



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:33 AM UTC

PDB ID : 1XO5 / pdb_00001xo5
Title : Crystal structure of CIB1, an EF-hand, integrin and kinase-binding protein
Authors : Gentry, H.R.; Singer, A.U.; Betts, L.; Yang, C.; Ferrara, J.D.; Parise, L.V.;
Sondek, J.
Deposited on : 2004-10-05
Resolution : 1.99 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

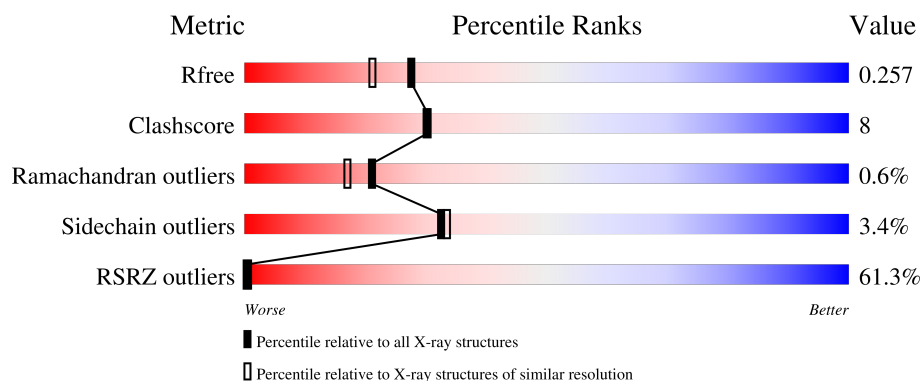
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	183	49% 78% 16% • 5%
1	B	183	66% 76% 17% 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3186 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 Calcium and integrin-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	174	Total	C	N	O	S	0	0	0
			1408	890	236	278	4			
1	B	170	Total	C	N	O	S	0	0	0
			1373	868	229	272	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	44	SER	THR	conflict	UNP Q99828
A	44	SER	THR	conflict	UNP Q99828

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Ca	0	0
			4	4		
2	B	4	Total	Ca	0	0
			4	4		

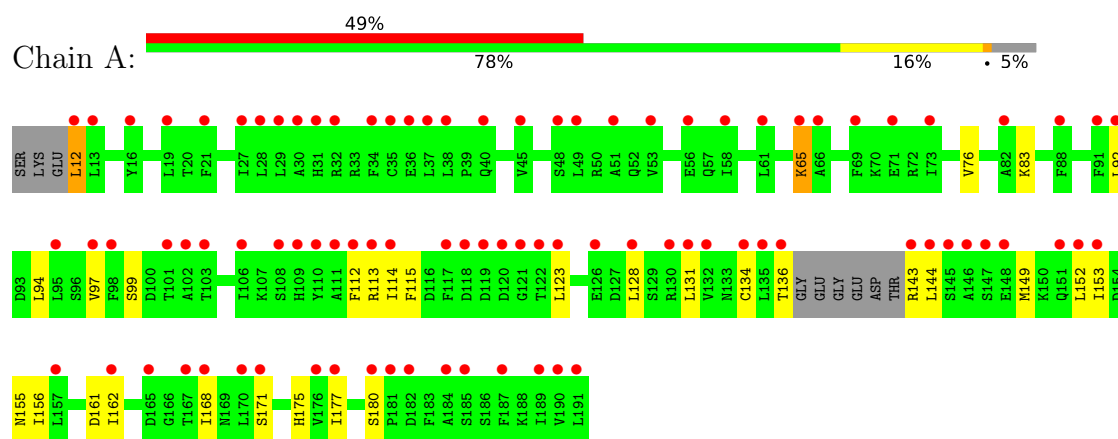
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	263	Total	O	0	0
			263	263		
3	B	134	Total	O	0	0
			134	134		

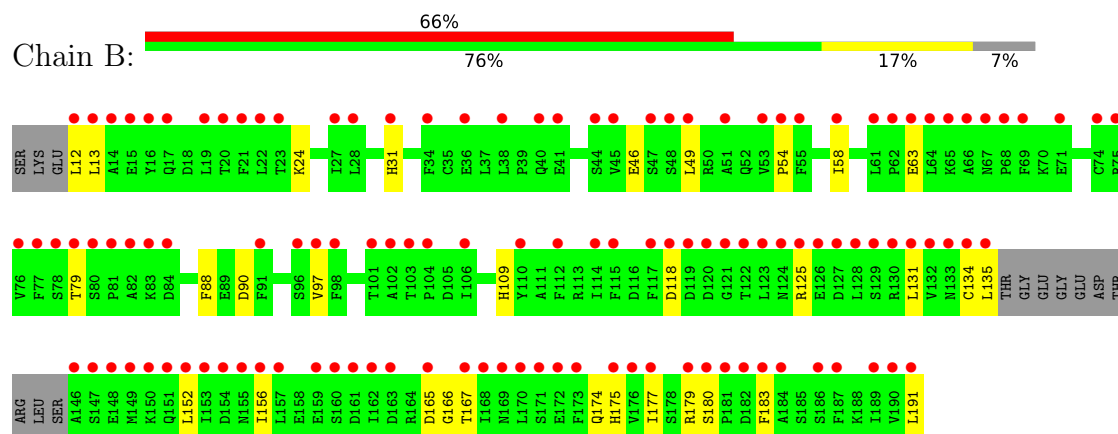
3 Residue-property plots

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: Calcium and integrin-binding protein 1



- Molecule 1: Calcium and integrin-binding protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.66Å 51.01Å 77.21Å 90.00° 103.12° 90.00°	Depositor
Resolution (Å)	40.32 – 1.99 40.32 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.1 (40.32-1.99) 95.1 (40.32-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.32 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.212 , 0.257 0.216 , 0.257	Depositor DCC
R_{free} test set	1430 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	30.3	Xtriage
Anisotropy	0.070	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.5	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	0.90	EDS
Total number of atoms	3186	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.88% 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: CA

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	0.62	0/1432	0.76	0/1932
1	B	0.53	0/1397	0.78	0/1885
All	All	0.58	0/2829	0.77	0/3817

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1408	0	1382	28	1
1	B	1373	0	1337	18	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	263	0	0	20	4
3	B	134	0	0	10	0
All	All	3186	0	2719	46	4

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 8.

All (46) 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:97:VAL:HB	3:A:696:HOH:O	1.62	0.99
1:B:54:PRO:O	3:B:620:HOH:O	1.82	0.96
1:A:115:PHE:O	3:A:821:HOH:O	1.86	0.92
1:A:180:SER:O	3:A:771:HOH:O	1.94	0.86
1:A:128:LEU:HD11	1:A:168:ILE:HD12	1.59	0.82
1:A:152:LEU:O	3:A:833:HOH:O	1.98	0.80
1:A:94:LEU:HA	3:A:696:HOH:O	1.91	0.69
1:B:131:LEU:O	3:B:784:HOH:O	2.09	0.69
1:B:165:ASP:O	1:B:167:THR:N	2.27	0.67
1:A:156:ILE:HG13	3:A:833:HOH:O	1.94	0.66
1:B:191:LEU:HD12	3:B:776:HOH:O	1.97	0.64
1:A:156:ILE:N	3:A:833:HOH:O	2.33	0.61
1:A:136:THR:HG21	1:A:144:LEU:HA	1.82	0.60
1:A:113:ARG:NH1	3:A:616:HOH:O	2.34	0.60
1:B:58:ILE:N	3:B:620:HOH:O	2.35	0.57
1:B:134:CYS:N	3:B:784:HOH:O	2.39	0.55
1:A:175:HIS:CE1	3:A:657:HOH:O	2.61	0.53
1:A:177:ILE:HA	3:A:771:HOH:O	2.10	0.51
1:B:12:LEU:N	3:B:674:HOH:O	2.43	0.50
1:A:161:ASP:HA	3:A:806:HOH:O	2.10	0.49
1:A:156:ILE:HB	3:A:701:HOH:O	2.13	0.48
1:B:109:HIS:CD2	3:B:831:HOH:O	2.66	0.48
1:A:149:MET:O	1:A:153:ILE:HG12	2.15	0.47
1:A:99:SER:CB	3:A:747:HOH:O	2.62	0.47
1:B:174:GLN:HA	1:B:177:ILE:HG22	1.98	0.46
1:A:76:VAL:HG21	1:A:114:ILE:HD13	1.98	0.45
1:A:155:ASN:HB2	3:A:833:HOH:O	2.16	0.45
1:B:97:VAL:HG12	1:B:191:LEU:HD13	1.98	0.45
1:A:12:LEU:N	3:A:643:HOH:O	2.49	0.45
1:B:180:SER:OG	1:B:183:PHE:HD1	1.99	0.45
1:B:46:GLU:HB2	3:B:795:HOH:O	2.17	0.44
1:A:143:ARG:N	3:A:736:HOH:O	2.51	0.44
1:A:112:PHE:CE1	1:A:123:LEU:HG	2.53	0.44
1:B:79:THR:HG22	1:B:90:ASP:OD1	2.17	0.44
1:B:31:HIS:HA	1:B:88:PHE:CE1	2.53	0.43
1:A:65:LYS:CB	1:A:65:LYS:NZ	2.82	0.42
1:A:94:LEU:CA	3:A:696:HOH:O	2.60	0.42
1:B:175:HIS:HB3	1:B:179:ARG:NH1	2.33	0.42
1:B:135:LEU:N	3:B:784:HOH:O	2.52	0.42
1:B:152:LEU:O	1:B:156:ILE:HG12	2.20	0.42
1:A:162:ILE:HD11	3:A:657:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:LYS:NZ	3:A:445:HOH:O	2.49	0.41
1:A:65:LYS:NZ	1:A:65:LYS:HB3	2.35	0.41
1:A:162:ILE:HG12	3:A:761:HOH:O	2.20	0.41
1:A:94:LEU:C	1:A:94:LEU:HD23	2.47	0.40
1:B:79:THR:HG23	3:B:583:HOH:O	2.21	0.40

All (4) 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)
3:A:608:HOH:O	3:A:851:HOH:O[2_555]	1.99	0.21
3:A:414:HOH:O	3:A:728:HOH:O[2_545]	2.08	0.12
1:A:175:HIS:NE2	3:A:760:HOH:O[2_645]	2.12	0.08
3:A:425:HOH:O	3:A:829:HOH:O[2_555]	2.16	0.04

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	170/183 (93%)	169 (99%)	1 (1%)	0	100	100
1	B	166/183 (91%)	160 (96%)	4 (2%)	2 (1%)	10	6
All	All	336/366 (92%)	329 (98%)	5 (2%)	2 (1%)	21	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	166	GLY
1	B	13	LEU

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	162/170 (95%)	156 (96%)	6 (4%)	30	30
1	B	157/170 (92%)	152 (97%)	5 (3%)	34	35
All	All	319/340 (94%)	308 (97%)	11 (3%)	32	33

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LEU
1	A	65	LYS
1	A	92	LEU
1	A	131	LEU
1	A	134	CYS
1	A	171	SER
1	B	24	LYS
1	B	49	LEU
1	B	63	GLU
1	B	118	ASP
1	B	125	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	GLN
1	B	174	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	174/183 (95%)	2.19	90 (51%) 0 0	35, 42, 52, 61	0
1	B	170/183 (92%)	2.51	121 (71%) 0 0	34, 45, 58, 59	0
All	All	344/366 (93%)	2.35	211 (61%) 0 0	34, 43, 55, 61	0

All (211) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	183	PHE	5.8
1	A	147	SER	4.9
1	B	175	HIS	4.8
1	B	12	LEU	4.8
1	B	117	PHE	4.7
1	A	27	ILE	4.5
1	B	162	ILE	4.4
1	B	53	VAL	4.4
1	B	82	ALA	4.4
1	A	152	LEU	4.3
1	A	117	PHE	4.2
1	B	181	PRO	4.0
1	A	146	ALA	4.0
1	A	131	LEU	4.0
1	B	62	PRO	4.0
1	B	170	LEU	3.9
1	A	65	LYS	3.9
1	B	177	ILE	3.8
1	B	21	PHE	3.8
1	B	153	ILE	3.8
1	B	187	PHE	3.8
1	B	125	ARG	3.8
1	B	157	LEU	3.7
1	B	156	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	135	LEU	3.7
1	B	49	LEU	3.7
1	B	179	ARG	3.7
1	A	49	LEU	3.7
1	A	114	ILE	3.7
1	A	101	THR	3.7
1	A	53	VAL	3.6
1	A	191	LEU	3.6
1	B	20	THR	3.6
1	B	115	PHE	3.6
1	A	30	ALA	3.6
1	B	146	ALA	3.6
1	B	184	ALA	3.6
1	B	64	LEU	3.6
1	A	91	PHE	3.5
1	A	126	GLU	3.5
1	B	147	SER	3.5
1	A	168	ILE	3.5
1	B	168	ILE	3.5
1	B	69	PHE	3.5
1	B	148	GLU	3.4
1	B	14	ALA	3.4
1	B	123	LEU	3.4
1	A	71	GLU	3.4
1	B	58	ILE	3.4
1	B	165	ASP	3.3
1	B	122	THR	3.3
1	B	151	GLN	3.3
1	B	155	ASN	3.3
1	B	61	LEU	3.3
1	B	131	LEU	3.3
1	A	181	PRO	3.3
1	A	112	PHE	3.3
1	A	148	GLU	3.2
1	A	12	LEU	3.2
1	B	79	THR	3.2
1	A	58	ILE	3.2
1	A	136	THR	3.2
1	B	97	VAL	3.2
1	B	135	LEU	3.2
1	B	190	VAL	3.2
1	B	159	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	92	LEU	3.1
1	A	128	LEU	3.1
1	B	80	SER	3.1
1	B	180	SER	3.1
1	B	173	PHE	3.1
1	B	127	ASP	3.1
1	A	189	ILE	3.1
1	A	123	LEU	3.1
1	B	132	VAL	3.1
1	A	88	PHE	3.1
1	B	169	ASN	3.1
1	B	66	ALA	3.1
1	A	69	PHE	3.0
1	A	185	SER	3.0
1	A	134	CYS	3.0
1	A	38	LEU	3.0
1	A	170	LEU	3.0
1	B	149	MET	3.0
1	B	160	SER	3.0
1	A	153	ILE	3.0
1	A	110	TYR	3.0
1	A	61	LEU	2.9
1	B	186	SER	2.9
1	B	102	ALA	2.9
1	B	124	ASN	2.9
1	A	120	ASP	2.9
1	A	19	LEU	2.9
1	A	190	VAL	2.9
1	B	51	ALA	2.9
1	B	134	CYS	2.9
1	B	19	LEU	2.9
1	A	40	GLN	2.8
1	A	82	ALA	2.8
1	A	187	PHE	2.8
1	A	118	ASP	2.8
1	B	22	LEU	2.8
1	A	56	GLU	2.8
1	B	55	PHE	2.8
1	B	91	PHE	2.8
1	B	45	VAL	2.8
1	A	165	ASP	2.8
1	B	48	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	65	LYS	2.8
1	A	122	THR	2.8
1	B	120	ASP	2.8
1	B	112	PHE	2.7
1	A	13	LEU	2.7
1	B	54	PRO	2.7
1	B	44	SER	2.7
1	B	154	ASP	2.6
1	A	103	THR	2.6
1	A	48	SER	2.6
1	B	27	ILE	2.6
1	A	102	ALA	2.6
1	B	110	TYR	2.6
1	A	35	CYS	2.6
1	A	34	PHE	2.6
1	B	130	ARG	2.6
1	A	97	VAL	2.6
1	A	132	VAL	2.6
1	B	15	GLU	2.5
1	A	162	ILE	2.5
1	A	111	ALA	2.5
1	A	151	GLN	2.5
1	A	119	ASP	2.5
1	B	77	PHE	2.5
1	B	189	ILE	2.5
1	B	67	ASN	2.5
1	A	145	SER	2.5
1	A	36	GLU	2.5
1	A	16	TYR	2.5
1	A	106	ILE	2.5
1	B	17	GLN	2.5
1	B	81	PRO	2.5
1	B	98	PHE	2.4
1	B	172	GLU	2.4
1	B	118	ASP	2.4
1	B	119	ASP	2.4
1	A	130	ARG	2.4
1	A	108	SER	2.4
1	A	113	ARG	2.4
1	B	126	GLU	2.4
1	B	133	ASN	2.4
1	A	28	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	152	LEU	2.4
1	A	98	PHE	2.4
1	B	163	ASP	2.4
1	B	104	PRO	2.4
1	A	45	VAL	2.4
1	A	29	LEU	2.3
1	A	157	LEU	2.3
1	B	28	LEU	2.3
1	A	21	PHE	2.3
1	A	109	HIS	2.3
1	B	129	SER	2.3
1	B	103	THR	2.3
1	A	184	ALA	2.3
1	B	150	LYS	2.3
1	B	13	LEU	2.3
1	B	38	LEU	2.3
1	B	191	LEU	2.3
1	A	167	THR	2.3
1	B	128	LEU	2.3
1	B	68	PRO	2.2
1	A	180	SER	2.2
1	B	96	SER	2.2
1	B	182	ASP	2.2
1	B	176	VAL	2.2
1	B	167	THR	2.2
1	A	37	LEU	2.2
1	A	144	LEU	2.2
1	B	41	GLU	2.2
1	B	171	SER	2.2
1	B	101	THR	2.2
1	A	171	SER	2.2
1	B	161	ASP	2.2
1	A	177	ILE	2.2
1	B	36	GLU	2.2
1	B	71	GLU	2.2
1	B	40	GLN	2.2
1	A	51	ALA	2.2
1	A	182	ASP	2.1
1	B	34	PHE	2.1
1	B	23	THR	2.1
1	A	176	VAL	2.1
1	B	31	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	84	ASP	2.1
1	A	32	ARG	2.1
1	B	47	SER	2.1
1	B	75	ARG	2.1
1	B	78	SER	2.1
1	B	83	LYS	2.1
1	B	76	VAL	2.1
1	A	73	ILE	2.0
1	B	16	TYR	2.0
1	A	121	GLY	2.0
1	B	121	GLY	2.0
1	A	95	LEU	2.0
1	B	74	CYS	2.0
1	A	66	ALA	2.0
1	B	63	GLU	2.0
1	A	31	HIS	2.0
1	B	106	ILE	2.0
1	B	114	ILE	2.0
1	A	143	ARG	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	CA	B	2	1/1	0.84	0.12	49,49,49,49	0
2	CA	B	6	1/1	0.87	0.16	50,50,50,50	0
2	CA	B	4	1/1	0.95	0.07	56,56,56,56	0
2	CA	A	1	1/1	0.95	0.06	41,41,41,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	B	8	1/1	0.95	0.12	50,50,50,50	0
2	CA	A	3	1/1	0.97	0.06	47,47,47,47	0
2	CA	A	5	1/1	0.98	0.06	40,40,40,40	0
2	CA	A	7	1/1	0.98	0.07	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.