



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:23 PM UTC

PDB ID : 6AGI / pdb_00006agi
Title : Crystal Structure of EFHA2 in Ca-binding State
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Deposited on : 2018-08-11
Resolution : 2.80 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

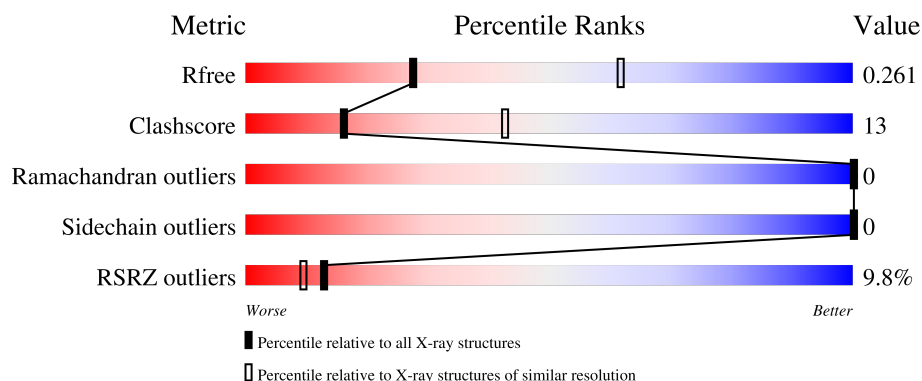
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

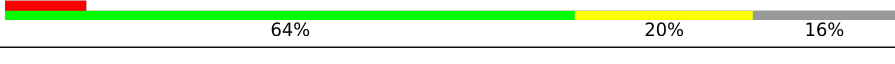
The reported resolution of this entry is 2.80 Å.

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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	382	 7% 60% 19% 21%
1	B	382	 9% 64% 20% 16%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5061 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 uptake protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2420	1569	385	456	10			
1	B	322	Total	C	N	O	S	0	0	0
			2575	1668	413	483	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	131	GLY	-	expression tag	UNP Q86XE3
A	132	SER	-	expression tag	UNP Q86XE3
B	131	GLY	-	expression tag	UNP Q86XE3
B	132	SER	-	expression tag	UNP Q86XE3

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

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

- Molecule 3 is IMIDAZOLE (CCD ID: IMD) (formula: C₃H₅N₂).

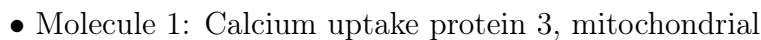


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	N	0	0
			5	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	27	Total	O	0	0
			27	27		
4	B	29	Total	O	0	0
			29	29		

- Molecule 1: Calcium uptake protein 3, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.39Å 77.18Å 172.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.70 – 2.80 48.70 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.2 (48.70-2.80) 96.2 (48.70-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.81Å)	Xtriage
Refinement program	PHENIX (dev_2666: ???)	Depositor
R, R_{free}	0.197 , 0.260 0.203 , 0.261	Depositor DCC
R_{free} test set	1939 reflections (8.49%)	wwPDB-VP
Wilson B-factor (Å ²)	28.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 68.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5061	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.11% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, IMD

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	0.48	0/2471	0.87	3/3337 (0.1%)
1	B	0.47	0/2629	0.84	2/3547 (0.1%)
All	All	0.48	0/5100	0.86	5/6884 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	350	LYS	N-CA-C	-13.71	86.17	108.52
1	B	267	LYS	N-CA-C	7.99	119.61	111.07
1	B	485	ASP	N-CA-C	-5.42	105.48	111.71
1	A	261	GLN	CA-C-N	5.12	127.86	120.38
1	A	261	GLN	C-N-CA	5.12	127.86	120.38

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	2420	0	2295	62	0
1	B	2575	0	2458	72	0
2	A	3	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	5	0	5	1	0
4	A	27	0	0	0	0
4	B	29	0	0	0	0
All	All	5061	0	4758	128	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 (128) 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:484:VAL:HG22	1:B:494:GLU:OE1	1.70	0.92
1:A:228:CYS:SG	1:A:232:LYS:NZ	2.45	0.88
1:B:206:SER:O	1:B:370:GLU:CD	2.18	0.86
1:B:229:ILE:HG12	1:B:364:MET:HE3	1.57	0.85
1:A:453:ILE:HD13	1:A:458:PHE:HB2	1.62	0.82
1:A:221:THR:HG21	1:A:261:GLN:HB3	1.59	0.81
1:B:228:CYS:SG	1:B:232:LYS:NZ	2.57	0.77
1:A:375:GLU:OE2	1:A:397:ARG:NH2	2.22	0.72
1:A:157:CYS:O	1:A:160:GLN:HB3	1.91	0.71
1:B:206:SER:O	1:B:370:GLU:CG	2.38	0.70
1:A:259:VAL:HG13	1:A:260:LEU:HD12	1.72	0.69
1:B:259:VAL:O	1:B:262:GLU:HG2	1.93	0.68
1:B:444:ASN:ND2	1:B:448:PHE:CD2	2.62	0.67
1:B:275:GLY:O	1:B:280:ARG:NH1	2.28	0.66
1:B:232:LYS:HD2	1:B:364:MET:HE1	1.78	0.66
1:B:396:LEU:HD11	1:B:407:PHE:HD2	1.60	0.66
1:B:232:LYS:HE2	1:B:240:ALA:HB2	1.76	0.66
1:B:210:ARG:HH21	1:B:370:GLU:HG3	1.61	0.65
1:A:415:ILE:HD11	1:A:480:LYS:HD2	1.79	0.65
1:B:484:VAL:O	1:B:486:LYS:HG2	1.96	0.65
1:B:396:LEU:HD11	1:B:407:PHE:CD2	2.31	0.64
1:B:484:VAL:CG2	1:B:494:GLU:OE1	2.42	0.64
1:A:264:PHE:HE2	1:B:445:MET:HE3	1.63	0.63
1:A:229:ILE:HG23	1:A:364:MET:HB3	1.79	0.63
1:A:415:ILE:HD11	1:A:480:LYS:CD	2.29	0.62
1:B:485:ASP:OD1	1:B:486:LYS:N	2.33	0.62
1:B:155:ILE:HB	1:B:162:PHE:HB2	1.81	0.62
1:B:487:ASP:OD1	1:B:489:GLN:N	2.30	0.61
1:A:264:PHE:CE2	1:B:445:MET:HE3	2.35	0.61
1:B:462:VAL:O	1:B:466:THR:OG1	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:LEU:HD21	1:A:407:PHE:CE2	2.37	0.60
1:A:414:SER:O	1:A:415:ILE:HD13	2.02	0.58
1:A:437:GLU:HB3	1:B:437:GLU:HG2	1.85	0.58
1:A:160:GLN:HG3	1:A:162:PHE:CZ	2.39	0.57
1:A:232:LYS:HE3	1:A:364:MET:HE1	1.85	0.57
1:B:411:VAL:O	1:B:415:ILE:HG22	2.03	0.57
1:A:396:LEU:HD11	1:A:407:PHE:HD2	1.69	0.57
1:B:259:VAL:O	1:B:263:ILE:HG12	2.04	0.57
1:B:150:ARG:NH1	1:B:286:GLN:OE1	2.38	0.56
1:A:160:GLN:HG3	1:A:162:PHE:CE2	2.41	0.56
1:A:199:PRO:O	1:A:345:HIS:HD2	1.89	0.56
1:B:250:GLU:HG2	3:B:603:IMD:HN3	1.71	0.55
1:B:491:SER:OG	1:B:494:GLU:HG3	2.05	0.55
1:B:206:SER:O	1:B:370:GLU:HG3	2.07	0.54
1:B:433:LEU:CD2	1:B:499:MET:HE2	2.38	0.54
1:B:205:SER:C	1:B:207:LYS:N	2.65	0.54
1:A:495:PHE:CE1	1:A:499:MET:HE3	2.43	0.53
1:B:135:ILE:O	1:B:150:ARG:NH2	2.41	0.53
1:B:145:ARG:HG3	1:B:145:ARG:HH11	1.73	0.53
1:B:135:ILE:N	1:B:150:ARG:HH22	2.05	0.53
1:A:479:PHE:CE2	1:A:490:LEU:HD23	2.43	0.53
1:B:205:SER:C	1:B:207:LYS:H	2.15	0.53
1:B:487:ASP:OD2	1:B:489:GLN:HB2	2.08	0.53
1:A:244:PHE:CD1	1:A:260:LEU:HD22	2.44	0.53
1:B:205:SER:O	1:B:207:LYS:N	2.41	0.53
1:A:158:GLU:C	1:A:160:GLN:H	2.16	0.52
1:A:201:VAL:HG13	1:A:345:HIS:O	2.09	0.52
1:B:232:LYS:HD2	1:B:364:MET:CE	2.40	0.51
1:A:490:LEU:HD12	1:A:495:PHE:HB2	1.92	0.51
1:B:455:GLN:HG2	1:B:479:PHE:CD2	2.46	0.50
1:A:459:LYS:HB2	1:A:475:VAL:HG21	1.92	0.50
1:B:444:ASN:ND2	1:B:448:PHE:HD2	2.08	0.50
1:A:257:PHE:O	1:A:261:GLN:HG3	2.12	0.49
1:B:444:ASN:ND2	1:B:444:ASN:O	2.45	0.49
1:A:451:ARG:NH2	1:B:268:ASN:CB	2.76	0.49
1:A:187:SER:OG	1:A:190:GLU:HG2	2.15	0.47
1:A:396:LEU:HD21	1:A:407:PHE:CD2	2.50	0.47
1:B:174:THR:HG22	1:B:175:ASP:N	2.30	0.46
1:A:256:GLU:O	1:A:259:VAL:HG12	2.16	0.46
1:B:206:SER:O	1:B:370:GLU:OE1	2.34	0.45
1:B:274:LYS:HA	1:B:274:LYS:HE2	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:THR:O	1:A:344:VAL:HG23	2.16	0.45
1:A:385:THR:HG22	1:A:422:THR:HG22	1.98	0.45
1:B:220:TYR:O	1:B:223:TYR:HB3	2.16	0.45
1:A:452:SER:HB3	1:A:489:GLN:HB3	1.99	0.44
1:B:205:SER:O	1:B:206:SER:C	2.60	0.44
1:B:141:TYR:CE2	1:B:279:LYS:HD3	2.52	0.44
1:A:225:PHE:O	1:A:229:ILE:HG13	2.18	0.44
1:B:479:PHE:CE1	1:B:490:LEU:HD12	2.52	0.44
1:B:139:ASP:OD1	1:B:147:ARG:HG2	2.18	0.44
1:B:435:ASN:HB3	1:B:466:THR:HG22	1.99	0.44
1:B:484:VAL:HG23	1:B:485:ASP:N	2.33	0.44
1:B:210:ARG:NH2	1:B:370:GLU:HG3	2.29	0.44
1:A:142:ALA:HB1	1:A:146:GLU:HB2	2.00	0.44
1:A:232:LYS:CE	1:A:364:MET:HE1	2.48	0.44
1:B:479:PHE:O	1:B:483:ASP:HB3	2.18	0.43
1:A:169:ILE:HG23	1:A:374:ILE:HD13	1.98	0.43
1:A:452:SER:HB2	1:A:489:GLN:OE1	2.18	0.43
1:B:223:TYR:CZ	1:B:227:LEU:HD11	2.53	0.43
1:B:237:PHE:CD1	1:B:364:MET:HE2	2.53	0.43
1:B:426:PHE:O	1:B:430:PHE:HD2	2.01	0.43
1:A:162:PHE:CD1	1:A:217:VAL:HG13	2.54	0.43
1:A:445:MET:SD	1:B:225:PHE:HA	2.59	0.43
1:B:395:LEU:HA	1:B:395:LEU:HD23	1.70	0.42
1:B:453:ILE:HD11	1:B:457:GLU:HB3	2.01	0.42
1:A:283:LEU:HD13	1:A:287:LEU:CD1	2.50	0.42
1:A:198:THR:HA	1:A:199:PRO:HD3	1.95	0.42
1:A:190:GLU:HG2	1:A:190:GLU:H	1.65	0.42
1:A:372:LEU:HD13	1:A:427:ARG:HA	2.02	0.42
1:A:415:ILE:HD11	1:A:480:LYS:HD3	2.01	0.41
1:A:387:SER:HB3	1:A:390:ASP:OD1	2.20	0.41
1:A:462:VAL:O	1:A:466:THR:OG1	2.34	0.41
1:A:234:HIS:HD2	1:A:237:PHE:CE2	2.38	0.41
1:A:479:PHE:CZ	1:A:490:LEU:HD23	2.55	0.41
1:B:433:LEU:HD21	1:B:499:MET:HE2	2.01	0.41
1:A:230:LEU:HD21	1:A:367:LEU:HD13	2.03	0.41
1:A:165:PRO:O	1:A:169:ILE:HG12	2.20	0.41
1:A:283:LEU:HD13	1:A:287:LEU:HD13	2.03	0.41
1:A:479:PHE:O	1:A:483:ASP:HB3	2.20	0.41
1:A:355:LEU:HD12	1:A:359:ASP:HB2	2.01	0.41
1:B:415:ILE:HD13	1:B:480:LYS:HG2	2.01	0.41
1:A:436:LEU:HD11	1:A:499:MET:HG3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:ALA:HB1	1:B:146:GLU:HB2	2.01	0.41
1:A:163:MET:HE3	1:A:168:PHE:HB2	2.02	0.41
1:A:495:PHE:HE1	1:A:499:MET:HE3	1.86	0.41
1:B:388:GLU:OE1	1:B:418:GLU:HG2	2.20	0.41
1:B:226:LEU:HD21	1:B:342:LEU:HD11	2.01	0.41
1:B:398:TYR:O	1:B:500:LYS:HG2	2.21	0.41
1:A:437:GLU:CB	1:B:437:GLU:HG2	2.49	0.40
1:A:483:ASP:HB2	1:A:490:LEU:HD22	2.03	0.40
1:B:170:LEU:O	1:B:174:THR:HB	2.21	0.40
1:B:444:ASN:ND2	1:B:444:ASN:C	2.77	0.40
1:B:229:ILE:HG12	1:B:364:MET:HG2	2.03	0.40
1:B:255:LYS:O	1:B:259:VAL:HG13	2.21	0.40
1:B:342:LEU:HD23	1:B:342:LEU:HA	1.82	0.40
1:A:446:TYR:CE2	1:A:453:ILE:HG22	2.57	0.40
1:A:491:SER:OG	1:A:494:GLU:HG3	2.22	0.40
1:B:433:LEU:HD23	1:B:433:LEU:HA	1.85	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	295/382 (77%)	282 (96%)	13 (4%)	0	100	100
1	B	316/382 (83%)	307 (97%)	9 (3%)	0	100	100
All	All	611/764 (80%)	589 (96%)	22 (4%)	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	255/346 (74%)	255 (100%)	0	100	100
1	B	270/346 (78%)	270 (100%)	0	100	100
All	All	525/692 (76%)	525 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	193	GLN
1	A	211	ASN
1	A	234	HIS
1	A	393	HIS
1	A	431	GLN
1	A	455	GLN
1	B	234	HIS
1	B	400	ASN
1	B	435	ASN
1	B	473	HIS
1	B	489	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 6 ligands modelled in this entry, 5 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	IMD	B	603	-	5,5,5	0.76	0	5,5,5	0.30	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	IMD	B	603	-	-	-	0/1/1/1

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	603	IMD	1	0

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	303/382 (79%)	0.51	27 (8%) 15 11	17, 49, 94, 126	0
1	B	322/382 (84%)	0.40	34 (10%) 11 8	10, 41, 92, 115	0
All	All	625/764 (81%)	0.45	61 (9%) 13 9	10, 44, 93, 126	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	337	VAL	4.6
1	B	401	VAL	4.3
1	A	260	LEU	4.2
1	B	415	ILE	4.0
1	B	179	VAL	3.9
1	A	182	THR	3.9
1	B	336	LEU	3.8
1	A	179	VAL	3.7
1	B	269	GLU	3.7
1	B	268	ASN	3.6
1	B	444	ASN	3.6
1	B	197	GLU	3.6
1	B	337	VAL	3.5
1	B	402	GLU	3.5
1	B	136	GLU	3.5
1	A	502	ARG	3.4
1	A	276	ASP	3.4
1	B	260	LEU	3.4
1	A	277	GLU	3.3
1	B	181	LYS	3.2
1	A	196	ALA	3.2
1	B	180	ALA	3.2
1	A	263	ILE	3.2
1	B	137	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	501	ASP	3.1
1	A	503	LEU	3.0
1	B	196	ALA	3.0
1	A	281	ALA	3.0
1	A	284	ARG	2.9
1	B	416	PRO	2.9
1	B	135	ILE	2.9
1	A	262	GLU	2.8
1	B	189	GLN	2.8
1	B	397	ARG	2.8
1	A	261	GLN	2.7
1	A	178	LYS	2.7
1	B	261	GLN	2.7
1	B	417	GLU	2.6
1	B	396	LEU	2.6
1	B	413	TYR	2.5
1	B	437	GLU	2.5
1	A	289	GLY	2.5
1	A	259	VAL	2.4
1	A	183	TRP	2.4
1	A	278	GLU	2.4
1	A	265	ARG	2.4
1	B	262	GLU	2.4
1	A	185	SER	2.3
1	B	398	TYR	2.3
1	A	197	GLU	2.3
1	A	175	ASP	2.3
1	B	406	VAL	2.3
1	B	407	PHE	2.3
1	B	282	MET	2.2
1	B	183	TRP	2.2
1	A	186	LEU	2.2
1	A	189	GLN	2.2
1	A	351	GLY	2.2
1	A	159	GLY	2.0
1	B	266	LYS	2.0
1	B	212	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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	IMD	B	603	5/5	0.91	0.13	36,44,47,48	0
2	CA	B	602	1/1	0.94	0.09	67,67,67,67	0
2	CA	A	603	1/1	0.95	0.33	78,78,78,78	0
2	CA	A	602	1/1	0.97	0.15	43,43,43,43	0
2	CA	A	601	1/1	0.98	0.08	74,74,74,74	0
2	CA	B	601	1/1	0.98	0.15	64,64,64,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.