



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:07 PM UTC

PDB ID : 3EAD / pdb_00003ead
Title : Crystal structure of CALX-CBD1
Authors : Zheng, L.; Wang, M.
Deposited on : 2008-08-25
Resolution : 2.25 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

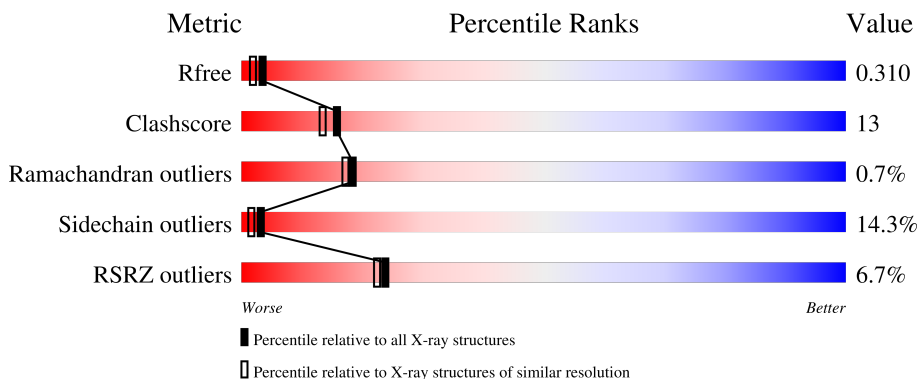
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	137	 4% 57% 18% 5% 19%
1	B	137	 5% 58% 18% 7% 17%
1	C	137	 4% 51% 28% 18%
1	D	137	 9% 57% 18% 6% 19%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3693 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 Na/Ca exchange protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	111	Total	C	N	O	S	0	0	0
			886	560	143	177	6			
1	B	114	Total	C	N	O	S	0	0	0
			908	574	148	180	6			
1	C	112	Total	C	N	O	S	0	0	0
			896	566	146	178	6			
1	D	111	Total	C	N	O	S	0	0	0
			886	560	143	177	6			

- 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		
2	C	4	Total	Ca	0	0
			4	4		
2	D	4	Total	Ca	0	0
			4	4		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0

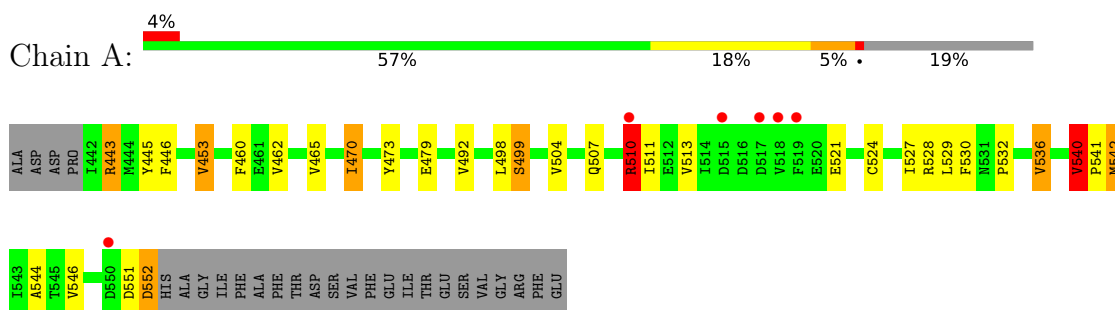
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	31	Total O 31 31	0	0
4	B	27	Total O 27 27	0	0
4	C	25	Total O 25 25	0	0
4	D	12	Total O 12 12	0	0

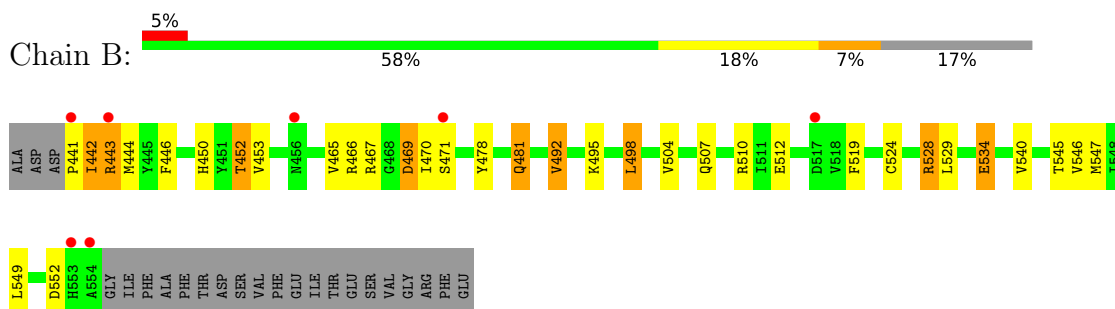
3 Residue-property plots [i](#)

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.

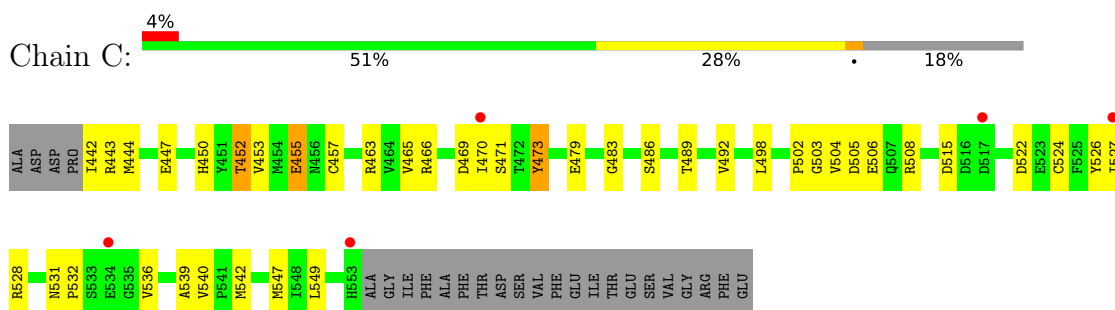
- Molecule 1: Na/Ca exchange protein



- Molecule 1: Na/Ca exchange protein

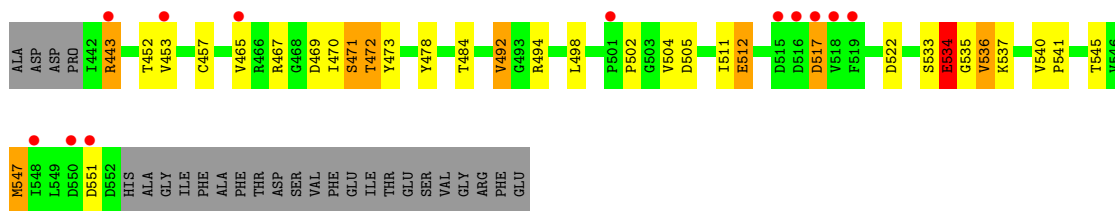


- Molecule 1: Na/Ca exchange protein



- Molecule 1: Na/Ca exchange protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.37Å 73.72Å 129.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.59 – 2.25 19.59 – 2.25	Depositor EDS
% Data completeness (in resolution range)	94.5 (19.59-2.25) 94.3 (19.59-2.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.26Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.210 , 0.269 0.266 , 0.310	Depositor DCC
R_{free} test set	1341 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	48.0	Xtrriage
Anisotropy	0.352	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 16.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3693	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% 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: GOL, 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	1.31	7/904 (0.8%)	1.20	4/1223 (0.3%)
1	B	1.03	0/928	1.15	5/1256 (0.4%)
1	C	1.01	0/915	1.04	0/1238
1	D	1.04	4/904 (0.4%)	0.99	2/1223 (0.2%)
All	All	1.10	11/3651 (0.3%)	1.10	11/4940 (0.2%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	552	ASP	CG-OD1	9.83	1.44	1.25
1	D	517	ASP	CG-OD1	8.21	1.41	1.25
1	A	542	MET	CG-SD	7.42	1.99	1.80
1	D	551	ASP	CG-OD1	6.92	1.38	1.25
1	A	527	ILE	CA-CB	-5.91	1.47	1.54
1	D	517	ASP	CG-OD2	5.53	1.35	1.25
1	A	510	ARG	CA-CB	5.29	1.61	1.53
1	D	551	ASP	CG-OD2	5.24	1.35	1.25
1	A	511	ILE	CA-CB	5.17	1.60	1.54
1	A	552	ASP	CB-CG	5.16	1.65	1.52
1	A	544	ALA	CA-CB	-5.10	1.45	1.53

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	542	MET	N-CA-C	-9.65	99.14	114.09
1	A	540	VAL	N-CA-CB	-6.13	104.38	110.08
1	A	536	VAL	N-CA-C	5.88	117.81	108.87
1	D	457	CYS	N-CA-C	-5.85	106.30	113.50
1	B	528	ARG	CB-CA-C	-5.65	99.94	109.72
1	B	443	ARG	N-CA-C	5.59	117.34	108.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	540	VAL	CB-CA-C	5.35	116.67	110.89
1	D	536	VAL	N-CA-C	5.20	115.34	107.80
1	B	470	ILE	CA-C-N	5.13	131.34	121.54
1	B	470	ILE	C-N-CA	5.13	131.34	121.54
1	B	442	ILE	N-CA-C	5.05	115.92	109.30

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	886	0	837	34	0
1	B	908	0	857	21	0
1	C	896	0	844	40	0
1	D	886	0	837	17	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
3	A	6	0	8	0	0
4	A	31	0	0	1	0
4	B	27	0	0	1	0
4	C	25	0	0	1	0
4	D	12	0	0	0	0
All	All	3693	0	3383	93	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 13.

All (93) 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:C:549:LEU:HB3	1:D:443:ARG:NH1	1.69	1.08
1:A:443:ARG:HH11	1:A:443:ARG:HG2	1.22	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:ARG:H	1:A:510:ARG:HD2	1.39	0.87
1:A:470:ILE:O	1:A:470:ILE:HG23	1.72	0.87
1:C:469:ASP:OD1	1:C:471:SER:HB3	1.75	0.85
1:C:470:ILE:O	1:C:470:ILE:HG22	1.79	0.82
1:A:443:ARG:HH11	1:A:443:ARG:CG	1.95	0.79
1:A:542:MET:HE2	1:C:526:TYR:CE1	2.19	0.78
1:A:443:ARG:HG2	1:A:443:ARG:NH1	1.96	0.77
1:A:540:VAL:O	1:B:452:THR:HG21	1.85	0.77
1:A:470:ILE:O	1:A:470:ILE:CG2	2.32	0.76
1:D:533:SER:O	1:D:534:GLU:C	2.30	0.74
1:A:542:MET:HE2	1:C:526:TYR:HE1	1.51	0.71
1:C:452:THR:HG21	1:D:540:VAL:O	1.89	0.71
1:A:542:MET:HE3	1:C:483:GLY:HA2	1.72	0.70
1:B:450:HIS:ND1	1:B:545:THR:HG23	2.06	0.70
1:A:542:MET:HE1	1:C:483:GLY:HA3	1.74	0.68
1:A:542:MET:CE	1:C:526:TYR:HE1	2.06	0.68
1:C:471:SER:O	1:C:502:PRO:HB3	1.95	0.67
1:A:443:ARG:HD3	1:B:549:LEU:HD13	1.77	0.67
1:C:549:LEU:HB3	1:D:443:ARG:HH12	1.55	0.66
1:A:510:ARG:HD2	1:A:510:ARG:N	2.10	0.66
1:C:470:ILE:O	1:C:470:ILE:CG2	2.45	0.65
1:A:542:MET:HE1	1:C:483:GLY:CA	2.27	0.64
1:A:542:MET:CE	1:C:483:GLY:CA	2.75	0.64
1:C:470:ILE:HG22	1:C:503:GLY:H	1.64	0.63
1:A:453:VAL:HG11	1:A:513:VAL:HG21	1.80	0.62
1:A:532:PRO:HB2	1:A:536:VAL:HB	1.84	0.59
1:C:450:HIS:NE2	1:C:452:THR:HG22	2.18	0.59
1:C:442:ILE:HG21	1:C:536:VAL:HG22	1.84	0.59
1:D:472:THR:OG1	1:D:473:TYR:N	2.35	0.58
1:C:528:ARG:NH2	4:C:146:HOH:O	2.37	0.58
1:A:479:GLU:OE2	1:A:528:ARG:NH1	2.37	0.57
1:A:507:GLN:NE2	4:A:1032:HOH:O	2.37	0.57
1:B:492:VAL:HG13	1:B:512:GLU:HB3	1.85	0.57
1:C:442:ILE:CG2	1:C:536:VAL:HG22	2.35	0.56
1:C:453:VAL:HG22	1:C:457:CYS:SG	2.46	0.55
1:C:473:TYR:C	1:C:473:TYR:CD2	2.84	0.55
1:A:541:PRO:HD3	1:B:452:THR:HG21	1.89	0.55
1:C:455:GLU:HG3	1:C:515:ASP:HA	1.88	0.54
1:B:441:PRO:O	1:B:443:ARG:HG2	2.08	0.54
1:A:446:PHE:CE2	1:A:462:VAL:CG1	2.91	0.54
1:A:541:PRO:HD3	1:B:452:THR:CG2	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:443:ARG:HE	1:C:539:ALA:HB2	1.73	0.54
1:A:446:PHE:HE2	1:A:462:VAL:CG1	2.20	0.53
1:B:444:MET:HA	1:B:465:VAL:O	2.09	0.52
1:C:470:ILE:HD13	1:C:505:ASP:HB3	1.92	0.51
1:D:522:ASP:HB3	1:D:547:MET:HE2	1.93	0.51
1:B:481:GLN:OE1	1:B:528:ARG:HG3	2.10	0.51
1:D:478:TYR:OH	1:D:494:ARG:NH2	2.43	0.51
1:C:506:GLU:OE2	1:C:508:ARG:NH2	2.45	0.50
1:D:469:ASP:OD2	1:D:471:SER:OG	2.30	0.50
1:B:469:ASP:OD2	1:B:471:SER:HB3	2.11	0.50
1:A:551:ASP:N	1:A:551:ASP:OD1	2.44	0.50
1:A:524:CYS:HA	1:A:546:VAL:O	2.12	0.49
1:C:470:ILE:CD1	1:C:505:ASP:HB3	2.42	0.49
1:D:533:SER:O	1:D:534:GLU:O	2.30	0.49
1:C:444:MET:HE3	1:C:536:VAL:HG21	1.94	0.49
1:B:481:GLN:OE1	1:B:528:ARG:HD2	2.13	0.49
1:A:542:MET:CE	1:C:483:GLY:HA3	2.41	0.48
1:A:460:PHE:O	1:A:510:ARG:HA	2.14	0.47
1:A:446:PHE:HE2	1:A:462:VAL:HG11	1.80	0.46
1:D:492:VAL:HG13	1:D:512:GLU:HB2	1.96	0.46
1:D:534:GLU:O	1:D:536:VAL:N	2.45	0.46
1:C:452:THR:HG21	1:D:541:PRO:HD3	1.98	0.46
1:B:507:GLN:NE2	4:B:46:HOH:O	2.47	0.46
1:A:446:PHE:CE2	1:A:462:VAL:HG11	2.52	0.45
1:B:519:PHE:HA	1:B:552:ASP:HB2	1.99	0.44
1:B:446:PHE:CE1	1:B:529:LEU:HG	2.53	0.44
1:B:450:HIS:NE2	1:B:452:THR:HG22	2.32	0.44
1:B:524:CYS:HA	1:B:546:VAL:O	2.17	0.44
1:C:453:VAL:CG2	1:C:457:CYS:SG	3.06	0.44
1:C:450:HIS:CD2	1:C:452:THR:HG22	2.52	0.44
1:C:452:THR:CG2	1:D:541:PRO:HD3	2.47	0.44
1:A:453:VAL:CG1	1:A:513:VAL:HG21	2.47	0.44
1:D:467:ARG:NH1	1:D:505:ASP:HB2	2.33	0.44
1:A:473:TYR:CE1	1:A:499:SER:HB3	2.53	0.44
1:C:452:THR:HB	1:C:547:MET:HB3	1.99	0.43
1:B:478:TYR:HA	1:B:528:ARG:O	2.17	0.43
1:C:549:LEU:HB3	1:D:443:ARG:HH11	1.68	0.43
1:C:447:GLU:O	1:C:463:ARG:HD3	2.19	0.43
1:D:494:ARG:HD3	1:D:511:ILE:HD13	2.00	0.42
1:A:542:MET:HE2	1:C:526:TYR:CZ	2.54	0.42
1:D:443:ARG:HB3	1:D:537:LYS:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:522:ASP:HB3	1:C:547:MET:HE2	2.02	0.42
1:B:478:TYR:CE1	1:B:498:LEU:HD13	2.54	0.41
1:B:450:HIS:CD2	1:B:452:THR:HG22	2.56	0.41
1:B:452:THR:HB	1:B:547:MET:HB3	2.03	0.41
1:B:534:GLU:H	1:B:534:GLU:HG2	1.48	0.41
1:C:531:ASN:N	1:C:532:PRO:CD	2.84	0.41
1:C:479:GLU:OE2	1:C:528:ARG:NH1	2.51	0.41
1:C:527:ILE:HD13	1:C:527:ILE:HG21	1.79	0.40
1:A:529:LEU:O	1:A:530:PHE:HB3	2.20	0.40

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	109/137 (80%)	103 (94%)	6 (6%)	0	100	100
1	B	112/137 (82%)	107 (96%)	5 (4%)	0	100	100
1	C	110/137 (80%)	105 (96%)	5 (4%)	0	100	100
1	D	109/137 (80%)	102 (94%)	4 (4%)	3 (3%)	4	2
All	All	440/548 (80%)	417 (95%)	20 (4%)	3 (1%)	18	17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	534	GLU
1	D	502	PRO
1	D	535	GLY

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	97/118 (82%)	84 (87%)	13 (13%)	4	2
1	B	99/118 (84%)	85 (86%)	14 (14%)	3	2
1	C	98/118 (83%)	85 (87%)	13 (13%)	4	2
1	D	97/118 (82%)	81 (84%)	16 (16%)	2	0
All	All	391/472 (83%)	335 (86%)	56 (14%)	3	1

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	443	ARG
1	A	445	TYR
1	A	453	VAL
1	A	465	VAL
1	A	470	ILE
1	A	492	VAL
1	A	498	LEU
1	A	499	SER
1	A	504	VAL
1	A	510	ARG
1	A	521	GLU
1	A	540	VAL
1	A	552	ASP
1	B	442	ILE
1	B	452	THR
1	B	453	VAL
1	B	466	ARG
1	B	467	ARG
1	B	469	ASP
1	B	481	GLN
1	B	492	VAL
1	B	495	LYS
1	B	498	LEU
1	B	504	VAL

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Mol	Chain	Res	Type
1	B	510	ARG
1	B	534	GLU
1	B	540	VAL
1	C	452	THR
1	C	455	GLU
1	C	465	VAL
1	C	466	ARG
1	C	473	TYR
1	C	486	SER
1	C	489	THR
1	C	492	VAL
1	C	498	LEU
1	C	504	VAL
1	C	524	CYS
1	C	540	VAL
1	C	542	MET
1	D	443	ARG
1	D	452	THR
1	D	453	VAL
1	D	465	VAL
1	D	470	ILE
1	D	471	SER
1	D	472	THR
1	D	484	THR
1	D	492	VAL
1	D	498	LEU
1	D	504	VAL
1	D	512	GLU
1	D	517	ASP
1	D	534	GLU
1	D	545	THR
1	D	547	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	450	HIS
1	A	481	GLN
1	A	507	GLN
1	B	507	GLN
1	C	481	GLN
1	C	507	GLN

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Mol	Chain	Res	Type
1	C	553	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](#)

Of 17 ligands modelled in this entry, 16 are monoatomic - leaving 1 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	$\# Z > 2$
3	GOL	A	1	-	5,5,5	0.43	0	5,5,5	0.67	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1	GOL	O1-C1-C2-C3
3	A	1	GOL	C1-C2-C3-O3
3	A	1	GOL	O2-C2-C3-O3

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	111/137 (81%)	0.64	6 (5%) 31 29	38, 46, 54, 60	0
1	B	114/137 (83%)	0.49	7 (6%) 27 25	43, 48, 54, 59	0
1	C	112/137 (81%)	0.44	5 (4%) 38 37	40, 48, 55, 58	0
1	D	111/137 (81%)	0.99	12 (10%) 11 10	44, 50, 57, 61	0
All	All	448/548 (81%)	0.64	30 (6%) 24 22	38, 48, 56, 61	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	517	ASP	7.4
1	D	518	VAL	4.8
1	C	553	HIS	4.0
1	D	517	ASP	3.9
1	D	550	ASP	3.6
1	A	510	ARG	3.4
1	B	443	ARG	3.2
1	D	515	ASP	3.1
1	C	534	GLU	2.8
1	B	553	HIS	2.8
1	A	519	PHE	2.8
1	D	519	PHE	2.8
1	D	551	ASP	2.6
1	B	554	ALA	2.5
1	B	441	PRO	2.5
1	A	518	VAL	2.5
1	B	517	ASP	2.5
1	B	471	SER	2.4
1	C	517	ASP	2.4
1	D	516	ASP	2.4
1	C	470	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	443	ARG	2.2
1	D	465	VAL	2.2
1	D	453	VAL	2.2
1	D	548	ILE	2.1
1	B	456	ASN	2.1
1	C	527	ILE	2.1
1	A	515	ASP	2.0
1	A	550	ASP	2.0
1	D	501	PRO	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	CA	D	1003	1/1	0.70	0.16	92,92,92,92	0
3	GOL	A	1	6/6	0.70	0.14	59,61,64,65	0
2	CA	D	1002	1/1	0.81	0.19	83,83,83,83	0
2	CA	D	1004	1/1	0.82	0.15	90,90,90,90	0
2	CA	D	1001	1/1	0.85	0.17	83,83,83,83	0
2	CA	A	1004	1/1	0.89	0.07	75,75,75,75	0
2	CA	A	1003	1/1	0.89	0.09	68,68,68,68	0
2	CA	A	1002	1/1	0.93	0.20	70,70,70,70	0
2	CA	A	1001	1/1	0.93	0.21	69,69,69,69	0
2	CA	C	1001	1/1	0.94	0.13	52,52,52,52	0
2	CA	C	1002	1/1	0.95	0.07	47,47,47,47	0
2	CA	C	1004	1/1	0.96	0.04	62,62,62,62	0
2	CA	B	1002	1/1	0.96	0.06	46,46,46,46	0
2	CA	B	1001	1/1	0.97	0.06	53,53,53,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CA	B	1004	1/1	0.97	0.04	58,58,58,58	0
2	CA	B	1003	1/1	0.98	0.03	49,49,49,49	0
2	CA	C	1003	1/1	0.99	0.05	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.