



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 04:59 PM UTC

PDB ID : 3UZS / pdb_00003uzs
Title : Structure of the C13.28 RNA Aptamer Bound to the G Protein-Coupled Receptor Kinase 2-Heterotrimeric G Protein Beta 1 and Gamma 2 Subunit Complex
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Deposited on : 2011-12-07
Resolution : 4.52 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

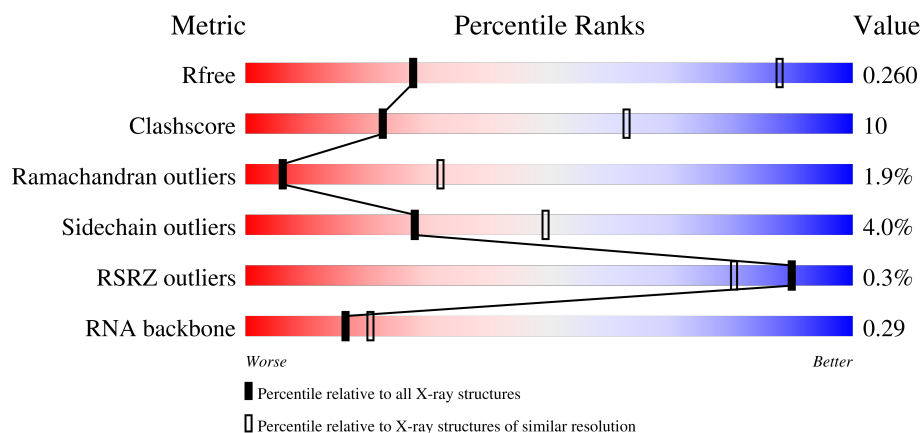
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.52 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	1131 (5.14-3.90)
Clashscore	190562	1005 (5.10-3.94)
Ramachandran outliers	187476	1061 (5.12-3.90)
Sidechain outliers	187428	1044 (5.12-3.90)
RSRZ outliers	180081	1126 (5.14-3.90)
RNA backbone	3983	1039 (5.90-3.10)

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	689	 68% 19% • 12%
2	B	340	 70% 27% •
3	G	74	 73% 16% • 9%
4	C	28	 43% 29% 29%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8535 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 Beta-adrenergic receptor kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	609	Total	C	N	O	S	0	0	0
			4984	3183	863	904	34			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	670	ALA	SER	engineered mutation	UNP P21146

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	339	Total	C	N	O	S	0	0	0
			2607	1607	468	511	21			

- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	67	Total	C	N	O	S	0	0	0
			520	326	91	99	4			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-5	HIS	-	expression tag	UNP P63212
G	-4	HIS	-	expression tag	UNP P63212
G	-3	HIS	-	expression tag	UNP P63212
G	-2	HIS	-	expression tag	UNP P63212
G	-1	HIS	-	expression tag	UNP P63212
G	0	HIS	-	expression tag	UNP P63212
G	68	CMT	-	expression tag	UNP P63212

- Molecule 4 is a RNA chain called C13.28 RNA Aptamer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	20	Total	C	N	O	P	0	0	0
			423	191	79	135	18			

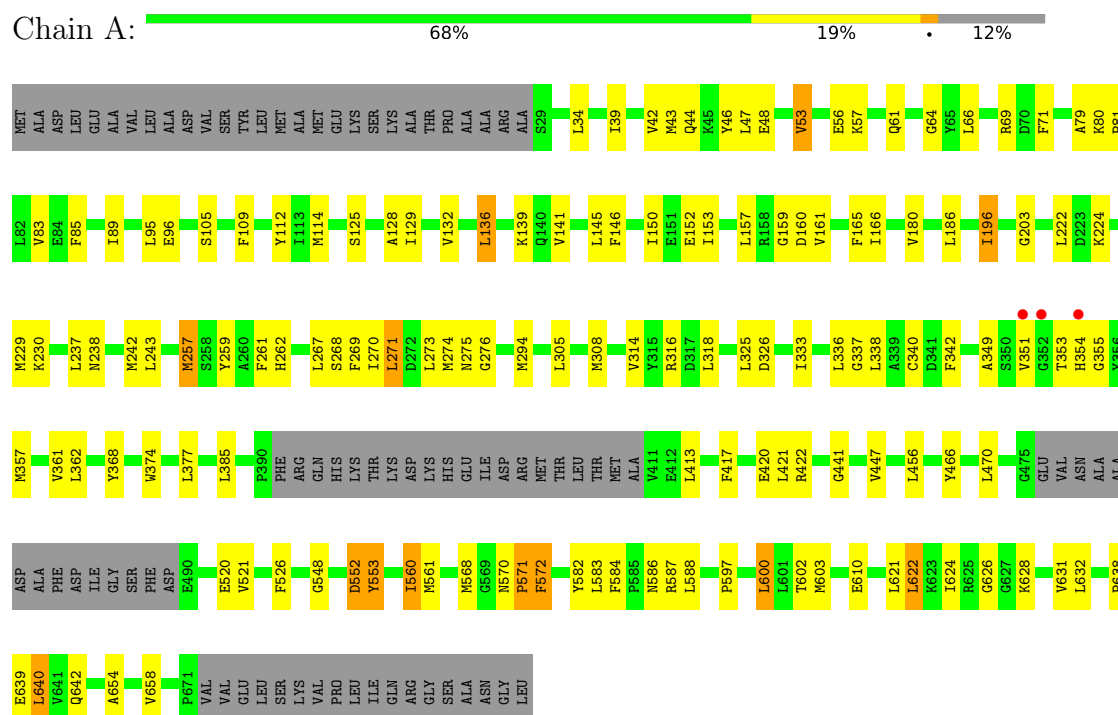
- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

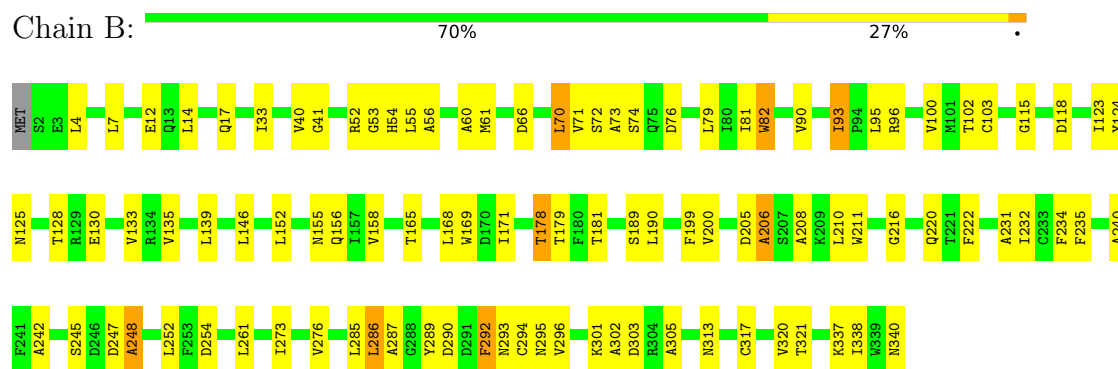
3 Residue-property plots

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: Beta-adrenergic receptor kinase 1



• Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



• Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2

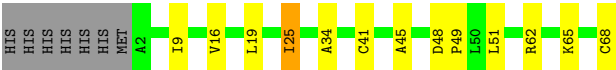
Chain G:

73%

16%

•

9%



● Molecule 4: C13.28 RNA Aptamer

Chain C:

43%

29%

29%



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 1 2	Depositor
Cell constants a, b, c, α , β , γ	257.28Å 257.28Å 99.43Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.99 – 4.52 19.99 – 4.52	Depositor EDS
% Data completeness (in resolution range)	56.9 (19.99-4.52) 57.0 (19.99-4.52)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 4.54Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.184 , 0.268 0.180 , 0.260	Depositor DCC
R_{free} test set	650 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	256.8	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.15 , 154.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.109 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8535	wwPDB-VP
Average B, all atoms (Å ²)	328.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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: MG, CMT

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	0.60	0/5097	0.71	0/6852
2	B	0.62	0/2654	0.69	0/3597
3	G	0.50	0/520	0.77	0/700
4	C	0.39	0/472	0.76	0/733
All	All	0.59	0/8743	0.71	0/11882

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 [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	4984	0	4978	103	0
2	B	2607	0	2510	70	0
3	G	520	0	527	12	0
4	C	423	0	221	0	0
5	A	1	0	0	0	0
All	All	8535	0	8236	176	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 (176) 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)
2:B:220:GLN:HE21	3:G:25:ILE:HD12	1.26	0.99
1:A:308:MET:HE1	1:A:333:ILE:HD12	1.46	0.97
1:A:294:MET:HE1	1:A:385:LEU:HD11	1.66	0.78
1:A:622:LEU:HD21	1:A:632:LEU:HD12	1.67	0.77
1:A:89:ILE:HG21	1:A:150:ILE:HD11	1.70	0.73
1:A:150:ILE:HD13	1:A:153:ILE:HD12	1.70	0.72
1:A:48:GLU:HA	1:A:53:VAL:HG21	1.73	0.71
2:B:33:ILE:HG21	3:G:34:ALA:HB1	1.74	0.70
1:A:314:VAL:HG23	1:A:342:PHE:CD2	2.27	0.69
2:B:73:ALA:HB2	2:B:103:CYS:HB3	1.77	0.66
1:A:270:ILE:C	1:A:271:LEU:HD23	2.21	0.65
2:B:79:LEU:HD12	2:B:95:LEU:HD21	1.78	0.65
2:B:294:CYS:SG	2:B:295:ASN:N	2.69	0.65
1:A:413:LEU:HD12	1:A:422:ARG:HG3	1.79	0.64
2:B:70:LEU:HD22	2:B:70:LEU:C	2.23	0.64
2:B:220:GLN:HE21	3:G:25:ILE:CD1	2.07	0.63
1:A:582:TYR:O	1:A:588:LEU:HD12	1.99	0.63
1:A:621:LEU:C	1:A:622:LEU:HD23	2.26	0.61
2:B:61:MET:HG3	2:B:317:CYS:SG	2.41	0.61
1:A:42:VAL:HG13	1:A:561:MET:HE1	1.84	0.59
1:A:85:PHE:CE2	1:A:153:ILE:HD11	2.37	0.59
1:A:583:LEU:HD12	1:A:584:PHE:H	1.67	0.59
3:G:41:CYS:O	3:G:45:ALA:HB2	2.02	0.58
2:B:294:CYS:C	2:B:295:ASN:HD22	2.11	0.57
1:A:621:LEU:HD12	1:A:622:LEU:N	2.20	0.57
1:A:600:LEU:HD23	2:B:55:LEU:HB3	1.87	0.55
2:B:254:ASP:HB2	2:B:261:LEU:HD11	1.88	0.55
2:B:71:VAL:CG1	2:B:79:LEU:HD22	2.37	0.55
2:B:287:ALA:HB3	2:B:289:TYR:CE1	2.41	0.55
2:B:205:ASP:O	2:B:206:ALA:HB3	2.05	0.55
2:B:242:ALA:HB2	2:B:252:LEU:HD13	1.89	0.55
2:B:123:ILE:HD11	2:B:139:LEU:HD12	1.88	0.55
1:A:150:ILE:HA	1:A:153:ILE:HD12	1.89	0.54
2:B:72:SER:O	2:B:79:LEU:HD23	2.08	0.54
1:A:61:GLN:O	1:A:64:GLY:N	2.41	0.54
1:A:316:ARG:NH2	1:A:351:VAL:HG11	2.23	0.54
1:A:336:LEU:O	1:A:338:LEU:N	2.41	0.54
1:A:262:HIS:HB2	1:A:267:LEU:HD23	1.90	0.54
2:B:231:ALA:CB	2:B:276:VAL:HG13	2.38	0.54
2:B:247:ASP:O	2:B:248:ALA:HB3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:ALA:HB2	1:A:152:GLU:OE2	2.08	0.53
1:A:145:LEU:HD23	1:A:146:PHE:CE2	2.44	0.53
1:A:34:LEU:HD23	1:A:180:VAL:HG21	1.90	0.53
1:A:521:VAL:HG12	1:A:526:PHE:HB2	1.90	0.53
2:B:292:PHE:CD1	2:B:313:ASN:C	2.87	0.53
1:A:139:LYS:O	1:A:141:VAL:HG13	2.07	0.53
1:A:186:LEU:HD11	1:A:259:TYR:HB3	1.90	0.53
1:A:361:VAL:HG22	1:A:368:TYR:CE1	2.44	0.52
2:B:115:GLY:HA3	2:B:146:LEU:HD23	1.90	0.52
2:B:337:LYS:O	2:B:338:ILE:HD13	2.09	0.52
2:B:273:ILE:N	2:B:273:ILE:HD12	2.24	0.52
2:B:208:ALA:HB3	2:B:222:PHE:HB2	1.92	0.52
1:A:243:LEU:HD22	1:A:257:MET:HB2	1.92	0.52
2:B:155:ASN:CA	2:B:171:ILE:HD12	2.40	0.52
2:B:286:LEU:HD22	2:B:286:LEU:N	2.25	0.52
1:A:47:LEU:HB3	1:A:53:VAL:HG22	1.91	0.51
2:B:320:VAL:HG12	2:B:321:THR:O	2.11	0.51
1:A:196:ILE:HD12	1:A:196:ILE:N	2.26	0.51
1:A:583:LEU:HD12	1:A:584:PHE:N	2.25	0.51
2:B:123:ILE:HD12	2:B:123:ILE:N	2.25	0.51
1:A:109:PHE:HD1	1:A:136:LEU:HD13	1.75	0.51
1:A:229:MET:HE3	1:A:230:LYS:HE2	1.92	0.50
1:A:308:MET:HE1	1:A:333:ILE:CD1	2.29	0.50
1:A:274:MET:HE2	1:A:326:ASP:N	2.27	0.50
2:B:124:TYR:CE2	2:B:135:VAL:HG22	2.47	0.50
2:B:220:GLN:NE2	3:G:25:ILE:HD12	2.10	0.50
1:A:105:SER:HB2	1:A:136:LEU:HD11	1.94	0.50
2:B:242:ALA:HB2	2:B:252:LEU:CD1	2.41	0.50
2:B:296:VAL:HB	2:B:305:ALA:HB3	1.92	0.49
1:A:262:HIS:CB	1:A:267:LEU:HD23	2.42	0.49
2:B:189:SER:OG	2:B:232:ILE:HG22	2.12	0.49
1:A:560:ILE:HD13	1:A:583:LEU:HG	1.93	0.49
2:B:158:VAL:HG22	2:B:168:LEU:HA	1.93	0.49
1:A:621:LEU:HD12	1:A:622:LEU:H	1.76	0.49
1:A:66:LEU:O	1:A:69:ARG:HG2	2.13	0.49
1:A:560:ILE:H	1:A:560:ILE:HD12	1.76	0.49
1:A:238:ASN:HD21	1:A:340:CYS:HA	1.77	0.49
1:A:318:LEU:HD23	1:A:377:LEU:N	2.28	0.49
1:A:624:ILE:HD12	1:A:628:LYS:HB3	1.93	0.49
1:A:39:ILE:HG22	1:A:43:MET:HB2	1.94	0.49
2:B:286:LEU:CD1	2:B:296:VAL:HG22	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:ILE:HG22	1:A:157:LEU:HD12	1.95	0.48
1:A:374:TRP:CZ3	1:A:447:VAL:HG21	2.48	0.48
1:A:361:VAL:HG22	1:A:368:TYR:CD1	2.48	0.48
1:A:654:ALA:O	1:A:658:VAL:HG23	2.14	0.48
2:B:14:LEU:HD13	3:G:19:LEU:HB3	1.96	0.48
2:B:14:LEU:HD13	3:G:19:LEU:CB	2.44	0.48
1:A:568:MET:HE2	1:A:631:VAL:HG21	1.94	0.48
1:A:624:ILE:HG22	1:A:626:GLY:H	1.78	0.48
1:A:109:PHE:O	1:A:114:MET:HB2	2.14	0.47
1:A:357:MET:CE	1:A:362:LEU:HD21	2.44	0.47
1:A:165:PHE:O	1:A:166:ILE:C	2.56	0.47
1:A:274:MET:HE2	1:A:325:LEU:C	2.40	0.47
2:B:199:PHE:CE2	2:B:211:TRP:HB2	2.50	0.47
2:B:56:ALA:HB3	2:B:76:ASP:N	2.29	0.47
2:B:7:LEU:HD22	3:G:16:VAL:HG21	1.96	0.47
2:B:199:PHE:O	2:B:210:LEU:HD12	2.14	0.47
1:A:79:ALA:O	1:A:83:VAL:HG23	2.15	0.47
1:A:109:PHE:CE1	1:A:132:VAL:HG12	2.49	0.47
1:A:237:LEU:C	1:A:237:LEU:HD23	2.40	0.47
1:A:71:PHE:CZ	1:A:165:PHE:HA	2.50	0.46
1:A:46:TYR:HA	1:A:642:GLN:HE21	1.79	0.46
1:A:242:MET:HA	1:A:242:MET:HE2	1.96	0.46
1:A:109:PHE:CD1	1:A:136:LEU:HD22	2.51	0.46
2:B:292:PHE:CD1	2:B:292:PHE:N	2.83	0.46
1:A:314:VAL:HG12	1:A:316:ARG:HG2	1.98	0.46
1:A:622:LEU:HD11	1:A:632:LEU:HG	1.97	0.46
2:B:285:LEU:C	2:B:286:LEU:HD22	2.41	0.46
1:A:125:SER:O	1:A:128:ALA:HB3	2.16	0.45
1:A:639:GLU:O	1:A:640:LEU:C	2.59	0.45
2:B:178:THR:HG22	2:B:179:THR:H	1.81	0.45
2:B:93:ILE:HD11	2:B:133:VAL:HB	1.98	0.45
1:A:638:PRO:O	1:A:639:GLU:C	2.58	0.45
1:A:305:LEU:CD1	1:A:377:LEU:HD22	2.46	0.45
2:B:178:THR:HG21	2:B:216:GLY:HA3	1.99	0.45
1:A:48:GLU:CA	1:A:53:VAL:HG21	2.46	0.45
1:A:80:LYS:N	1:A:81:PRO:HD2	2.32	0.45
1:A:586:ASN:C	1:A:603:MET:HG2	2.42	0.44
2:B:74:SER:O	2:B:100:VAL:HG11	2.16	0.44
1:A:42:VAL:HG13	1:A:561:MET:CE	2.47	0.44
1:A:43:MET:O	1:A:44:GLN:C	2.60	0.44
2:B:82:TRP:CD1	2:B:82:TRP:N	2.84	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:LEU:HD23	1:A:96:GLU:N	2.32	0.44
2:B:123:ILE:HD11	2:B:139:LEU:CD1	2.47	0.44
1:A:357:MET:HE3	1:A:362:LEU:HD21	2.00	0.44
1:A:160:ASP:O	1:A:161:VAL:C	2.61	0.44
2:B:235:PHE:HB3	2:B:240:ALA:HB3	1.99	0.44
2:B:245:SER:H	2:B:273:ILE:HD13	1.83	0.44
1:A:203:GLY:HA3	1:A:222:LEU:HA	1.99	0.43
2:B:286:LEU:HD12	2:B:296:VAL:HG22	2.00	0.43
2:B:200:VAL:HG23	2:B:232:ILE:HD11	2.01	0.43
2:B:93:ILE:HD11	2:B:133:VAL:CG1	2.48	0.43
1:A:269:PHE:HB3	1:A:271:LEU:HD21	2.00	0.43
1:A:308:MET:CE	1:A:333:ILE:HD12	2.32	0.43
1:A:456:LEU:HD22	1:A:466:TYR:CE2	2.54	0.43
1:A:85:PHE:HE2	1:A:153:ILE:HD11	1.83	0.43
1:A:141:VAL:O	1:A:141:VAL:HG23	2.19	0.43
1:A:294:MET:CE	1:A:385:LEU:HD21	2.48	0.43
2:B:60:ALA:HB3	2:B:102:THR:HA	1.99	0.43
1:A:109:PHE:CD2	1:A:114:MET:HE2	2.54	0.42
2:B:155:ASN:HA	2:B:171:ILE:HD12	2.01	0.42
1:A:560:ILE:HD12	1:A:560:ILE:N	2.34	0.42
1:A:552:ASP:O	1:A:553:TYR:C	2.62	0.42
1:A:85:PHE:CD1	1:A:112:TYR:HB3	2.55	0.42
1:A:570:ASN:O	1:A:572:PHE:N	2.52	0.42
2:B:205:ASP:O	2:B:206:ALA:CB	2.68	0.42
1:A:43:MET:O	1:A:46:TYR:N	2.53	0.42
1:A:417:PHE:CD1	1:A:421:LEU:HD23	2.55	0.42
1:A:81:PRO:O	1:A:85:PHE:HB2	2.18	0.42
1:A:224:LYS:HE2	1:A:267:LEU:HD21	2.02	0.42
2:B:301:LYS:O	2:B:302:ALA:HB3	2.19	0.42
1:A:584:PHE:HB2	1:A:587:ARG:HG2	2.02	0.42
2:B:168:LEU:HD12	2:B:169:TRP:H	1.85	0.42
2:B:79:LEU:HD21	2:B:103:CYS:HB3	2.02	0.42
2:B:4:LEU:HD21	3:G:9:ILE:HG13	2.02	0.42
2:B:54:HIS:ND1	2:B:76:ASP:OD2	2.49	0.42
2:B:152:LEU:HD12	2:B:156:GLN:HB3	2.02	0.41
1:A:243:LEU:HD13	1:A:257:MET:HG3	2.02	0.41
1:A:353:THR:O	1:A:355:GLY:N	2.53	0.41
2:B:118:ASP:OD1	2:B:118:ASP:N	2.53	0.41
1:A:261:PHE:CE2	1:A:268:SER:HB2	2.55	0.41
1:A:85:PHE:CD2	1:A:153:ILE:HD11	2.55	0.41
2:B:231:ALA:HB1	2:B:276:VAL:H	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:VAL:HG13	1:A:368:TYR:CZ	2.56	0.41
2:B:40:VAL:HG23	2:B:41:GLY:N	2.35	0.41
1:A:325:LEU:HD12	1:A:325:LEU:N	2.36	0.41
3:G:48:ASP:HA	3:G:49:PRO:HD3	1.93	0.41
1:A:349:ALA:HB3	1:A:351:VAL:HG23	2.03	0.41
2:B:81:ILE:O	2:B:90:VAL:N	2.54	0.41
2:B:165:THR:HG22	2:B:181:THR:HA	2.03	0.41
2:B:231:ALA:HB1	2:B:276:VAL:HG13	2.02	0.40
1:A:571:PRO:HG3	1:A:631:VAL:HG23	2.04	0.40
2:B:125:ASN:O	2:B:133:VAL:HG13	2.21	0.40
1:A:273:LEU:HD23	1:A:273:LEU:C	2.46	0.40
3:G:48:ASP:HB3	3:G:51:LEU:HD12	2.03	0.40
3:G:48:ASP:CB	3:G:51:LEU:HD12	2.52	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	603/689 (88%)	519 (86%)	72 (12%)	12 (2%)	6	31
2	B	337/340 (99%)	291 (86%)	41 (12%)	5 (2%)	8	38
3	G	65/74 (88%)	59 (91%)	4 (6%)	2 (3%)	3	22
All	All	1005/1103 (91%)	869 (86%)	117 (12%)	19 (2%)	6	32

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	337	GLY
1	A	553	TYR
1	A	276	GLY
1	A	354	HIS

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Mol	Chain	Res	Type
2	B	206	ALA
1	A	159	GLY
1	A	552	ASP
1	A	571	PRO
1	A	572	PHE
1	A	640	LEU
2	B	128	THR
2	B	130	GLU
2	B	248	ALA
3	G	62	ARG
3	G	65	LYS
2	B	53	GLY
1	A	597	PRO
1	A	441	GLY
1	A	548	GLY

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	547/611 (90%)	530 (97%)	17 (3%)	35	56
2	B	282/283 (100%)	265 (94%)	17 (6%)	17	39
3	G	54/61 (88%)	53 (98%)	1 (2%)	50	66
All	All	883/955 (92%)	848 (96%)	35 (4%)	28	49

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	VAL
1	A	56	GLU
1	A	57	LYS
1	A	129	ILE
1	A	136	LEU
1	A	196	ILE
1	A	257	MET

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Mol	Chain	Res	Type
1	A	271	LEU
1	A	275	ASN
1	A	420	GLU
1	A	470	LEU
1	A	520	GLU
1	A	560	ILE
1	A	600	LEU
1	A	602	THR
1	A	610	GLU
1	A	622	LEU
2	B	12	GLU
2	B	17	GLN
2	B	52	ARG
2	B	66	ASP
2	B	70	LEU
2	B	82	TRP
2	B	93	ILE
2	B	96	ARG
2	B	178	THR
2	B	190	LEU
2	B	234	PHE
2	B	286	LEU
2	B	290	ASP
2	B	292	PHE
2	B	293	ASN
2	B	303	ASP
2	B	340	ASN
3	G	25	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	147	GLN
1	A	189	ASN
1	A	238	ASN
1	A	275	ASN
1	A	310	ASN
1	A	503	GLN
1	A	508	ASN
1	A	530	ASN
1	A	546	GLN
1	A	598	GLN

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Mol	Chain	Res	Type
1	A	607	GLN
1	A	613	GLN
1	A	642	GLN
2	B	17	GLN
2	B	220	GLN
2	B	237	ASN
2	B	295	ASN
2	B	340	ASN
3	G	24	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	C	18/28 (64%)	8 (44%)	2 (11%)

All (8) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	C	50	U
4	C	51	A
4	C	52	C
4	C	53	G
4	C	54	G
4	C	55	G
4	C	65	U
4	C	68	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	C	51	A
4	C	53	G

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

1 non-standard protein/DNA/RNA residue 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	CMT	G	68	3	7,7,7	2.05	1 (14%)	6,8,8	2.06	3 (50%)

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	CMT	G	68	3	-	3/8/8/8	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	68	CMT	OXT-C	5.26	1.46	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	68	CMT	OXT-C-CA	3.75	121.05	111.50
3	G	68	CMT	OXT-C-O	-2.64	118.71	123.85
3	G	68	CMT	C1-OXT-C	2.02	120.50	115.92

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	68	CMT	CA-C-OXT-C1
3	G	68	CMT	O-C-OXT-C1
3	G	68	CMT	OXT-C-CA-N

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	609/689 (88%)	-0.83	3 (0%) 87 75	173, 330, 468, 554	0
2	B	339/340 (99%)	-0.87	0 100 100	160, 281, 419, 548	0
3	G	66/74 (89%)	-0.86	0 100 100	227, 379, 518, 566	0
4	C	20/28 (71%)	-0.21	0 100 100	457, 537, 641, 662	0
All	All	1034/1131 (91%)	-0.83	3 (0%) 90 80	160, 309, 480, 662	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	352	GLY	4.0
1	A	351	VAL	2.7
1	A	354	HIS	2.6

6.2 Non-standard residues in protein, DNA, RNA chains [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
3	CMT	G	68	8/8	0.69	0.07	389,419,424,434	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

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
5	MG	A	701	1/1	0.94	0.12	441,441,441,441	0

6.5 Other polymers

There are no such residues in this entry.