



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:06 PM GMT

PDB ID : 1ISS
Title : Crystal Structure of Metabotropic Glutamate Receptor Subtype 1 Complexed with an antagonist
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Deposited on : 2001-12-21
Resolution : 3.30 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

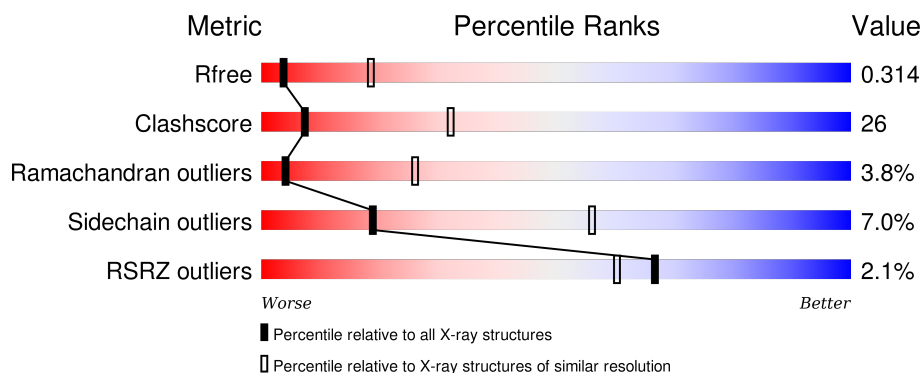
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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}	91344	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	490	<div> <div> <div>0%</div> <div>50%</div> <div>38%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	490	<div> <div>2%</div> <div>49%</div> <div>38%</div> <div>5%</div> <div>8%</div> </div>

2 Entry composition [i](#)

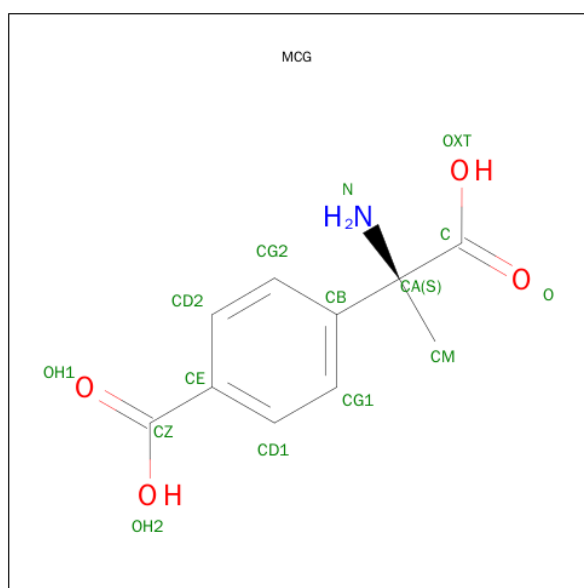
There are 2 unique types of molecules in this entry. The entry contains 7124 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Metabotropic Glutamate Receptor subtype 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	0	0
			3547	2250	613	664	20			
1	B	452	Total	C	N	O	S	0	0	0
			3547	2250	613	664	20			

- Molecule 2 is (S)-(ALPHA)-METHYL-4-CARBOXYPHENYLGLYCINE (three-letter code: MCG) (formula: C₁₀H₁₁NO₄).

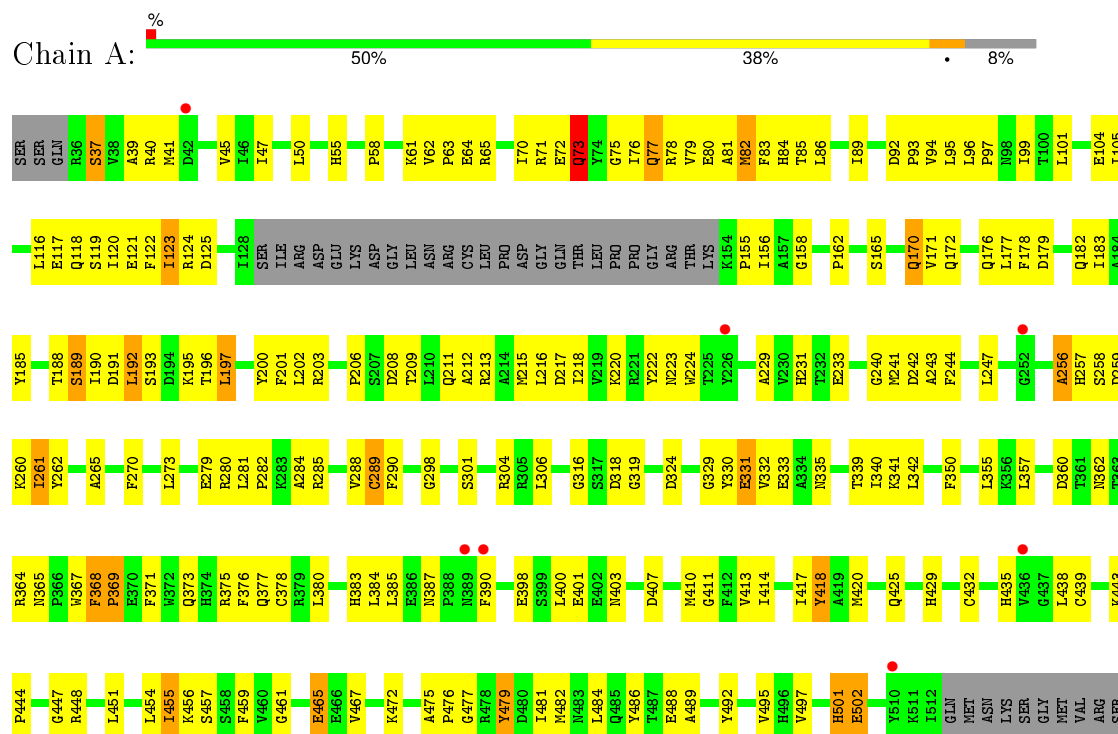


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	10	1	4		
2	B	1	Total	C	N	O	0	0
			15	10	1	4		

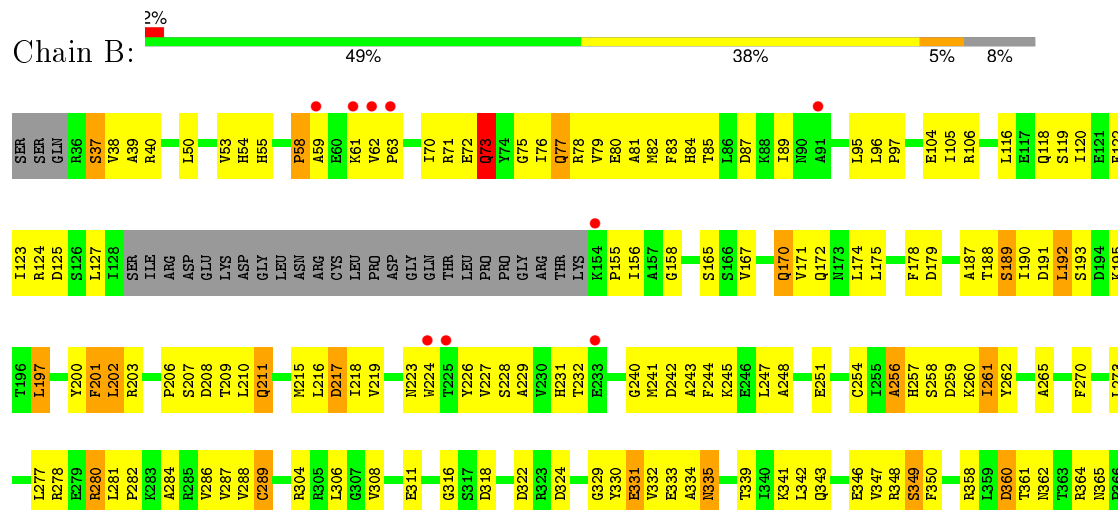
3 Residue-property plots

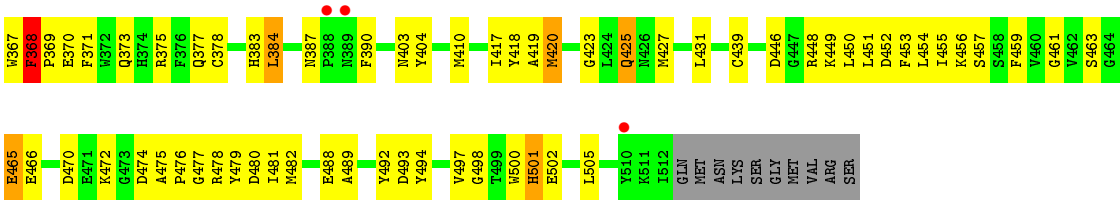
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: Metabotropic Glutamate Receptor subtype 1



• Molecule 1: Metabotropic Glutamate Receptor subtype 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	112.14Å 112.14Å 289.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.30 19.97 – 3.30	Depositor EDS
% Data completeness (in resolution range)	91.1 (20.00-3.30) 97.4 (19.97-3.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 3.29Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.257 , 0.314 0.266 , 0.314	Depositor DCC
R_{free} test set	2224 reflections (7.99%)	DCC
Wilson B-factor (Å ²)	90.1	Xtriage
Anisotropy	0.600	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 64.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Outliers	0 of 27833 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7124	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MCG

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	0.47	0/3627	0.67	0/4913
1	B	0.47	0/3627	0.68	0/4913
All	All	0.47	0/7254	0.67	0/9826

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	185	TYR	Sidechain

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	3547	0	3421	186	0
1	B	3547	0	3421	181	0
2	A	15	0	9	0	0
2	B	15	0	9	0	0
All	All	7124	0	6860	361	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 26.

All (361) 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:39:ALA:HB3	1:B:105:ILE:HB	1.44	0.97
1:A:123:ILE:HD12	1:A:178:PHE:CE1	2.09	0.88
1:B:368:PHE:HB3	1:B:369:PRO:HD3	1.57	0.86
1:A:39:ALA:HB3	1:A:105:ILE:HB	1.59	0.82
1:B:218:ILE:HD11	1:B:481:ILE:HD12	1.63	0.79
1:A:79:VAL:HG22	1:A:105:ILE:HG21	1.63	0.78
1:A:182:GLN:O	1:A:202:LEU:HD23	1.84	0.77
1:A:192:LEU:HD13	1:A:201:PHE:CZ	2.19	0.77
1:A:368:PHE:HB3	1:A:369:PRO:HD3	1.66	0.76
1:B:70:ILE:HD13	1:B:371:PHE:HB2	1.67	0.76
1:B:70:ILE:CD1	1:B:371:PHE:HB2	2.15	0.75
1:B:83:PHE:CE1	1:B:364:ARG:HG3	2.22	0.74
1:B:76:ILE:HD12	1:B:365:ASN:HD21	1.52	0.74
1:B:158:GLY:HA3	1:B:420:MET:CE	2.18	0.73
1:A:41:MET:CE	1:A:364:ARG:HH11	2.02	0.72
1:A:47:ILE:HD13	1:A:420:MET:HG3	1.71	0.72
1:A:70:ILE:HD13	1:A:371:PHE:HB2	1.71	0.71
1:B:158:GLY:HA3	1:B:420:MET:HE1	1.73	0.71
1:A:362:ASN:HD21	1:A:365:ASN:HB3	1.55	0.70
1:A:89:ILE:HG12	1:A:418:TYR:HE2	1.56	0.69
1:A:362:ASN:ND2	1:A:365:ASN:HB3	2.07	0.69
1:A:339:THR:OG1	1:A:482:MET:HB2	1.92	0.69
1:B:261:ILE:HD11	1:B:265:ALA:HB3	1.73	0.68
1:B:280:ARG:O	1:B:284:ALA:HB3	1.94	0.68
1:A:41:MET:HE3	1:A:364:ARG:HH11	1.57	0.68
1:A:47:ILE:HD13	1:A:420:MET:CG	2.25	0.67
1:A:70:ILE:CD1	1:A:371:PHE:HB2	2.25	0.67
1:A:83:PHE:CE1	1:A:364:ARG:HG3	2.28	0.67
1:B:201:PHE:CD2	1:B:202:LEU:N	2.62	0.67
1:B:211:GLN:HE22	1:B:318:ASP:H	1.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:322:ASP:HA	1:B:494:TYR:CE2	2.30	0.66
1:A:89:ILE:HG12	1:A:418:TYR:CE2	2.31	0.66
1:A:280:ARG:O	1:A:284:ALA:HB3	1.94	0.66
1:A:80:GLU:HG3	1:A:357:LEU:HD11	1.78	0.66
1:B:202:LEU:N	1:B:202:LEU:HD23	2.11	0.65
1:A:200:TYR:OH	1:A:448:ARG:HG2	1.96	0.65
1:A:335:ASN:HA	1:A:484:LEU:HG	1.80	0.64
1:A:216:LEU:HB2	1:A:244:PHE:HE1	1.60	0.64
1:B:172:GLN:NE2	1:B:201:PHE:HB2	2.12	0.64
1:B:206:PRO:HB3	1:B:477:GLY:HA2	1.78	0.64
1:B:227:VAL:HG12	1:B:286:VAL:HB	1.80	0.64
1:B:330:TYR:O	1:B:332:VAL:N	2.31	0.63
1:B:122:PHE:CD1	1:B:156:ILE:HG13	2.32	0.63
1:B:122:PHE:HD1	1:B:156:ILE:HG13	1.63	0.63
1:B:330:TYR:C	1:B:332:VAL:H	2.01	0.62
1:A:206:PRO:HB3	1:A:477:GLY:HA2	1.81	0.62
1:A:407:ASP:HB3	1:A:410:MET:HE2	1.81	0.62
1:B:106:ARG:HD3	1:B:118:GLN:OE1	2.00	0.62
1:A:413:VAL:HG12	1:A:414:ILE:N	2.15	0.62
1:A:122:PHE:CD1	1:A:156:ILE:HG13	2.34	0.62
1:A:172:GLN:O	1:A:176:GLN:HG2	2.00	0.62
1:B:339:THR:OG1	1:B:482:MET:HB2	2.00	0.61
1:B:470:ASP:OD1	1:B:474:ASP:HB2	2.01	0.61
1:B:165:SER:HB3	1:B:189:SER:OG	2.01	0.61
1:A:241:MET:O	1:A:244:PHE:N	2.32	0.61
1:B:371:PHE:CE1	1:B:375:ARG:HB2	2.36	0.61
1:B:229:ALA:O	1:B:258:SER:HA	2.01	0.61
1:B:40:ARG:HG3	1:B:104:GLU:HG3	1.83	0.61
1:A:82:MET:HG2	1:A:105:ILE:HD11	1.83	0.60
1:A:162:PRO:HG3	1:A:171:VAL:HG21	1.83	0.60
1:B:475:ALA:HB1	1:B:476:PRO:HD2	1.82	0.60
1:A:373:GLN:HG2	1:A:378:CYS:O	2.01	0.60
1:A:285:ARG:HH11	1:A:285:ARG:HG2	1.66	0.60
1:A:454:LEU:O	1:A:457:SER:HB2	2.02	0.60
1:A:376:PHE:HZ	1:A:400:LEU:HD23	1.67	0.60
1:B:461:GLY:HA3	1:B:465:GLU:HG2	1.84	0.59
1:B:192:LEU:HD13	1:B:201:PHE:CZ	2.36	0.59
1:B:72:GLU:H	1:B:73:GLN:HE21	1.49	0.59
1:A:165:SER:HB3	1:A:189:SER:OG	2.03	0.59
1:A:398:GLU:OE1	1:A:398:GLU:N	2.34	0.59
1:A:375:ARG:HH11	1:A:375:ARG:HG3	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:MET:HG2	1:B:105:ILE:HD11	1.85	0.59
1:B:281:LEU:HB3	1:B:282:PRO:HA	1.85	0.59
1:B:53:VAL:HG12	1:B:54:HIS:ND1	2.18	0.58
1:A:123:ILE:HD12	1:A:178:PHE:CZ	2.38	0.58
1:A:39:ALA:HB2	1:A:367:TRP:CZ3	2.39	0.58
1:A:373:GLN:HE21	1:A:380:LEU:HD12	1.69	0.58
1:B:120:ILE:HD13	1:B:174:LEU:HD21	1.85	0.58
1:A:55:HIS:CE1	1:A:71:ARG:HG2	2.38	0.58
1:A:216:LEU:HB2	1:A:244:PHE:CE1	2.38	0.57
1:A:376:PHE:CZ	1:A:400:LEU:HD23	2.39	0.57
1:A:123:ILE:CG1	1:A:124:ARG:N	2.68	0.57
1:B:341:LYS:HG2	1:B:342:LEU:N	2.18	0.57
1:A:229:ALA:O	1:A:258:SER:HA	2.05	0.57
1:A:448:ARG:O	1:A:451:LEU:HB3	2.05	0.57
1:B:216:LEU:HD21	1:B:251:GLU:HG3	1.86	0.56
1:B:241:MET:O	1:B:244:PHE:N	2.38	0.56
1:A:330:TYR:C	1:A:332:VAL:H	2.08	0.56
1:B:373:GLN:HG2	1:B:378:CYS:O	2.04	0.56
1:B:85:THR:O	1:B:89:ILE:HG13	2.05	0.56
1:B:368:PHE:HB3	1:B:369:PRO:CD	2.32	0.56
1:B:39:ALA:HB2	1:B:367:TRP:CZ3	2.40	0.56
1:B:454:LEU:O	1:B:457:SER:HB2	2.06	0.56
1:A:192:LEU:HD22	1:A:201:PHE:CD1	2.41	0.56
1:A:240:GLY:O	1:A:243:ALA:HB3	2.05	0.56
1:A:330:TYR:O	1:A:332:VAL:N	2.38	0.56
1:B:39:ALA:HB2	1:B:367:TRP:HZ3	1.69	0.56
1:A:261:ILE:HD11	1:A:265:ALA:HB3	1.88	0.56
1:A:333:GLU:H	1:A:333:GLU:CD	2.07	0.56
1:A:195:LYS:C	1:A:197:LEU:H	2.10	0.55
1:A:58:PRO:HD2	1:A:61:LYS:HB2	1.88	0.55
1:B:72:GLU:H	1:B:73:GLN:NE2	2.04	0.55
1:B:216:LEU:HD22	1:B:247:LEU:HB3	1.89	0.55
1:A:172:GLN:NE2	1:A:201:PHE:HB2	2.22	0.54
1:B:192:LEU:HD22	1:B:201:PHE:CD1	2.43	0.54
1:A:82:MET:CB	1:A:105:ILE:HD11	2.38	0.54
1:B:215:MET:O	1:B:218:ILE:HB	2.08	0.54
1:B:95:LEU:O	1:B:96:LEU:C	2.45	0.54
1:A:281:LEU:HB3	1:A:282:PRO:HA	1.89	0.54
1:A:78:ARG:O	1:A:81:ALA:HB3	2.07	0.54
1:A:158:GLY:HA3	1:A:420:MET:CE	2.37	0.54
1:B:308:VAL:HB	1:B:311:GLU:OE1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:ILE:HD11	1:B:481:ILE:CD1	2.33	0.54
1:A:414:ILE:O	1:A:417:ILE:HB	2.08	0.54
1:A:99:ILE:HD13	1:A:438:LEU:CD2	2.37	0.54
1:B:72:GLU:N	1:B:73:GLN:HE21	2.06	0.54
1:A:501:HIS:O	1:A:502:GLU:HB2	2.08	0.54
1:B:79:VAL:HG22	1:B:105:ILE:HG21	1.91	0.53
1:A:244:PHE:CE2	1:A:288:VAL:HG11	2.42	0.53
1:A:218:ILE:HD11	1:A:481:ILE:HD12	1.89	0.53
1:A:216:LEU:CB	1:A:244:PHE:HE1	2.21	0.53
1:A:461:GLY:HA3	1:A:465:GLU:HG2	1.90	0.53
1:A:217:ASP:HA	1:A:220:LYS:HD3	1.89	0.53
1:B:123:ILE:HG13	1:B:124:ARG:N	2.23	0.53
1:A:367:TRP:O	1:A:368:PHE:C	2.45	0.53
1:A:41:MET:CE	1:A:364:ARG:NH1	2.71	0.53
1:A:191:ASP:O	1:A:193:SER:N	2.41	0.53
1:A:183:ILE:HA	1:A:202:LEU:O	2.08	0.53
1:A:373:GLN:NE2	1:A:380:LEU:HD12	2.24	0.53
1:B:208:ASP:O	1:B:211:GLN:HB2	2.08	0.53
1:A:123:ILE:CD1	1:A:178:PHE:CE1	2.89	0.52
1:A:259:ASP:OD1	1:A:260:LYS:N	2.41	0.52
1:B:76:ILE:HG13	1:B:371:PHE:CG	2.45	0.52
1:A:285:ARG:NH1	1:A:285:ARG:HG2	2.22	0.52
1:B:83:PHE:CD1	1:B:364:ARG:HG3	2.44	0.52
1:A:195:LYS:C	1:A:197:LEU:N	2.63	0.52
1:B:73:GLN:H	1:B:73:GLN:HE21	1.57	0.52
1:A:461:GLY:HA3	1:A:465:GLU:OE2	2.10	0.52
1:A:40:ARG:HG3	1:A:104:GLU:HG3	1.91	0.52
1:A:377:GLN:HA	1:A:390:PHE:CE1	2.44	0.52
1:B:89:ILE:HG12	1:B:418:TYR:CE2	2.45	0.52
1:A:261:ILE:HG12	1:A:262:TYR:N	2.25	0.52
1:A:123:ILE:HG12	1:A:124:ARG:N	2.25	0.51
1:B:40:ARG:CD	1:B:104:GLU:HG3	2.40	0.51
1:A:216:LEU:HD13	1:A:244:PHE:CE1	2.45	0.51
1:A:195:LYS:HE2	1:A:195:LYS:HA	1.92	0.51
1:A:172:GLN:HG3	1:A:176:GLN:HE21	1.75	0.51
1:B:171:VAL:HG12	1:B:175:LEU:HD12	1.91	0.51
1:A:193:SER:O	1:A:472:LYS:HD3	2.11	0.51
1:B:203:ARG:NH2	1:B:207:SER:HB3	2.26	0.51
1:B:78:ARG:O	1:B:81:ALA:HB3	2.11	0.51
1:B:119:SER:O	1:B:122:PHE:HB2	2.09	0.51
1:B:425:GLN:HE21	1:B:425:GLN:HA	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:GLY:O	1:B:243:ALA:HB3	2.10	0.51
1:B:55:HIS:CE1	1:B:71:ARG:HG2	2.46	0.51
1:A:368:PHE:HB3	1:A:369:PRO:CD	2.39	0.51
1:B:330:TYR:C	1:B:332:VAL:N	2.65	0.51
1:B:306:LEU:O	1:B:306:LEU:HG	2.11	0.51
1:B:261:ILE:HG12	1:B:262:TYR:N	2.26	0.50
1:A:455:ILE:C	1:A:457:SER:H	2.14	0.50
1:B:270:PHE:O	1:B:273:LEU:HB3	2.12	0.50
1:B:367:TRP:O	1:B:368:PHE:C	2.50	0.50
1:A:301:SER:HB2	1:A:330:TYR:HE1	1.77	0.50
1:A:62:VAL:N	1:A:63:PRO:CD	2.74	0.50
1:B:70:ILE:HD11	1:B:371:PHE:HB2	1.91	0.50
1:A:257:HIS:CG	1:A:258:SER:H	2.29	0.50
1:A:191:ASP:C	1:A:193:SER:H	2.14	0.50
1:A:124:ARG:O	1:A:125:ASP:C	2.48	0.50
1:A:65:ARG:NH2	1:B:127:LEU:O	2.45	0.50
1:A:479:TYR:N	1:A:479:TYR:CD1	2.79	0.50
1:B:244:PHE:CE2	1:B:288:VAL:HG11	2.47	0.50
1:A:432:CYS:HB3	1:A:435:HIS:HB2	1.94	0.49
1:B:165:SER:OG	1:B:187:ALA:HA	2.13	0.49
1:A:215:MET:O	1:A:218:ILE:HB	2.12	0.49
1:A:95:LEU:O	1:A:96:LEU:C	2.50	0.49
1:B:158:GLY:HA3	1:B:420:MET:HE3	1.92	0.49
1:A:241:MET:O	1:A:242:ASP:C	2.49	0.49
1:A:459:PHE:CZ	1:A:467:VAL:HG11	2.47	0.49
1:B:304:ARG:NH2	1:B:333:GLU:OE2	2.46	0.49
1:A:261:ILE:HG12	1:A:262:TYR:O	2.12	0.49
1:B:257:HIS:CG	1:B:258:SER:N	2.81	0.49
1:B:190:ILE:HG22	1:B:190:ILE:O	2.13	0.49
1:B:289:CYS:O	1:B:316:GLY:HA2	2.13	0.48
1:B:124:ARG:O	1:B:125:ASP:C	2.51	0.48
1:B:228:SER:HB3	1:B:287:VAL:HG22	1.95	0.48
1:A:117:GLU:O	1:A:120:ILE:HB	2.13	0.48
1:B:70:ILE:HG12	1:B:71:ARG:N	2.29	0.48
1:A:99:ILE:HD13	1:A:438:LEU:HD21	1.95	0.48
1:A:77:GLN:HG2	1:A:350:PHE:CZ	2.48	0.48
1:A:329:GLY:N	1:A:331:GLU:OE1	2.41	0.48
1:A:233:GLU:OE1	1:A:260:LYS:HD2	2.12	0.48
1:B:257:HIS:CG	1:B:258:SER:H	2.32	0.48
1:B:201:PHE:C	1:B:201:PHE:CD2	2.86	0.48
1:B:190:ILE:O	1:B:190:ILE:CG2	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:ASP:O	1:A:211:GLN:HB2	2.14	0.48
1:B:497:VAL:HG23	1:B:498:GLY:N	2.28	0.48
1:A:425:GLN:NE2	1:A:429:HIS:NE2	2.62	0.48
1:A:41:MET:HE3	1:A:364:ARG:NH1	2.27	0.48
1:B:501:HIS:O	1:B:502:GLU:HB2	2.14	0.48
1:B:216:LEU:O	1:B:218:ILE:N	2.48	0.47
1:B:70:ILE:HD13	1:B:371:PHE:CB	2.41	0.47
1:A:82:MET:CG	1:A:105:ILE:HD11	2.44	0.47
1:A:201:PHE:CD2	1:A:202:LEU:N	2.83	0.47
1:A:92:ASP:OD1	1:A:94:VAL:N	2.44	0.47
1:B:76:ILE:CD1	1:B:365:ASN:HD21	2.25	0.47
1:B:322:ASP:HA	1:B:494:TYR:CD2	2.49	0.47
1:A:179:ASP:HA	1:A:200:TYR:CE1	2.50	0.47
1:A:257:HIS:CG	1:A:258:SER:N	2.81	0.47
1:A:495:VAL:O	1:A:497:VAL:HG13	2.15	0.47
1:A:306:LEU:HG	1:A:306:LEU:O	2.15	0.47
1:B:77:GLN:OE1	1:B:404:TYR:HE1	1.97	0.47
1:B:341:LYS:O	1:B:479:TYR:HB3	2.15	0.47
1:A:304:ARG:NH2	1:A:333:GLU:OE2	2.35	0.47
1:B:179:ASP:HA	1:B:200:TYR:CE1	2.50	0.47
1:A:162:PRO:HD2	1:A:182:GLN:NE2	2.30	0.47
1:B:195:LYS:C	1:B:197:LEU:N	2.66	0.47
1:A:120:ILE:O	1:A:121:GLU:C	2.53	0.47
1:A:330:TYR:C	1:A:332:VAL:N	2.69	0.46
1:B:346:GLU:HG2	1:B:347:VAL:H	1.80	0.46
1:B:448:ARG:O	1:B:451:LEU:HB3	2.14	0.46
1:A:270:PHE:CZ	1:A:298:GLY:HA3	2.50	0.46
1:B:75:GLY:O	1:B:76:ILE:C	2.54	0.46
1:A:158:GLY:HA3	1:A:420:MET:HE3	1.97	0.46
1:B:256:ALA:CB	1:B:284:ALA:HB2	2.45	0.46
1:B:191:ASP:C	1:B:193:SER:H	2.19	0.46
1:B:377:GLN:HA	1:B:390:PHE:CE1	2.50	0.46
1:B:425:GLN:HA	1:B:425:GLN:NE2	2.31	0.46
1:B:260:LYS:O	1:B:261:ILE:HB	2.16	0.46
1:A:85:THR:OG1	1:A:414:ILE:HG23	2.16	0.46
1:B:425:GLN:HE21	1:B:425:GLN:CA	2.29	0.46
1:A:70:ILE:HD13	1:A:371:PHE:CB	2.44	0.45
1:A:332:VAL:HB	1:A:333:GLU:OE2	2.15	0.45
1:A:158:GLY:HA3	1:A:420:MET:HE1	1.98	0.45
1:A:455:ILE:O	1:A:457:SER:N	2.49	0.45
1:A:41:MET:HE1	1:A:364:ARG:HH11	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:HIS:O	1:A:260:LYS:HA	2.16	0.45
1:A:47:ILE:CD1	1:A:420:MET:HG3	2.45	0.45
1:A:84:HIS:O	1:A:85:THR:C	2.55	0.45
1:B:72:GLU:N	1:B:73:GLN:NE2	2.64	0.45
1:B:348:ARG:O	1:B:349:SER:C	2.54	0.45
1:B:244:PHE:O	1:B:247:LEU:N	2.49	0.45
1:A:447:GLY:O	1:A:448:ARG:C	2.54	0.45
1:B:195:LYS:HA	1:B:195:LYS:HE2	1.98	0.45
1:A:417:ILE:O	1:A:420:MET:HB3	2.17	0.45
1:B:50:LEU:HD23	1:B:50:LEU:HA	1.73	0.45
1:A:123:ILE:HG12	1:A:124:ARG:H	1.82	0.45
1:B:75:GLY:O	1:B:78:ARG:N	2.50	0.44
1:A:362:ASN:HD21	1:A:365:ASN:CB	2.26	0.44
1:A:82:MET:HG3	1:A:86:LEU:HD12	1.99	0.44
1:B:40:ARG:CG	1:B:104:GLU:HG3	2.46	0.44
1:B:423:GLY:HA3	1:B:454:LEU:HD23	1.98	0.44
1:B:362:ASN:ND2	1:B:365:ASN:HB3	2.31	0.44
1:B:218:ILE:HA	1:B:505:LEU:HD21	2.00	0.44
1:B:81:ALA:O	1:B:82:MET:C	2.56	0.44
1:A:410:MET:O	1:A:411:GLY:C	2.55	0.44
1:B:80:GLU:OE2	1:B:365:ASN:HB2	2.18	0.44
1:B:331:GLU:HB3	1:B:492:TYR:CD2	2.53	0.44
1:B:452:ASP:CG	1:B:456:LYS:HZ1	2.21	0.44
1:B:339:THR:O	1:B:482:MET:N	2.42	0.44
1:A:55:HIS:ND1	1:A:71:ARG:HG2	2.33	0.44
1:B:123:ILE:HD12	1:B:178:PHE:CE1	2.52	0.44
1:A:41:MET:HE1	1:A:364:ARG:NH1	2.32	0.44
1:A:289:CYS:O	1:A:316:GLY:HA2	2.17	0.44
1:A:339:THR:HG1	1:A:482:MET:HB2	1.80	0.43
1:B:167:VAL:O	1:B:170:GLN:N	2.51	0.43
1:B:466:GLU:H	1:B:478:ARG:HH12	1.65	0.43
1:A:47:ILE:HD13	1:A:420:MET:HG2	2.00	0.43
1:B:470:ASP:OD2	1:B:472:LYS:N	2.47	0.43
1:B:455:ILE:C	1:B:457:SER:H	2.21	0.43
1:B:500:TRP:HD1	1:B:505:LEU:HD13	1.82	0.43
1:B:172:GLN:CD	1:B:201:PHE:HB2	2.39	0.43
1:A:188:THR:O	1:A:189:SER:C	2.56	0.43
1:B:195:LYS:C	1:B:197:LEU:H	2.21	0.43
1:B:410:MET:HA	1:B:410:MET:HE2	2.00	0.43
1:B:417:ILE:O	1:B:420:MET:N	2.45	0.43
1:A:72:GLU:H	1:A:73:GLN:NE2	2.16	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:ILE:HD11	1:B:120:ILE:HG13	2.01	0.43
1:A:375:ARG:NH1	1:A:375:ARG:HG3	2.33	0.43
1:B:348:ARG:O	1:B:350:PHE:N	2.50	0.43
1:B:245:LYS:O	1:B:248:ALA:HB3	2.19	0.43
1:A:75:GLY:O	1:A:76:ILE:C	2.57	0.43
1:A:70:ILE:HD11	1:A:76:ILE:HD11	2.01	0.43
1:B:224:TRP:CD2	1:B:286:VAL:HG21	2.54	0.43
1:A:177:LEU:CD1	1:B:174:LEU:HB2	2.49	0.43
1:B:59:ALA:O	1:B:62:VAL:HG23	2.19	0.43
1:B:216:LEU:O	1:B:219:VAL:N	2.52	0.43
1:B:343:GLN:HA	1:B:480:ASP:OD2	2.19	0.43
1:A:170:GLN:HE21	1:A:170:GLN:HB2	1.63	0.43
1:A:222:TYR:O	1:A:224:TRP:N	2.52	0.43
1:A:39:ALA:HB2	1:A:367:TRP:HZ3	1.81	0.43
1:A:121:GLU:OE1	1:B:124:ARG:NH1	2.52	0.43
1:B:241:MET:O	1:B:242:ASP:C	2.57	0.42
1:B:333:GLU:CD	1:B:333:GLU:H	2.22	0.42
1:B:278:ARG:HH11	1:B:306:LEU:HD21	1.83	0.42
1:A:190:ILE:HG22	1:A:190:ILE:O	2.19	0.42
1:A:81:ALA:O	1:A:82:MET:C	2.57	0.42
1:A:212:ALA:O	1:A:213:ARG:C	2.58	0.42
1:B:83:PHE:HB3	1:B:364:ARG:CZ	2.49	0.42
1:B:329:GLY:N	1:B:331:GLU:OE1	2.53	0.42
1:A:101:LEU:HD23	1:A:101:LEU:HA	1.83	0.42
1:B:365:ASN:OD1	1:B:367:TRP:HE3	2.02	0.42
1:B:446:ASP:OD1	1:B:446:ASP:C	2.58	0.42
1:A:362:ASN:HD22	1:A:368:PHE:HB2	1.85	0.42
1:B:358:ARG:HB2	1:B:361:THR:OG1	2.20	0.42
1:B:369:PRO:O	1:B:370:GLU:C	2.58	0.42
1:A:417:ILE:O	1:A:420:MET:N	2.45	0.42
1:A:375:ARG:HH11	1:A:375:ARG:CG	2.32	0.42
1:A:120:ILE:HD11	1:B:123:ILE:CD1	2.49	0.42
1:B:449:LYS:O	1:B:450:LEU:C	2.58	0.42
1:B:58:PRO:HD2	1:B:61:LYS:HB2	2.01	0.42
1:B:229:ALA:HB1	1:B:241:MET:CE	2.49	0.42
1:A:459:PHE:CD1	1:A:459:PHE:C	2.93	0.42
1:A:355:LEU:HD22	1:A:401:GLU:HG2	2.01	0.42
1:B:118:GLN:O	1:B:119:SER:C	2.58	0.42
1:A:243:ALA:O	1:A:247:LEU:HG	2.20	0.42
1:A:233:GLU:HG3	1:A:262:TYR:CD1	2.55	0.42
1:B:191:ASP:O	1:B:193:SER:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:ILE:HD12	1:A:178:PHE:CD1	2.52	0.42
1:A:270:PHE:O	1:A:273:LEU:HB3	2.19	0.42
1:A:118:GLN:O	1:A:119:SER:C	2.58	0.42
1:A:213:ARG:CZ	1:A:217:ASP:OD1	2.68	0.41
1:B:208:ASP:O	1:B:209:THR:C	2.57	0.41
1:B:188:THR:O	1:B:189:SER:C	2.58	0.41
1:B:38:VAL:HG12	1:B:39:ALA:O	2.20	0.41
1:B:360:ASP:OD1	1:B:360:ASP:N	2.53	0.41
1:A:475:ALA:HB1	1:A:476:PRO:HD2	2.02	0.41
1:B:83:PHE:HB3	1:B:364:ARG:NH2	2.36	0.41
1:B:120:ILE:HA	1:B:120:ILE:HD13	1.72	0.41
1:B:259:ASP:OD1	1:B:260:LYS:N	2.45	0.41
1:B:343:GLN:H	1:B:479:TYR:HA	1.86	0.41
1:A:208:ASP:O	1:A:209:THR:C	2.59	0.41
1:A:383:HIS:HE1	1:A:385:LEU:HD12	1.86	0.41
1:A:75:GLY:O	1:A:78:ARG:N	2.53	0.41
1:A:240:GLY:HA3	1:A:290:PHE:CZ	2.54	0.41
1:A:481:ILE:HD12	1:A:481:ILE:HG23	1.83	0.41
1:A:120:ILE:CD1	1:B:123:ILE:HD11	2.50	0.41
1:A:340:ILE:HG22	1:A:479:TYR:CD2	2.56	0.41
1:B:427:MET:HA	1:B:453:PHE:CE1	2.56	0.41
1:A:201:PHE:HE2	1:A:203:ARG:HD3	1.85	0.41
1:B:231:HIS:O	1:B:260:LYS:HA	2.21	0.41
1:B:332:VAL:C	1:B:334:ALA:H	2.24	0.41
1:A:50:LEU:HD23	1:A:50:LEU:HA	1.82	0.41
1:A:318:ASP:O	1:A:319:GLY:C	2.58	0.41
1:B:84:HIS:O	1:B:87:ASP:N	2.54	0.41
1:B:431:LEU:O	1:B:439:CYS:SG	2.79	0.41
1:A:191:ASP:C	1:A:193:SER:N	2.74	0.41
1:B:174:LEU:HD12	1:B:174:LEU:O	2.21	0.40
1:B:216:LEU:C	1:B:218:ILE:N	2.75	0.40
1:B:226:TYR:CE2	1:B:256:ALA:HB2	2.55	0.40
1:A:45:VAL:HB	1:A:101:LEU:CD2	2.51	0.40
1:B:419:ALA:HA	1:B:459:PHE:CE2	2.56	0.40
1:B:470:ASP:OD2	1:B:470:ASP:C	2.60	0.40
1:B:383:HIS:ND1	1:B:384:LEU:N	2.70	0.40
1:B:70:ILE:CG1	1:B:71:ARG:N	2.84	0.40
1:B:76:ILE:HA	1:B:76:ILE:HD13	1.98	0.40
1:A:256:ALA:CB	1:A:284:ALA:HB2	2.51	0.40
1:A:435:HIS:CG	1:A:439:CYS:HB3	2.57	0.40
1:B:449:LYS:C	1:B:451:LEU:N	2.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:TYR:HD1	1:A:492:TYR:CE1	2.39	0.40
1:A:443:LYS:HA	1:A:444:PRO:HA	1.91	0.40
1:B:62:VAL:HB	1:B:63:PRO:HD3	2.03	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	448/490 (91%)	352 (79%)	79 (18%)	17 (4%)	4	26
1	B	448/490 (91%)	353 (79%)	78 (17%)	17 (4%)	4	26
All	All	896/980 (91%)	705 (79%)	157 (18%)	34 (4%)	4	26

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	223	ASN
1	B	223	ASN
1	B	256	ALA
1	B	331	GLU
1	B	489	ALA
1	A	37	SER
1	A	192	LEU
1	A	256	ALA
1	A	331	GLU
1	A	456	LYS
1	A	489	ALA
1	B	37	SER
1	A	73	GLN
1	A	97	PRO
1	A	189	SER

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Mol	Chain	Res	Type
1	B	73	GLN
1	B	192	LEU
1	B	217	ASP
1	A	82	MET
1	A	384	LEU
1	B	97	PRO
1	B	189	SER
1	B	335	ASN
1	B	349	SER
1	B	384	LEU
1	A	279	GLU
1	A	368	PHE
1	B	210	LEU
1	B	261	ILE
1	B	368	PHE
1	A	502	GLU
1	A	261	ILE
1	A	455	ILE
1	B	58	PRO

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	376/422 (89%)	352 (94%)	24 (6%)	22	60
1	B	376/422 (89%)	347 (92%)	29 (8%)	16	51
All	All	752/844 (89%)	699 (93%)	53 (7%)	19	56

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	SER
1	A	64	GLU
1	A	73	GLN
1	A	77	GLN

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Mol	Chain	Res	Type
1	A	93	PRO
1	A	116	LEU
1	A	123	ILE
1	A	155	PRO
1	A	170	GLN
1	A	196	THR
1	A	197	LEU
1	A	289	CYS
1	A	324	ASP
1	A	341	LYS
1	A	342	LEU
1	A	360	ASP
1	A	369	PRO
1	A	387	ASN
1	A	403	ASN
1	A	418	TYR
1	A	465	GLU
1	A	479	TYR
1	A	488	GLU
1	A	501	HIS
1	B	37	SER
1	B	73	GLN
1	B	77	GLN
1	B	116	LEU
1	B	155	PRO
1	B	170	GLN
1	B	197	LEU
1	B	201	PHE
1	B	202	LEU
1	B	211	GLN
1	B	217	ASP
1	B	232	THR
1	B	254	CYS
1	B	277	LEU
1	B	280	ARG
1	B	289	CYS
1	B	324	ASP
1	B	335	ASN
1	B	360	ASP
1	B	368	PHE
1	B	387	ASN
1	B	403	ASN

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Mol	Chain	Res	Type
1	B	420	MET
1	B	425	GLN
1	B	463	SER
1	B	465	GLU
1	B	488	GLU
1	B	493	ASP
1	B	501	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	170	GLN
1	A	173	ASN
1	A	176	GLN
1	A	231	HIS
1	A	250	GLN
1	A	362	ASN
1	A	403	ASN
1	B	73	GLN
1	B	77	GLN
1	B	173	ASN
1	B	176	GLN
1	B	211	GLN
1	B	250	GLN
1	B	335	ASN
1	B	403	ASN
1	B	425	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

2 ligands are 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$
2	MCG	A	1001	-	8,15,15	1.37	0	11,22,22	0.89	0
2	MCG	B	2001	-	8,15,15	1.53	1 (12%)	11,22,22	0.95	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
2	MCG	A	1001	-	-	0/6/16/16	0/1/1/1
2	MCG	B	2001	-	-	0/6/16/16	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2001	MCG	CA-CB	-3.03	1.50	1.53

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	452/490 (92%)	-0.37	7 (1%) 76 71	10, 65, 119, 164	0
1	B	452/490 (92%)	-0.24	12 (2%) 58 51	14, 67, 123, 162	0
All	All	904/980 (92%)	-0.31	19 (2%) 67 60	10, 66, 121, 164	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	389	ASN	4.7
1	A	510	TYR	4.2
1	A	389	ASN	4.1
1	B	62	VAL	3.9
1	B	388	PRO	3.0
1	B	510	TYR	2.9
1	A	226	TYR	2.8
1	B	233	GLU	2.7
1	B	225	THR	2.6
1	A	436	VAL	2.6
1	B	63	PRO	2.6
1	B	59	ALA	2.4
1	B	91	ALA	2.3
1	A	42	ASP	2.3
1	B	61	LYS	2.3
1	B	154	LYS	2.2
1	B	224	TRP	2.1
1	A	390	PHE	2.1
1	A	252	GLY	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	MCG	A	1001	15/15	0.93	0.23	1.12	50,59,67,71	0
2	MCG	B	2001	15/15	0.94	0.20	0.44	56,70,75,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.