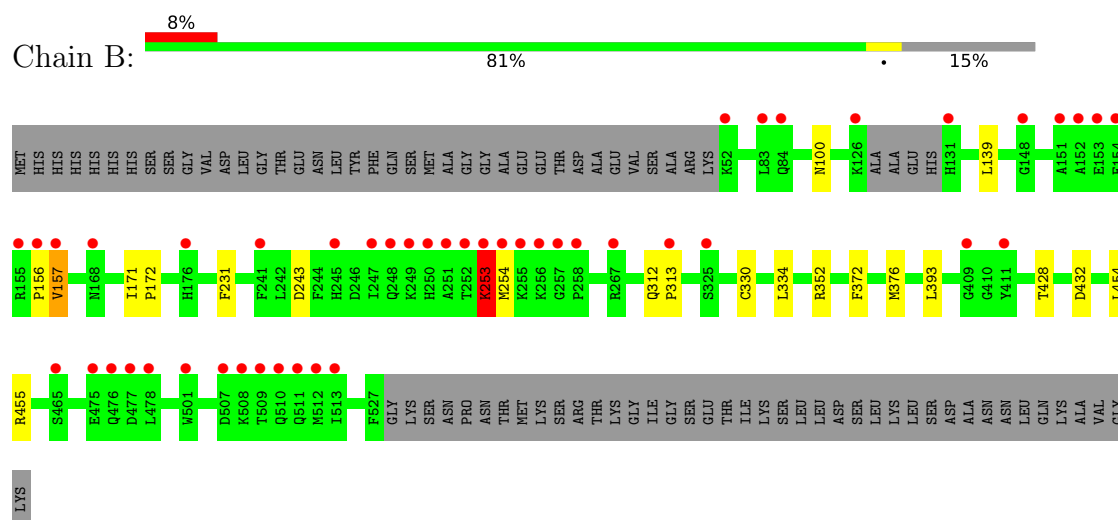
3 Residue-property plots [i](#)

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: MITOCHONDRIAL PROTEIN



• Molecule 1: MITOCHONDRIAL PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.39Å 94.37Å 191.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.00 – 1.82 38.00 – 1.82	Depositor EDS
% Data completeness (in resolution range)	100.0 (38.00-1.82) 100.0 (38.00-1.82)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 1.82Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.222 , 0.245 0.225 , 0.248	Depositor DCC
R_{free} test set	4878 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	30.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 29.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8229	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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: CL

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	0.42	0/3870	0.66	3/5246 (0.1%)
1	B	0.40	0/3949	0.68	4/5352 (0.1%)
All	All	0.41	0/7819	0.67	7/10598 (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	B	0	1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	253	LYS	CB-CA-C	9.75	131.45	110.19
1	B	253	LYS	CA-C-N	6.60	134.15	121.54
1	B	253	LYS	C-N-CA	6.60	134.15	121.54
1	B	253	LYS	N-CA-C	-6.25	102.73	110.41
1	A	293	TYR	N-CA-C	6.21	119.81	111.24
1	A	292	GLY	CA-C-N	5.34	130.53	122.68
1	A	292	GLY	C-N-CA	5.34	130.53	122.68

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	253	LYS	Peptide

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	3751	0	3690	14	0
1	B	3805	0	3761	15	0
2	A	1	0	0	0	0
2	B	3	0	0	0	0
3	A	343	0	0	0	0
3	B	326	0	0	1	0
All	All	8229	0	7451	29	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 2.

All (29) 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:376[A]:MET:HA	1:A:376[A]:MET:HE2	1.58	0.86
1:A:180:ILE:HG22	1:A:184[A]:MET:HE2	1.63	0.79
1:B:376[A]:MET:HE2	1:B:376[A]:MET:HA	1.69	0.73
1:A:180:ILE:HG22	1:A:184[A]:MET:CE	2.23	0.68
1:A:180:ILE:CG2	1:A:184[A]:MET:HE2	2.24	0.67
1:A:334:LEU:HD21	1:A:376[A]:MET:HE3	1.82	0.62
1:B:334:LEU:HD21	1:B:376[A]:MET:HE3	1.87	0.56
1:B:312[A]:GLN:NE2	1:B:312[A]:GLN:HA	2.25	0.52
1:A:334:LEU:HD21	1:A:376[A]:MET:CE	2.41	0.50
1:B:376[B]:MET:HE3	1:B:454:LEU:HD22	1.96	0.48
1:B:253:LYS:HD2	1:B:254:MET:H	1.80	0.47
1:B:334:LEU:HD21	1:B:376[A]:MET:CE	2.45	0.46
1:A:275:THR:HG23	1:A:322:VAL:CG2	2.46	0.46
1:A:184[A]:MET:HE1	1:A:431:LEU:O	2.15	0.46
1:A:100:ASN:ND2	1:A:312:GLN:O	2.49	0.46
1:B:139:LEU:HD11	3:B:2186:HOH:O	2.17	0.44
1:B:156:PRO:HB2	1:B:157:VAL:HG13	2.00	0.44
1:A:393:LEU:HB3	1:A:455:ARG:HA	2.00	0.43
1:B:231:PHE:O	1:B:352[A]:ARG:NH2	2.52	0.43
1:A:216:PHE:CE1	1:A:278:ILE:HD13	2.54	0.42
1:A:171:ILE:HB	1:A:172:PRO:HD3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:THR:HG23	1:A:322:VAL:HG23	2.02	0.41
1:B:330[B]:CYS:SG	1:B:372:PHE:CE1	3.14	0.41
1:B:171:ILE:HB	1:B:172:PRO:HD3	2.02	0.41
1:A:312:GLN:N	1:A:313:PRO:CD	2.84	0.41
1:B:393:LEU:HB3	1:B:455:ARG:HA	2.03	0.41

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	476/555 (86%)	468 (98%)	8 (2%)	0	100	100
1	B	486/555 (88%)	478 (98%)	8 (2%)	0	100	100
All	All	962/1110 (87%)	946 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	415/497 (84%)	412 (99%)	3 (1%)	76	70
1	B	423/497 (85%)	418 (99%)	5 (1%)	63	54
All	All	838/994 (84%)	830 (99%)	8 (1%)	76	60

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	SER
1	A	157	VAL
1	A	432	ASP
1	B	157	VAL
1	B	428[A]	THR
1	B	428[B]	THR
1	B	432[A]	ASP
1	B	432[B]	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	GLN
1	A	131	HIS
1	A	150	GLN
1	A	406	HIS
1	A	440	GLN
1	A	483	ASN
1	A	504	GLN
1	B	189	ASN
1	B	488	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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

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	470/555 (84%)	0.76	48 (10%)	12 14	12, 32, 54, 69	9 (1%)
1	B	472/555 (85%)	0.63	47 (9%)	12 14	12, 29, 60, 87	19 (4%)
All	All	942/1110 (84%)	0.69	95 (10%)	12 14	12, 31, 55, 87	28 (2%)

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	154	GLU	6.0
1	A	247	ILE	6.0
1	B	247	ILE	6.0
1	B	509	THR	5.5
1	B	252	THR	5.3
1	B	151	ALA	5.2
1	A	293	TYR	5.1
1	B	250	HIS	5.0
1	B	513	ILE	4.9
1	B	152	ALA	4.9
1	B	512	MET	4.3
1	B	156	PRO	4.0
1	A	244	PHE	3.8
1	B	508	LYS	3.7
1	A	400	ALA	3.7
1	B	245	HIS	3.7
1	A	313	PRO	3.6
1	A	245	HIS	3.6
1	A	254	MET	3.6
1	B	507	ASP	3.5
1	B	131	HIS	3.4
1	A	312	GLN	3.3
1	B	256	LYS	3.3
1	A	432	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	255	LYS	3.3
1	B	251	ALA	3.2
1	B	501	TRP	3.2
1	A	461	ASN	3.1
1	A	463	PRO	3.1
1	A	292	GLY	3.1
1	A	464	GLU	3.0
1	A	477	ASP	3.0
1	A	256	LYS	3.0
1	B	253	LYS	3.0
1	B	254	MET	3.0
1	B	157	VAL	2.9
1	A	411	TYR	2.9
1	A	246	ASP	2.9
1	A	465	SER	2.9
1	B	465	SER	2.9
1	A	478	LEU	2.9
1	B	148	GLY	2.9
1	A	407	VAL	2.8
1	A	471	TRP	2.8
1	B	267	ARG	2.8
1	B	248	GLN	2.7
1	B	258	PRO	2.7
1	B	411	TYR	2.6
1	B	155	ARG	2.6
1	A	52	LYS	2.6
1	B	475	GLU	2.6
1	A	398	GLU	2.5
1	B	477	ASP	2.5
1	B	241	PHE	2.5
1	B	249	LYS	2.5
1	A	402	GLU	2.5
1	A	77	LEU	2.5
1	B	511	GLN	2.5
1	A	133	VAL	2.5
1	A	311	HIS	2.4
1	B	153	GLU	2.4
1	A	149	SER	2.4
1	B	126	LYS	2.4
1	A	476	GLN	2.4
1	B	168	ASN	2.4
1	B	325	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	462	LYS	2.4
1	B	409	GLY	2.3
1	A	76	LYS	2.3
1	A	147	PRO	2.3
1	A	319	ASP	2.3
1	B	257	GLY	2.2
1	A	278	ILE	2.2
1	A	408	ILE	2.2
1	B	52	LYS	2.2
1	A	475	GLU	2.2
1	A	396	LEU	2.2
1	B	83[A]	LEU	2.2
1	B	84	GLN	2.2
1	A	148	GLY	2.2
1	A	404	ASP	2.2
1	B	176[A]	HIS	2.2
1	A	255	LYS	2.2
1	A	419	LEU	2.1
1	A	487	PRO	2.1
1	B	478	LEU	2.1
1	A	80	LYS	2.1
1	A	150	GLN	2.1
1	B	510	GLN	2.1
1	A	290	GLY	2.0
1	A	395	GLN	2.0
1	B	313	PRO	2.0
1	A	295	SER	2.0
1	A	422	ILE	2.0
1	B	476	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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($\text{\AA}^2$)	Q<0.9
2	CL	B	1529	1/1	0.97	0.06	34,34,34,34	0
2	CL	B	1530	1/1	0.97	0.07	50,50,50,50	0
2	CL	A	1528	1/1	0.99	0.04	28,28,28,28	0
2	CL	B	1528	1/1	0.99	0.10	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.