



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 11:10 AM UTC

PDB ID : 3KXD / pdb_00003kxd
Title : Crystal structure of the mthk rck in complex with cadmium
Authors : Dvir, H.; Choe, S.
Deposited on : 2009-12-02
Resolution : 2.20 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

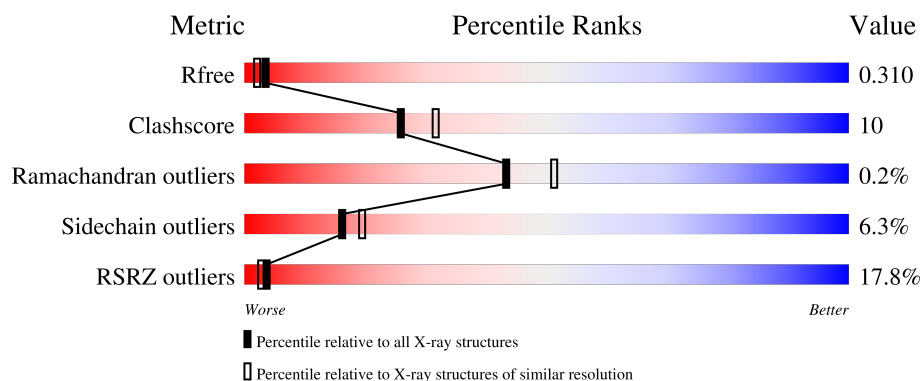
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	224	16% 74% 24% .
1	B	224	20% 72% 23% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3494 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-gated potassium channel mthK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1706	1067	296	336	7			
1	B	219	Total	C	N	O	S	0	0	0
			1672	1045	296	324	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	337	LEU	-	expression tag	UNP O27564
A	338	VAL	-	expression tag	UNP O27564
A	339	PRO	-	expression tag	UNP O27564
B	337	LEU	-	expression tag	UNP O27564
B	338	VAL	-	expression tag	UNP O27564
B	339	PRO	-	expression tag	UNP O27564

- Molecule 2 is CADMIUM ION (CCD ID: CD) (formula: Cd).

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

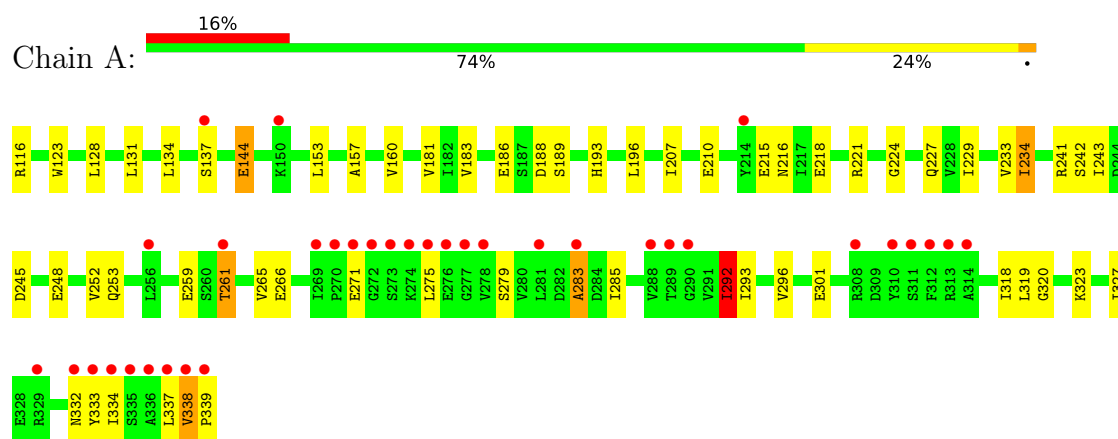
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	67	Total	O	0	0
			67	67		
3	B	45	Total	O	0	0
			45	45		

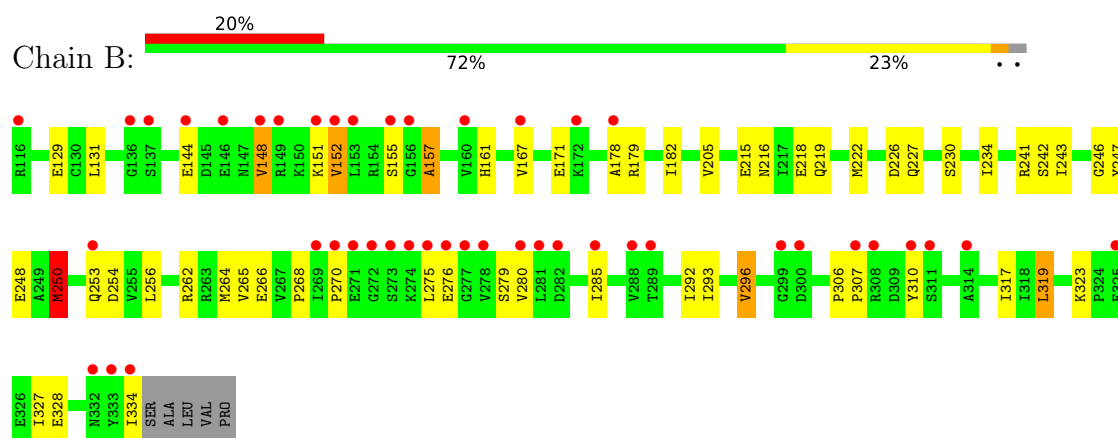
3 Residue-property plots

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-gated potassium channel mthK



- Molecule 1: Calcium-gated potassium channel mthK



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.02Å 38.29Å 96.63Å 90.00° 95.10° 90.00°	Depositor
Resolution (Å)	57.83 – 2.20 57.83 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (57.83-2.20) 99.3 (57.83-2.20)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.04 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.184 , 0.254 0.254 , 0.310	Depositor DCC
R_{free} test set	1108 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	35.7	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.1	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	0.93	EDS
Total number of atoms	3494	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.04% 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: CD

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	1.36	8/1728 (0.5%)	1.30	4/2340 (0.2%)
1	B	1.18	2/1693 (0.1%)	1.15	6/2290 (0.3%)
All	All	1.27	10/3421 (0.3%)	1.23	10/4630 (0.2%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	234	ILE	C-O	-6.22	1.16	1.24
1	A	160	VAL	C-O	-5.95	1.17	1.24
1	A	183	VAL	N-CA	-5.88	1.39	1.46
1	A	224	GLY	C-O	-5.57	1.18	1.24
1	A	207	ILE	CA-CB	5.55	1.61	1.54
1	A	283	ALA	CA-CB	-5.46	1.44	1.53
1	A	229	ILE	CA-CB	5.29	1.60	1.54
1	B	250	MET	C-O	-5.24	1.18	1.24
1	A	181	VAL	CA-CB	5.13	1.61	1.54
1	B	247	TYR	C-O	-5.03	1.18	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	292	ILE	CB-CA-C	-9.39	98.95	111.15
1	B	247	TYR	N-CA-C	5.96	117.78	111.28
1	B	152	VAL	N-CA-C	5.88	116.07	110.42
1	B	230	SER	CA-C-N	5.73	125.41	119.05
1	B	230	SER	C-N-CA	5.73	125.41	119.05
1	A	261	THR	N-CA-C	5.64	117.42	111.28
1	B	254	ASP	N-CA-C	5.57	117.15	111.14
1	A	196	LEU	N-CA-C	-5.37	105.59	111.82
1	B	226	ASP	N-CA-C	-5.31	106.64	113.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	144	GLU	CA-CB-CG	5.13	124.36	114.10

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	1706	0	1691	34	0
1	B	1672	0	1665	39	0
2	A	3	0	0	0	0
2	B	1	0	0	0	0
3	A	67	0	0	3	0
3	B	45	0	0	0	0
All	All	3494	0	3356	64	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 10.

All (64) 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:265:VAL:HG21	1:B:327:ILE:HD12	1.35	1.05
1:A:265:VAL:HG21	1:A:327:ILE:HD12	1.49	0.90
1:B:285:ILE:HG21	1:B:293:ILE:HD11	1.56	0.86
1:B:265:VAL:HG21	1:B:327:ILE:CD1	2.09	0.81
1:B:265:VAL:CG2	1:B:327:ILE:HD12	2.11	0.80
1:B:262:ARG:HH11	1:B:262:ARG:HG3	1.46	0.78
1:A:116:ARG:HA	3:A:60:HOH:O	1.89	0.73
1:A:265:VAL:CG2	1:A:327:ILE:HD12	2.23	0.68
1:B:167:VAL:O	1:B:171:GLU:HG3	1.93	0.67
1:A:252:VAL:HG21	1:B:256:LEU:HD11	1.79	0.65
1:A:221:ARG:HG2	3:A:44:HOH:O	1.95	0.64
1:B:144:GLU:O	1:B:161:HIS:HE1	1.81	0.63
1:A:285:ILE:HG21	1:A:293:ILE:HD11	1.81	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:GLU:O	1:B:222:MET:HG3	1.99	0.63
1:B:265:VAL:CG2	1:B:327:ILE:CD1	2.75	0.62
1:B:131:LEU:HD11	1:B:157:ALA:HB2	1.81	0.62
1:A:275:LEU:HD12	1:A:334:ILE:HG22	1.81	0.62
1:A:296:VAL:HG22	1:A:318:ILE:HD13	1.83	0.61
1:B:262:ARG:HG3	1:B:262:ARG:NH1	2.14	0.59
1:B:151:LYS:O	1:B:155:SER:HB2	2.03	0.58
1:A:188:ASP:CG	1:A:216:ASN:ND2	2.64	0.56
1:B:148:VAL:O	1:B:152:VAL:HG23	2.06	0.55
1:B:243:ILE:HG22	1:B:243:ILE:O	2.08	0.54
1:B:279:SER:HA	1:B:310:TYR:O	2.09	0.53
1:B:144:GLU:O	1:B:161:HIS:CE1	2.61	0.53
1:B:241:ARG:NH1	1:B:248:GLU:OE1	2.41	0.52
1:A:189:SER:O	1:A:193:HIS:CD2	2.62	0.52
1:B:148:VAL:O	1:B:148:VAL:HG23	2.11	0.51
1:A:242:SER:HB3	1:B:227:GLN:OE1	2.11	0.51
1:B:266:GLU:HG2	1:B:319:LEU:HD23	1.93	0.50
1:B:262:ARG:NH2	1:B:323:LYS:HE2	2.27	0.50
1:A:233:VAL:HA	1:B:129:GLU:HG2	1.94	0.49
1:B:266:GLU:HG2	1:B:319:LEU:CD2	2.44	0.47
1:B:275:LEU:HD12	1:B:334:ILE:HD11	1.96	0.47
1:A:245:ASP:C	1:A:245:ASP:OD1	2.58	0.46
1:A:218:GLU:OE2	1:A:221:ARG:HD2	2.15	0.46
1:A:243:ILE:HD11	1:B:182:ILE:HD11	1.98	0.46
1:A:227:GLN:OE1	1:B:242:SER:HB3	2.16	0.46
1:A:241:ARG:NH1	1:A:248:GLU:OE1	2.49	0.45
1:A:188:ASP:CG	1:A:216:ASN:HD21	2.23	0.45
1:B:178:ALA:O	1:B:205:VAL:HG23	2.17	0.44
1:A:292:ILE:O	1:A:320:GLY:HA2	2.18	0.44
1:A:134:LEU:O	1:A:137:SER:HB3	2.17	0.44
1:A:189:SER:O	1:A:193:HIS:HD2	2.00	0.44
1:B:280:VAL:HG23	1:B:310:TYR:HB3	1.99	0.43
1:B:268:PRO:O	1:B:270:PRO:HD3	2.18	0.43
1:A:248:GLU:OE1	1:B:264:MET:HE3	2.18	0.43
1:A:323:LYS:O	1:A:327:ILE:HG12	2.19	0.43
1:A:234:ILE:HG21	1:B:234:ILE:HG21	2.00	0.42
1:A:332:ASN:N	1:A:332:ASN:HD22	2.17	0.42
1:A:319:LEU:N	1:A:319:LEU:HD12	2.35	0.42
1:B:296:VAL:HA	1:B:317:ILE:O	2.20	0.41
1:A:218:GLU:HG3	3:A:48:HOH:O	2.20	0.41
1:B:262:ARG:NH1	1:B:262:ARG:CG	2.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:GLU:HG3	1:B:248:GLU:OE2	2.21	0.41
1:A:131:LEU:HD11	1:A:157:ALA:HB2	2.01	0.41
1:A:243:ILE:CG2	1:B:179:ARG:HD3	2.51	0.41
1:A:271:GLU:OE1	1:A:271:GLU:HA	2.20	0.41
1:A:338:VAL:O	1:A:339:PRO:O	2.39	0.41
1:B:306:PRO:HA	1:B:307:PRO:HD3	1.94	0.41
1:A:123:TRP:CH2	1:A:131:LEU:HD12	2.56	0.41
1:A:283:ALA:O	1:A:333:TYR:OH	2.37	0.40
1:B:246:GLY:O	1:B:250:MET:HB2	2.21	0.40
1:B:216:ASN:O	1:B:219:GLN:HB2	2.22	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	222/224 (99%)	217 (98%)	5 (2%)	0	100	100
1	B	217/224 (97%)	205 (94%)	11 (5%)	1 (0%)	24	27
All	All	439/448 (98%)	422 (96%)	16 (4%)	1 (0%)	43	51

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	157	ALA

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	184/192 (96%)	170 (92%)	14 (8%)	12	14
1	B	180/192 (94%)	171 (95%)	9 (5%)	22	28
All	All	364/384 (95%)	341 (94%)	23 (6%)	16	19

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	128	LEU
1	A	144	GLU
1	A	153	LEU
1	A	186	GLU
1	A	210	GLU
1	A	215	GLU
1	A	253	GLN
1	A	259	GLU
1	A	261	THR
1	A	279	SER
1	A	292	ILE
1	A	301	GLU
1	A	337	LEU
1	A	338	VAL
1	B	148	VAL
1	B	215	GLU
1	B	250	MET
1	B	253	GLN
1	B	276	GLU
1	B	292	ILE
1	B	296	VAL
1	B	319	LEU
1	B	328	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	ASN
1	A	193	HIS
1	A	253	GLN
1	A	332	ASN

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Mol	Chain	Res	Type
1	B	158	ASN
1	B	161	HIS
1	B	216	ASN
1	B	253	GLN
1	B	286	HIS
1	B	332	ASN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	224/224 (100%)	0.80	35 (15%) 5 4	13, 41, 96, 166	0
1	B	219/224 (97%)	1.10	44 (20%) 3 2	20, 56, 99, 112	0
All	All	443/448 (98%)	0.95	79 (17%) 4 3	13, 48, 97, 166	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	337	LEU	5.4
1	A	339	PRO	4.8
1	A	281	LEU	4.4
1	A	272	GLY	3.9
1	B	277	GLY	3.9
1	A	288	VAL	3.9
1	B	288	VAL	3.9
1	A	333	TYR	3.7
1	A	313	ARG	3.7
1	A	275	LEU	3.7
1	A	269	ILE	3.6
1	A	278	VAL	3.6
1	B	278	VAL	3.5
1	A	261	THR	3.4
1	A	311	SER	3.4
1	A	338	VAL	3.3
1	A	273	SER	3.2
1	A	314	ALA	3.1
1	A	329	ARG	3.1
1	A	334	ILE	3.0
1	B	271	GLU	3.0
1	B	136	GLY	3.0
1	A	312	PHE	3.0
1	B	276	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	153	LEU	3.0
1	A	274	LYS	2.9
1	A	336	ALA	2.9
1	A	335	SER	2.8
1	B	310	TYR	2.8
1	A	276	GLU	2.8
1	B	272	GLY	2.7
1	B	333	TYR	2.7
1	B	167	VAL	2.7
1	B	155	SER	2.7
1	B	156	GLY	2.7
1	B	308	ARG	2.7
1	B	299	GLY	2.6
1	A	214	TYR	2.5
1	B	314	ALA	2.5
1	A	271	GLU	2.5
1	A	277	GLY	2.5
1	B	148	VAL	2.5
1	B	275	LEU	2.5
1	B	307	PRO	2.5
1	B	332	ASN	2.4
1	B	116	ARG	2.4
1	B	149	ARG	2.4
1	B	178	ALA	2.4
1	B	152	VAL	2.4
1	A	290	GLY	2.3
1	B	282	ASP	2.3
1	A	289	THR	2.3
1	B	311	SER	2.3
1	B	334	ILE	2.3
1	A	256	LEU	2.3
1	B	281	LEU	2.3
1	B	274	LYS	2.3
1	A	137	SER	2.3
1	B	285	ILE	2.3
1	B	160	VAL	2.3
1	A	270	PRO	2.3
1	B	151	LYS	2.3
1	B	269	ILE	2.3
1	A	308	ARG	2.2
1	A	283	ALA	2.2
1	B	144	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	280	VAL	2.2
1	A	310	TYR	2.1
1	B	137	SER	2.1
1	B	172	LYS	2.1
1	B	289	THR	2.1
1	A	332	ASN	2.1
1	B	300	ASP	2.1
1	B	270	PRO	2.1
1	B	325	GLU	2.0
1	B	146	GLU	2.0
1	B	273	SER	2.0
1	B	253	GLN	2.0
1	A	150	LYS	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(Å ²)	Q<0.9
2	CD	A	603	1/1	0.87	0.26	128,128,128,128	0
2	CD	A	604	1/1	0.89	0.13	124,124,124,124	0
2	CD	A	602	1/1	0.93	0.17	95,95,95,95	0
2	CD	B	601	1/1	0.98	0.07	71,71,71,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.