



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 12:22 AM EDT

PDB ID : 1OE9 / pdb_00001oe9
Title : Crystal structure of Myosin V motor with essential light chain-nucleotide-free
Authors : Coureux, P.-D.; Wells, A.L.; Menetrey, J.; Yengo, C.M.; Morris, C.A.; Sweeney, H.L.; Houdusse, A.
Deposited on : 2003-03-21
Resolution : 2.05 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
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

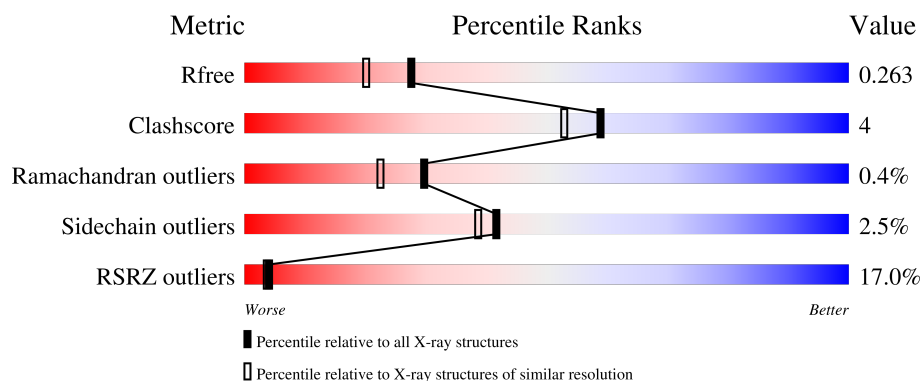
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	795	14% 82% 10% 8%
2	B	151	24% 76% 15% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7263 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 MYOSIN VA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	731	5866	3760	1004	1065	37	0	3	1

- Molecule 2 is a protein called MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE A ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	139	1059	673	174	206	6	0	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

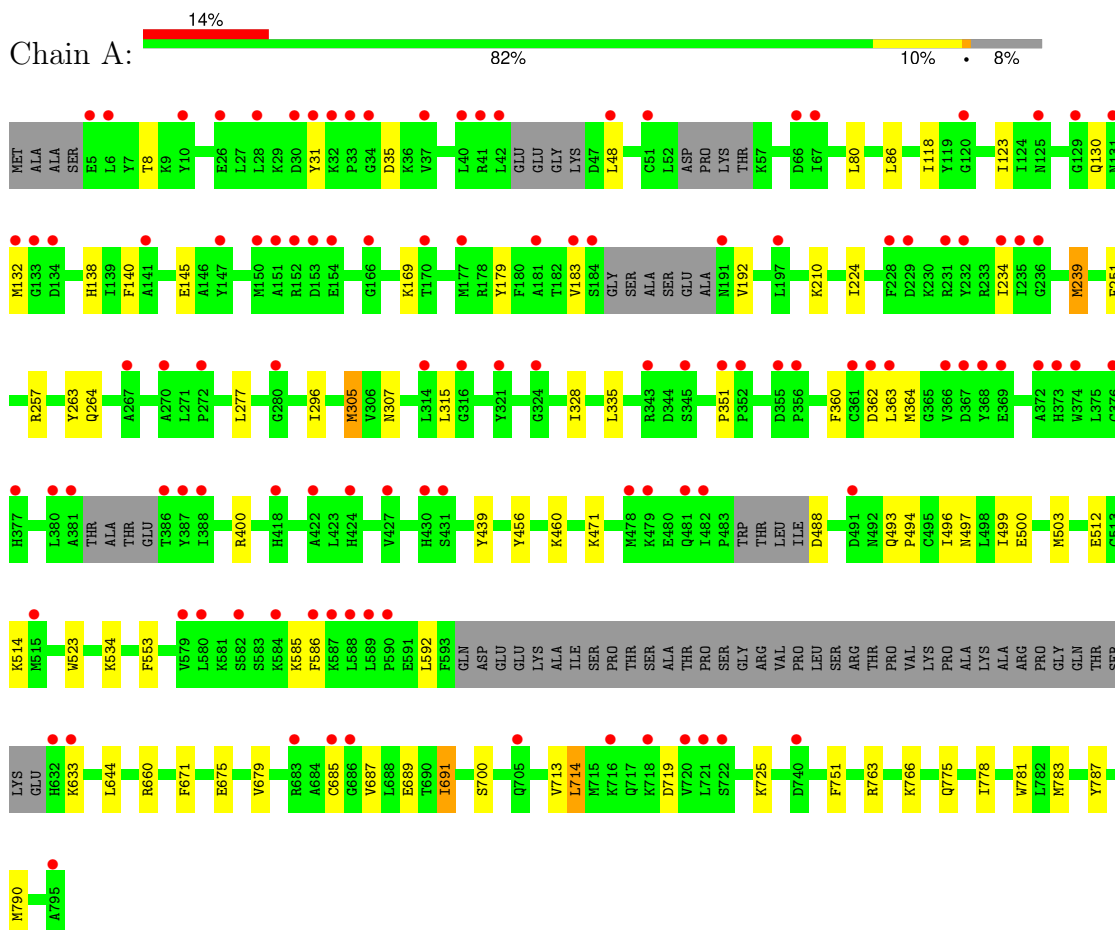
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	314	Total 314	O 314	0	0
4	B	19	Total 19	O 19	0	0

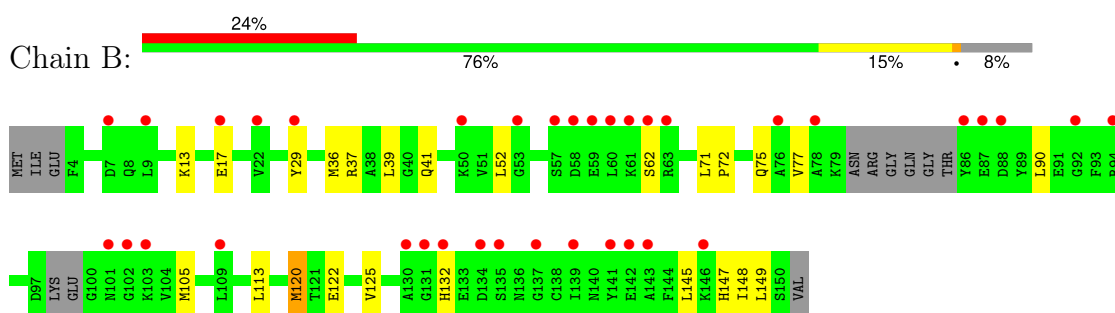
3 Residue-property plots

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: MYOSIN VA



• Molecule 2: MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE A ISOFORM



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.93Å 98.25Å 111.38Å 90.00° 101.43° 90.00°	Depositor
Resolution (Å)	40.00 – 2.05 40.00 – 2.05	Depositor EDS
% Data completeness (in resolution range)	96.8 (40.00-2.05) 96.7 (40.00-2.05)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.220 , 0.264 0.223 , 0.263	Depositor DCC
R_{free} test set	3680 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	32.0	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7263	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	A	0.85	2/6005 (0.0%)	0.90	0/8108
2	B	0.67	1/1075 (0.1%)	0.87	0/1448
All	All	0.83	3/7080 (0.0%)	0.90	0/9556

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	305	MET	SD-CE	-8.78	1.57	1.79
2	B	120	MET	SD-CE	-8.18	1.59	1.79
1	A	239	MET	CG-SD	-5.85	1.66	1.80

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5866	0	5755	47	0
2	B	1059	0	998	16	0
3	A	5	0	0	0	0
4	A	314	0	0	10	0
4	B	19	0	0	2	0
All	All	7263	0	6753	60	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 4.

All (60) 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:328:ILE:HD13	1:A:592:LEU:HD11	1.66	0.75
1:A:138:HIS:HD2	1:A:140:PHE:H	1.32	0.73
1:A:660:ARG:NH1	4:A:2261:HOH:O	2.20	0.73
1:A:192:VAL:HG21	1:A:234:ILE:HG22	1.82	0.60
1:A:714:LEU:HD11	1:A:763:ARG:HA	1.83	0.59
1:A:713:VAL:O	1:A:766:LYS:HE2	2.05	0.57
1:A:31:TYR:CE1	1:A:35:ASP:HB2	2.42	0.55
1:A:86:LEU:HD13	1:A:679:VAL:HG22	1.90	0.53
1:A:118:ILE:HA	1:A:123:ILE:HD13	1.90	0.52
2:B:120:MET:HE3	2:B:125:VAL:HG22	1.91	0.52
1:A:138:HIS:CD2	1:A:140:PHE:H	2.21	0.51
1:A:675:GLU:O	1:A:679:VAL:HG23	2.10	0.51
2:B:37:ARG:NH1	4:B:2005:HOH:O	2.38	0.50
1:A:700:SER:HB2	1:A:751:PHE:HB2	1.93	0.50
1:A:685[A]:CYS:SG	4:A:2275:HOH:O	2.60	0.50
1:A:264:GLN:C	1:A:305:MET:HE2	2.38	0.49
1:A:363:LEU:C	1:A:364:MET:HE2	2.38	0.48
1:A:80:LEU:HG	1:A:691:ILE:HG23	1.96	0.48
2:B:72:PRO:HA	2:B:75:GLN:HE21	1.79	0.48
1:A:512:GLU:HG2	1:A:523:TRP:HB2	1.96	0.47
1:A:192:VAL:HG21	1:A:234:ILE:CG2	2.44	0.46
1:A:456:TYR:CD1	1:A:499:ILE:HG21	2.49	0.46
1:A:123:ILE:HD12	4:A:2045:HOH:O	2.16	0.46
1:A:725:LYS:NZ	4:A:2293:HOH:O	2.47	0.46
2:B:113:LEU:HB3	2:B:120:MET:CE	2.46	0.45
1:A:132:MET:HB2	1:A:145:GLU:CG	2.46	0.45
1:A:179:TYR:CZ	1:A:183:VAL:HG11	2.52	0.45
1:A:210:LYS:HB2	1:A:296:ILE:HD11	1.99	0.45
2:B:90:LEU:HD12	2:B:145:LEU:HD23	1.98	0.44
1:A:493:GLN:N	1:A:494:PRO:CD	2.79	0.44
2:B:71:LEU:HB3	2:B:72:PRO:HD3	2.00	0.44
1:A:471:LYS:NZ	4:A:2191:HOH:O	2.42	0.44
1:A:685[B]:CYS:SG	1:A:687:VAL:HG23	2.58	0.44
1:A:251:PHE:CD2	1:A:251:PHE:C	2.96	0.43
1:A:787:TYR:HA	1:A:790:MET:HG2	2.00	0.43
1:A:460:LYS:HG3	1:A:644:LEU:HD21	1.99	0.43
1:A:257:ARG:HB3	1:A:263:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:GLN:NE2	4:A:2055:HOH:O	2.48	0.43
1:A:132:MET:HB2	1:A:145:GLU:HG2	2.01	0.42
2:B:132:HIS:NE2	2:B:147:HIS:CD2	2.87	0.42
1:A:360:PHE:O	1:A:364:MET:HG2	2.20	0.42
1:A:778:ILE:HD12	2:B:120:MET:HE1	2.02	0.42
2:B:37:ARG:HA	2:B:41:GLN:O	2.20	0.42
1:A:335:LEU:O	1:A:400:ARG:HD2	2.20	0.42
1:A:553:PHE:CE2	1:A:689:GLU:HB3	2.54	0.42
2:B:29:TYR:CD2	2:B:52:LEU:HD22	2.55	0.42
2:B:36:MET:SD	2:B:77:VAL:HG21	2.60	0.42
1:A:781:TRP:CD1	2:B:148:ILE:HA	2.55	0.42
2:B:13:LYS:O	2:B:17:GLU:HG2	2.20	0.41
1:A:169:LYS:NZ	4:A:2075:HOH:O	2.41	0.41
1:A:497:ASN:ND2	4:A:2200:HOH:O	2.52	0.41
1:A:778:ILE:CD1	2:B:120:MET:HE1	2.51	0.41
2:B:113:LEU:HB3	2:B:120:MET:HE2	2.03	0.41
1:A:496:ILE:O	1:A:500:GLU:HG2	2.20	0.41
1:A:362:ASP:OD1	1:A:585:LYS:NZ	2.54	0.41
1:A:783:MET:HE2	4:A:2311:HOH:O	2.21	0.41
2:B:37:ARG:HD2	4:B:2005:HOH:O	2.21	0.41
1:A:8:THR:OG1	4:A:2002:HOH:O	2.22	0.40
1:A:224:ILE:HD13	1:A:239:MET:HG3	2.02	0.40
1:A:503:MET:HA	1:A:503:MET:HE2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	720/795 (91%)	700 (97%)	17 (2%)	3 (0%)	30	22
2	B	133/151 (88%)	131 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	853/946 (90%)	831 (97%)	19 (2%)	3 (0%)	30	22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	633	LYS
1	A	671	PHE
1	A	351	PRO

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	622/696 (89%)	609 (98%)	13 (2%)	47	46
2	B	108/129 (84%)	103 (95%)	5 (5%)	24	18
All	All	730/825 (88%)	712 (98%)	18 (2%)	42	39

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	LEU
1	A	277	LEU
1	A	307	ASN
1	A	315	LEU
1	A	439	TYR
1	A	488	ASP
1	A	514	LYS
1	A	534	LYS
1	A	586	PHE
1	A	691	ILE
1	A	714	LEU
1	A	719	ASP
1	A	775	GLN
2	B	39	LEU
2	B	62	SER

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Mol	Chain	Res	Type
2	B	105	MET
2	B	122	GLU
2	B	149	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	138	HIS
1	A	406	HIS
1	A	410	ASN
1	A	424	HIS
1	A	430	HIS
1	A	463	GLN
1	A	493	GLN
1	A	497	ASN
1	A	525	GLN
1	A	726	GLN
2	B	75	GLN
2	B	111	HIS
2	B	147	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
3	SO4	A	1796	-	4,4,4	0.26	0	6,6,6	0.44	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 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	731/795 (91%)	0.88	112 (15%) 5 5	21, 39, 59, 73	3 (0%)
2	B	139/151 (92%)	1.54	36 (25%) 1 1	40, 54, 67, 70	0
All	All	870/946 (91%)	0.99	148 (17%) 4 4	21, 42, 63, 73	3 (0%)

All (148) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	10	TYR	5.8
2	B	101	ASN	5.2
1	A	133	GLY	5.1
1	A	151	ALA	4.9
1	A	632	HIS	4.7
2	B	143	ALA	4.3
2	B	137	GLY	4.0
1	A	6	LEU	4.0
1	A	125	ASN	3.9
1	A	586	PHE	3.9
1	A	587	LYS	3.9
2	B	102	GLY	3.8
1	A	387	TYR	3.7
2	B	103	LYS	3.7
2	B	58	ASP	3.7
2	B	92	GLY	3.7
1	A	590	PRO	3.6
1	A	422	ALA	3.6
1	A	191	ASN	3.6
1	A	197	LEU	3.6
1	A	427	VAL	3.6
1	A	181	ALA	3.5
1	A	478	MET	3.5
1	A	352	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	380	LEU	3.4
1	A	270	ALA	3.3
1	A	40	LEU	3.3
2	B	86	TYR	3.3
1	A	515	MET	3.3
2	B	131	GLY	3.3
1	A	42	LEU	3.2
1	A	234	ILE	3.2
1	A	345	SER	3.2
2	B	53	GLY	3.2
1	A	232	TYR	3.1
1	A	28	LEU	3.1
2	B	17	GLU	3.1
1	A	367	ASP	3.0
2	B	78	ALA	3.0
1	A	579	VAL	3.0
2	B	88	ASP	3.0
1	A	184	SER	3.0
1	A	363	LEU	2.9
1	A	718	LYS	2.9
1	A	228	PHE	2.9
2	B	141	TYR	2.9
2	B	76	ALA	2.9
2	B	60	LEU	2.8
2	B	62	SER	2.8
1	A	351	PRO	2.8
1	A	32	LYS	2.8
2	B	134	ASP	2.8
2	B	94	ARG	2.8
1	A	362	ASP	2.8
1	A	34	GLY	2.8
1	A	685[A]	CYS	2.8
1	A	361	CYS	2.7
1	A	369	GLU	2.7
1	A	31	TYR	2.7
2	B	57	SER	2.7
1	A	152	ARG	2.7
1	A	373	HIS	2.7
1	A	41	ARG	2.7
2	B	135	SER	2.6
1	A	720	VAL	2.6
1	A	150	MET	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	424	HIS	2.6
1	A	633	LYS	2.6
1	A	231	ARG	2.6
1	A	37	VAL	2.6
1	A	368	TYR	2.6
1	A	388	ILE	2.6
1	A	481	GLN	2.6
1	A	26	GLU	2.6
1	A	721	LEU	2.6
1	A	166	GLY	2.5
1	A	479	LYS	2.5
1	A	740	ASP	2.5
1	A	66	ASP	2.4
1	A	229	ASP	2.4
1	A	356	PRO	2.4
2	B	132	HIS	2.4
1	A	324	GLY	2.4
1	A	51[A]	CYS	2.4
2	B	29	TYR	2.4
1	A	716	LYS	2.4
2	B	142	GLU	2.4
2	B	22	VAL	2.4
1	A	377	HIS	2.4
2	B	87	GLU	2.4
1	A	316	GLY	2.4
1	A	582	SER	2.4
1	A	584	LYS	2.4
1	A	170	THR	2.4
1	A	588	LEU	2.3
2	B	50	LYS	2.3
1	A	235	ILE	2.3
1	A	30	ASP	2.3
1	A	132	MET	2.3
1	A	418	HIS	2.3
1	A	366	VAL	2.3
1	A	386	THR	2.3
1	A	5	GLU	2.3
1	A	154	GLU	2.3
1	A	430	HIS	2.3
1	A	722	SER	2.3
1	A	131	ASN	2.3
1	A	795	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	129	GLY	2.3
2	B	139	ILE	2.2
1	A	374	TRP	2.2
1	A	381	ALA	2.2
2	B	9	LEU	2.2
1	A	321	TYR	2.2
2	B	63	ARG	2.2
1	A	482	ILE	2.2
1	A	589	LEU	2.2
1	A	683	ARG	2.2
1	A	355	ASP	2.2
1	A	67	ILE	2.1
1	A	141	ALA	2.1
1	A	314	LEU	2.1
2	B	109	LEU	2.1
1	A	153	ASP	2.1
1	A	686	GLY	2.1
2	B	61	LYS	2.1
1	A	177	MET	2.1
1	A	33	PRO	2.1
1	A	272	PRO	2.1
1	A	372	ALA	2.1
1	A	431	SER	2.1
1	A	580	LEU	2.1
1	A	147	TYR	2.1
1	A	376	CYS	2.0
1	A	705	GLN	2.0
1	A	280	GLY	2.0
1	A	183	VAL	2.0
2	B	59	GLU	2.0
1	A	267	ALA	2.0
2	B	130	ALA	2.0
1	A	48	LEU	2.0
1	A	134	ASP	2.0
1	A	491	ASP	2.0
2	B	7	ASP	2.0
1	A	343	ARG	2.0
2	B	146	LYS	2.0
1	A	120	GLY	2.0
1	A	236	GLY	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
3	SO4	A	1796	5/5	0.79	0.20	44,46,49,50	5

6.5 Other polymers [i](#)

There are no such residues in this entry.