



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:46 AM UTC

PDB ID : 1ISS / pdb_00001iss
Title : Crystal Structure of Metabotropic Glutamate Receptor Subtype 1 Complexed with an antagonist
Authors : Tsuchiya, D.; Kunishima, N.; Kamiya, N.; Jingami, H.; Morikawa, K.
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

<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

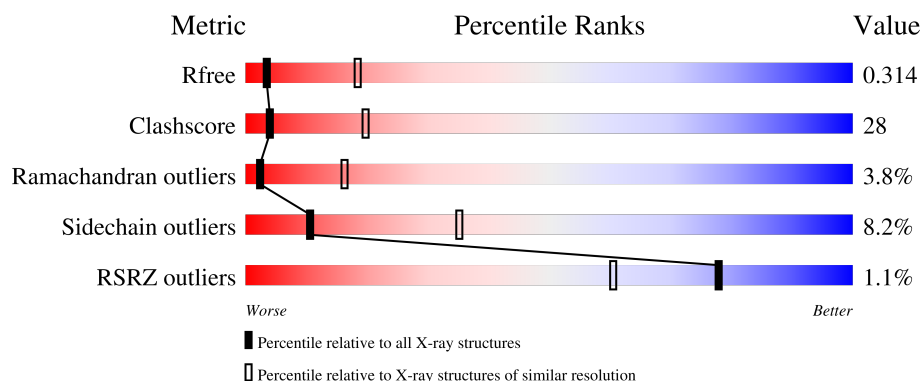
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	490	
1	B	490	

2 Entry composition [i](#)

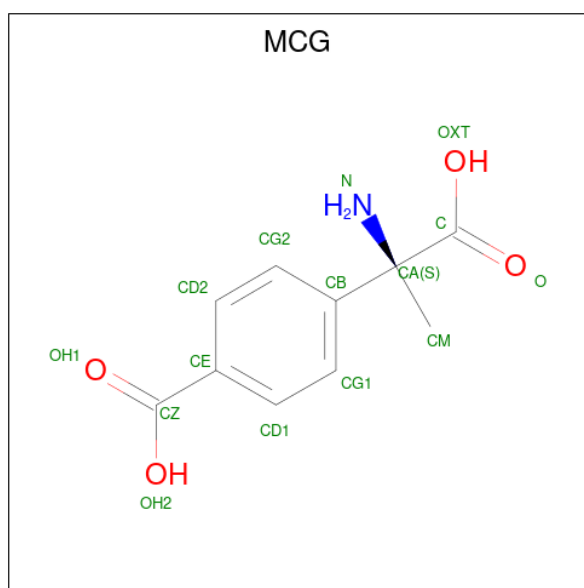
There are 2 unique types of molecules in this entry. The entry contains 7124 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 (CCD ID: MCG) (formula: C₁₀H₁₁NO₄).

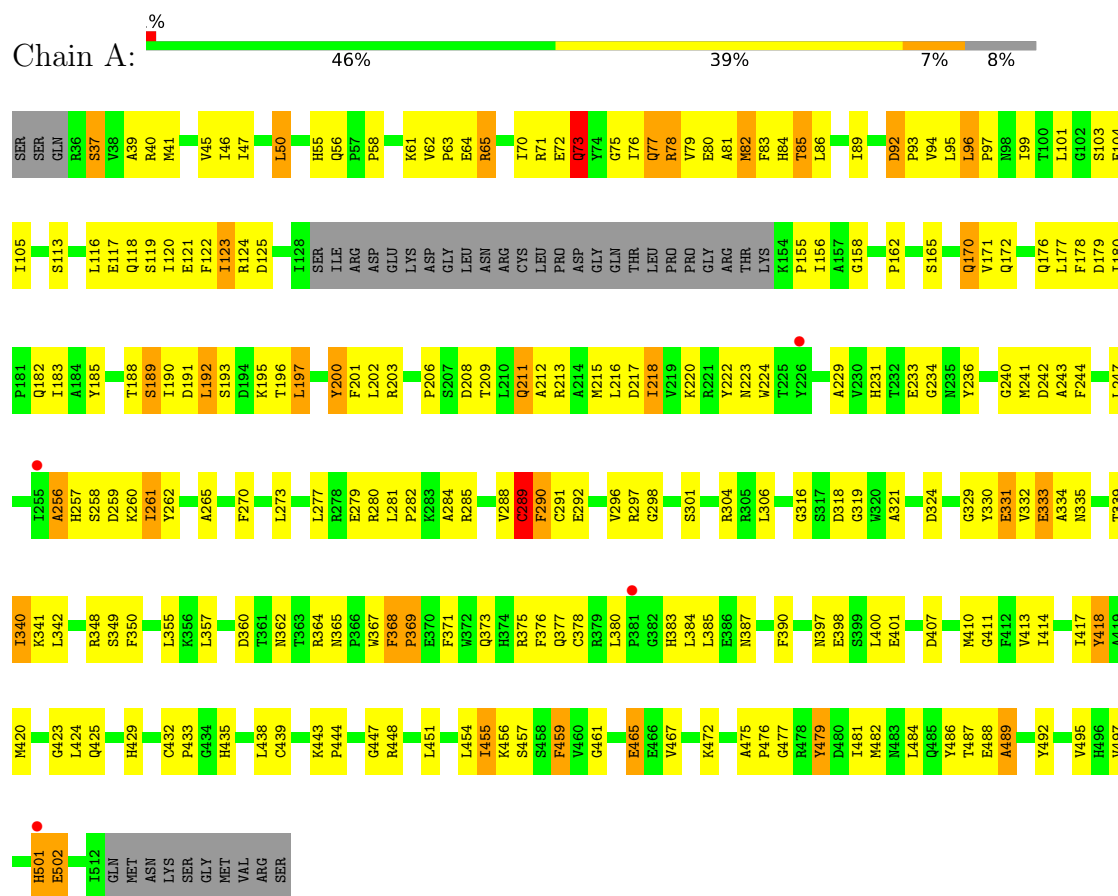


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	10	1	4		
2	B	1	Total	C	N	O	0	0
			15	10	1	4		

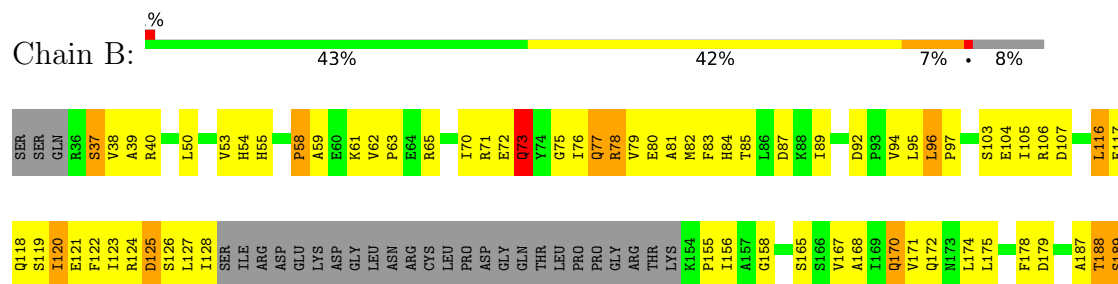
3 Residue-property plots

These plots are drawn for all protein, RNA, 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: Metabotropic Glutamate Receptor subtype 1



• Molecule 1: Metabotropic Glutamate Receptor subtype 1



ASN	K443	S349	S263	I190
LYS	P444	F350	N264	D191
SER	I445		A265	L192
GLY	D446	R358		S193
MET	G447	L359	F270	D194
VAL	R448	D360	L273	K195
ARG	K449	T361		T196
SER	L450	N362	L277	L197
	L451	T363	R278	Y200
	F453	R364	E279	F201
	L454	N365	R280	L202
	I455	P366	L281	R203
	K456	V367	P282	V204
	S457	F368	K283	V205
	S458	P369	A284	P206
	F459	E370	R285	S207
	V460	F371	V286	D208
	G461	Q372	V287	T209
	V462	Q373	V288	L210
	S463	H374	C289	Q211
	G464	R375	F290	
	E465	F376		M215
	E466	Q377	R304	L216
	V467	C378	R305	D217
			L306	I218
	D470	H383	G307	V219
	E471	L384	V308	
	K472	E386	E311	N223
	G473	N387		V224
	D474	P388	G316	T225
	A475	H389	S317	Y226
	P476	F390	S318	V227
	G477		G319	S228
	R478	Y404	W320	A229
	Y479		A321	V230
	D480	M410	D322	H231
	I481	G411	R323	T232
	M482	F412	D324	
		V413		G240
		I414	I327	M241
	E488		E328	D242
	A489	I417	G329	A243
	N490	Y418	Y330	F244
	R491	A419	E331	K245
	Y492	M420	V332	E246
	D493		E333	L247
	Y494	G423	A334	A248
		L424		
	V497	Q425	H385	E251
	G498	M426	T339	C254
	T499	N427	I340	T255
	W500		K341	A256
	H501	L431	L342	H257
	E502		Q343	S258
		V436		D259
	L505			K260
				T261
	I512	G439	E346	Y262
	GLN	V347	V347	
	MET	R348	R348	

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 20.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	91.1 (20.00-3.30) 96.8 (20.00-3.30)	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%)	wwPDB-VP
Wilson B-factor (Å ²)	90.1	Xtriage
Anisotropy	0.600	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 78.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	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, 0.333 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: 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	0.57	0/3627	1.04	23/4913 (0.5%)
1	B	0.59	0/3627	1.02	16/4913 (0.3%)
All	All	0.58	0/7254	1.03	39/9826 (0.4%)

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.

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	209	THR	N-CA-C	-7.24	102.19	111.02
1	A	96	LEU	CA-C-N	7.09	128.70	119.84
1	A	96	LEU	C-N-CA	7.09	128.70	119.84
1	A	340	ILE	CB-CA-C	-6.37	102.18	110.84
1	B	321	ALA	CB-CA-C	-6.33	109.25	116.54
1	A	290	PHE	N-CA-C	-6.29	97.57	108.52
1	B	340	ILE	CB-CA-C	-6.18	102.43	110.84
1	A	65	ARG	N-CA-C	6.17	120.14	112.24
1	A	180	ILE	N-CA-C	6.07	114.65	107.73
1	B	290	PHE	N-CA-C	-6.07	97.96	108.52
1	B	125	ASP	N-CA-C	-5.98	104.09	111.33
1	B	78	ARG	N-CA-C	-5.83	104.84	111.07
1	B	467	VAL	N-CA-C	5.67	116.03	107.75
1	A	56	GLN	CA-C-N	5.66	123.73	119.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	56	GLN	C-N-CA	5.66	123.73	119.66
1	A	423	GLY	N-CA-C	-5.65	105.65	112.49
1	A	321	ALA	CB-CA-C	-5.64	110.06	116.54
1	A	218	ILE	N-CA-C	-5.62	105.63	110.74
1	A	78	ARG	N-CA-C	-5.59	104.88	110.97
1	A	46	ILE	N-CA-C	5.55	116.10	107.99
1	A	289	CYS	N-CA-C	5.55	118.35	107.57
1	A	103	SER	N-CA-C	5.55	117.28	108.79
1	B	423	GLY	N-CA-C	-5.47	106.16	112.50
1	A	50	LEU	N-CA-C	5.46	116.24	108.54
1	A	92	ASP	CA-C-N	5.45	126.65	119.84
1	A	92	ASP	C-N-CA	5.45	126.65	119.84
1	B	65	ARG	N-CA-C	5.43	119.19	112.24
1	A	291	CYS	N-CA-C	5.38	118.34	109.72
1	A	292	GLU	N-CA-C	-5.38	102.91	110.50
1	A	113	SER	N-CA-C	5.38	116.83	111.07
1	B	103	SER	N-CA-C	5.37	117.01	108.79
1	B	92	ASP	CA-C-N	5.33	126.18	120.47
1	B	92	ASP	C-N-CA	5.33	126.18	120.47
1	A	459	PHE	N-CA-C	5.30	116.26	107.73
1	B	96	LEU	CA-C-N	5.22	126.36	119.84
1	B	96	LEU	C-N-CA	5.22	126.36	119.84
1	B	204	VAL	N-CA-C	-5.06	107.53	112.29
1	B	188	THR	N-CA-C	5.04	119.43	113.28
1	A	200	TYR	N-CA-C	5.04	119.15	113.15

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	199	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3547	0	3421	199	0
2	A	15	0	9	0	0
2	B	15	0	9	0	0
All	All	7124	0	6860	392	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 28.

All (392) 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:41:MET:HE1	1:A:364:ARG:HH11	1.35	0.92
1:A:41:MET:HE1	1:A:364:ARG:NH1	1.86	0.91
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: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:B:330:TYR:C	1:B:332:VAL:H	2.01	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:GLN:HE22	1:B:318:ASP:H	1.42	0.67
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:407:ASP:HB3	1:A:410:MET:HE2	1.78	0.66
1:A:80:GLU:HG3	1:A:357:LEU:HD11	1.78	0.66
1:B:158:GLY:HA3	1:B:420:MET:HE1	1.78	0.66
1:A:200:TYR:OH	1:A:448:ARG:HG2	1.96	0.65
1:B:202:LEU:N	1:B:202:LEU:HD23	2.11	0.65
1:A:216:LEU:HB2	1:A:244:PHE:HE1	1.60	0.64
1:A:335:ASN:HA	1:A:484:LEU:HG	1.80	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:A:206:PRO:HB3	1:A:477:GLY:HA2	1.81	0.62
1:B:106:ARG:HD3	1:B:118:GLN:OE1	2.00	0.62
1:A:122:PHE:CD1	1:A:156:ILE:HG13	2.34	0.62
1:A:413:VAL:HG12	1:A:414:ILE:N	2.15	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:A:330:TYR:C	1:A:332:VAL:H	2.08	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:40:ARG:HG3	1:B:104:GLU:HG3	1.83	0.61
1:B:229:ALA:O	1:B:258:SER:HA	2.01	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:A:333:GLU:H	1:A:333:GLU:CD	2.07	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:HG2	1:A:285:ARG:HH11	1.66	0.60
1:A:376:PHE:HZ	1:A:400:LEU:HD23	1.67	0.60
1:A:454:LEU:O	1:A:457:SER:HB2	2.02	0.60
1:A:195:LYS:C	1:A:197:LEU:H	2.10	0.59
1:B:461:GLY:HA3	1:B:465:GLU:HG2	1.84	0.59
1:B:72:GLU:H	1:B:73:GLN:HE21	1.49	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:LEU:HD13	1:B:201:PHE:CZ	2.36	0.59
1:A:165:SER:HB3	1:A:189:SER:OG	2.03	0.59
1:A:398:GLU:N	1:A:398:GLU:OE1	2.34	0.59
1:A:375:ARG:HH11	1:A:375:ARG:HG3	1.66	0.59
1:B:95:LEU:O	1:B:96:LEU:C	2.45	0.59
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:367:TRP:O	1:A:368:PHE:C	2.45	0.57
1:A:123:ILE:CG1	1:A:124:ARG:N	2.68	0.57
1:A:229:ALA:O	1:A:258:SER:HA	2.05	0.57
1:B:341:LYS:HG2	1:B:342:LEU:N	2.18	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:B:85:THR:O	1:B:89:ILE:HG13	2.05	0.56
1:B:373:GLN:HG2	1:B:378:CYS:O	2.04	0.56
1:A:82:MET:HE2	1:A:86:LEU:HD11	1.87	0.56
1:B:39:ALA:HB2	1:B:367:TRP:CZ3	2.40	0.56
1:B:158:GLY:HA3	1:B:420:MET:HE3	1.86	0.56
1:B:368:PHE:HB3	1:B:369:PRO:CD	2.32	0.56
1:B:454:LEU:O	1:B:457:SER:HB2	2.06	0.56
1:A:231:HIS:HB3	1:A:241:MET:HE2	1.87	0.56
1:A:192:LEU:HD22	1:A:201:PHE:CD1	2.41	0.56
1:A:195:LYS:C	1:A:197:LEU:N	2.63	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:A:261:ILE:HD11	1:A:265:ALA:HB3	1.88	0.56
1:B:39:ALA:HB2	1:B:367:TRP:HZ3	1.69	0.56
1:A:158:GLY:HA3	1:A:420:MET:HE1	1.87	0.55
1:A:455:ILE:C	1:A:457:SER:H	2.14	0.55
1:A:58:PRO:HD2	1:A:61:LYS:HB2	1.88	0.55
1:B:367:TRP:O	1:B:368:PHE:C	2.50	0.55
1:B:72:GLU:H	1:B:73:GLN:NE2	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:216:LEU:HD22	1:B:247:LEU:HB3	1.89	0.55
1:A:124:ARG:O	1:A:125:ASP:C	2.48	0.55
1:A:191:ASP:C	1:A:193:SER:H	2.14	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:A:95:LEU:O	1:A:96:LEU:C	2.50	0.54
1:A:281:LEU:HB3	1:A:282:PRO:HA	1.89	0.54
1:B:215:MET:O	1:B:218:ILE:HB	2.08	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
1:A:241:MET:O	1:A:242:ASP:C	2.49	0.54
1:A:414:ILE:O	1:A:417:ILE:HB	2.08	0.54
1:B:218:ILE:HD11	1:B:481:ILE:CD1	2.33	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:B:79:VAL:HG22	1:B:105:ILE:HG21	1.91	0.53
1:A:218:ILE:HD11	1:A:481:ILE:HD12	1.89	0.53
1:A:244:PHE:CE2	1:A:288:VAL:HG11	2.42	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:124:ARG:O	1:B:125:ASP:C	2.51	0.53
1:B:123:ILE:HG13	1:B:124:ARG:N	2.23	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:501:HIS:O	1:A:502:GLU:HB2	2.08	0.53
1:A:373:GLN:NE2	1:A:380:LEU:HD12	2.24	0.53
1:B:201:PHE:CD2	1:B:201:PHE:C	2.86	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:A:285:ARG:HG2	1:A:285:ARG:NH1	2.22	0.52
1:B:76:ILE:HG13	1:B:371:PHE:CG	2.45	0.52
1:B:83:PHE:CD1	1:B:364:ARG:HG3	2.44	0.52
1:B:195:LYS:C	1:B:197:LEU:N	2.66	0.52
1:A:40:ARG:HG3	1:A:104:GLU:HG3	1.91	0.52
1:A:461:GLY:HA3	1:A:465:GLU:OE2	2.10	0.52
1:B:73:GLN:HE21	1:B:73:GLN:H	1.57	0.52
1:A:377:GLN:HA	1:A:390:PHE:CE1	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:ILE:HG12	1:A:262:TYR:N	2.25	0.52
1:B:89:ILE:HG12	1:B:418:TYR:CE2	2.45	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:120:ILE:O	1:A:121:GLU:C	2.53	0.51
1:A:195:LYS:HA	1:A:195:LYS:HE2	1.92	0.51
1:A:216:LEU:HD13	1:A:244:PHE:CE1	2.45	0.51
1:A:330:TYR:C	1:A:332:VAL:N	2.69	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:75:GLY:O	1:B:76:ILE:C	2.54	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:240:GLY:O	1:B:243:ALA:HB3	2.10	0.51
1:B:425:GLN:HE21	1:B:425:GLN:HA	1.76	0.51
1:B:191:ASP:C	1:B:193:SER:H	2.19	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:306:LEU:HG	1:B:306:LEU:O	2.11	0.51
1:B:261:ILE:HG12	1:B:262:TYR:N	2.26	0.50
1:B:270:PHE:O	1:B:273:LEU:HB3	2.12	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:A:257:HIS:CG	1:A:258:SER:H	2.29	0.50
1:B:70:ILE:HD11	1:B:371:PHE:HB2	1.91	0.50
1:B:452:ASP:CG	1:B:456:LYS:HZ1	2.20	0.50
1:A:65:ARG:NH2	1:B:127:LEU:O	2.45	0.50
1:A:84:HIS:O	1:A:85:THR:C	2.55	0.50
1:A:479:TYR:N	1:A:479:TYR:CD1	2.79	0.50
1:B:348:ARG:O	1:B:349:SER:C	2.54	0.50
1:A:447:GLY:O	1:A:448:ARG:C	2.54	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:330:TYR:C	1:B:332:VAL:N	2.65	0.49
1:A:215:MET:O	1:A:218:ILE:HB	2.12	0.49
1:B:165:SER:OG	1:B:187:ALA:HA	2.13	0.49
1:B:453:PHE:O	1:B:457:SER:OG	2.29	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:ILE:HG12	1:A:262:TYR:O	2.12	0.49
1:B:81:ALA:O	1:B:82:MET:C	2.56	0.49
1:A:410:MET:O	1:A:411:GLY:C	2.55	0.49
1:B:190:ILE:O	1:B:190:ILE:HG22	2.13	0.49
1:B:257:HIS:CG	1:B:258:SER:N	2.81	0.49
1:B:289:CYS:O	1:B:316:GLY:HA2	2.13	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:333:GLU:CD	1:B:333:GLU:H	2.22	0.48
1:A:77:GLN:HG2	1:A:350:PHE:CZ	2.48	0.48
1:A:99:ILE:HD13	1:A:438:LEU:HD21	1.95	0.48
1:B:70:ILE:HG12	1:B:71:ARG:N	2.29	0.48
1:A:329:GLY:N	1:A:331:GLU:OE1	2.41	0.48
1:B:455:ILE:C	1:B:457:SER:H	2.21	0.48
1:A:233:GLU:OE1	1:A:260:LYS:HD2	2.12	0.48
1:A:188:THR:O	1:A:189:SER:C	2.56	0.48
1:B:172:GLN:CD	1:B:201:PHE:HB2	2.39	0.48
1:A:208:ASP:O	1:A:211:GLN:HB2	2.14	0.48
1:B:190:ILE:O	1:B:190:ILE:CG2	2.61	0.48
1:B:257:HIS:CG	1:B:258:SER:H	2.32	0.48
1:A:425:GLN:NE2	1:A:429:HIS:NE2	2.62	0.48
1:B:497:VAL:HG23	1:B:498:GLY:N	2.28	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:A:82:MET:CG	1:A:105:ILE:HD11	2.44	0.47
1:A:92:ASP:OD1	1:A:94:VAL:N	2.44	0.47
1:A:201:PHE:CD2	1:A:202:LEU:N	2.83	0.47
1:B:70:ILE:HD13	1:B:371:PHE:CB	2.41	0.47
1:B:76:ILE:CD1	1:B:365:ASN:HD21	2.25	0.47
1:A:75:GLY:O	1:A:76:ILE:C	2.57	0.47
1:A:179:ASP:HA	1:A:200:TYR:CE1	2.50	0.47
1:B:195:LYS:C	1:B:197:LEU:H	2.21	0.47
1:B:241:MET:O	1:B:242:ASP:C	2.57	0.47
1:B:322:ASP:HA	1:B:494:TYR:CD2	2.49	0.47
1:A:212:ALA:O	1:A:213:ARG:C	2.58	0.47
1:A:257:HIS:CG	1:A:258:SER:N	2.81	0.47
1:A:306:LEU:O	1:A:306:LEU:HG	2.15	0.47
1:A:495:VAL:O	1:A:497:VAL:HG13	2.15	0.47
1:B:77:GLN:OE1	1:B:404:TYR:HE1	1.97	0.47
1:A:81:ALA:O	1:A:82:MET:C	2.57	0.47
1:A:304:ARG:NH2	1:A:333:GLU:OE2	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:LYS:O	1:B:479:TYR:HB3	2.15	0.47
1:B:179:ASP:HA	1:B:200:TYR:CE1	2.50	0.47
1:B:446:ASP:OD1	1:B:446:ASP:C	2.58	0.47
1:A:162:PRO:HD2	1:A:182:GLN:NE2	2.30	0.47
1:B:369:PRO:O	1:B:370:GLU:C	2.58	0.47
1:B:449:LYS:O	1:B:450:LEU:C	2.58	0.47
1:B:229:ALA:HB1	1:B:241:MET:HE3	1.97	0.47
1:A:459:PHE:CD1	1:A:459:PHE:C	2.93	0.47
1:B:118:GLN:O	1:B:119:SER:C	2.58	0.47
1:A:118:GLN:O	1:A:119:SER:C	2.58	0.46
1:B:346:GLU:HG2	1:B:347:VAL:H	1.80	0.46
1:A:270:PHE:CZ	1:A:298:GLY:HA3	2.50	0.46
1:B:448:ARG:O	1:B:451:LEU:HB3	2.14	0.46
1:B:188:THR:O	1:B:189:SER:C	2.58	0.46
1:B:208:ASP:O	1:B:209:THR:C	2.57	0.46
1:B:256:ALA:CB	1:B:284:ALA:HB2	2.45	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:A:208:ASP:O	1:A:209:THR:C	2.59	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:318:ASP:O	1:A:319:GLY:C	2.58	0.45
1:A:332:VAL:HB	1:A:333:GLU:OE2	2.15	0.45
1:B:332:VAL:C	1:B:334:ALA:H	2.24	0.45
1:A:455:ILE:O	1:A:457:SER:N	2.49	0.45
1:A:231:HIS:O	1:A:260:LYS:HA	2.16	0.45
1:B:216:LEU:C	1:B:218:ILE:N	2.75	0.45
1:B:470:ASP:OD2	1:B:470:ASP:C	2.60	0.45
1:A:47:ILE:CD1	1:A:420:MET:HG3	2.45	0.45
1:B:72:GLU:N	1:B:73:GLN:NE2	2.64	0.45
1:A:191:ASP:C	1:A:193:SER:N	2.74	0.45
1:B:195:LYS:HE2	1:B:195:LYS:HA	1.98	0.45
1:B:244:PHE:O	1:B:247:LEU:N	2.49	0.45
1:A:417:ILE:O	1:A:420:MET:HB3	2.17	0.45
1:B:50:LEU:HA	1:B:50:LEU:HD23	1.73	0.45
1:A:123:ILE:HG12	1:A:124:ARG:H	1.82	0.45
1:B:449:LYS:C	1:B:451:LEU:N	2.75	0.45
1:A:82:MET:HG3	1:A:86:LEU:HD12	1.99	0.44
1:A:362:ASN:HD21	1:A:365:ASN:CB	2.26	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:ARG:CG	1:B:104:GLU:HG3	2.46	0.44
1:B:75:GLY:O	1:B:78:ARG:N	2.50	0.44
1:B:423:GLY:HA3	1:B:454:LEU:HD23	1.98	0.44
1:B:218:ILE:HA	1:B:505:LEU:HD21	2.00	0.44
1:B:362:ASN:ND2	1:B:365:ASN:HB3	2.31	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: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:B:339:THR:O	1:B:482:MET:N	2.42	0.44
1:A:234:GLY:C	1:A:236:TYR:H	2.26	0.44
1:A:289:CYS:O	1:A:316:GLY:HA2	2.17	0.44
1:A:332:VAL:C	1:A:334:ALA:H	2.26	0.44
1:A:398:GLU:CD	1:A:398:GLU:H	2.18	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:A:432:CYS:O	1:A:433:PRO:C	2.60	0.43
1:B:500:TRP:HD1	1:B:505:LEU:HD13	1.82	0.43
1:A:72:GLU:H	1:A:73:GLN:NE2	2.16	0.43
1:B:417:ILE:O	1:B:420:MET:N	2.45	0.43
1:A:123:ILE:HD11	1:B:120:ILE:HG13	2.01	0.43
1:A:375:ARG:HG3	1:A:375:ARG:NH1	2.33	0.43
1:B:245:LYS:O	1:B:248:ALA:HB3	2.19	0.43
1:B:348:ARG:O	1:B:350:PHE:N	2.50	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:B:442:MET:O	1:B:444:PRO:C	2.61	0.43
1:A:177:LEU:CD1	1:B:174:LEU:HB2	2.49	0.43
1:A:413:VAL:O	1:A:414:ILE:C	2.60	0.43
1:B:59:ALA:O	1:B:62:VAL:HG23	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:B:167:VAL:O	1:B:168:ALA:C	2.62	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: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:116:LEU:O	1:B:117:GLU:C	2.61	0.43
1:B:452:ASP:O	1:B:453:PHE:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:ILE:O	1:A:190:ILE:HG22	2.19	0.42
1:B:278:ARG:HH11	1:B:306:LEU:HD21	1.83	0.42
1:A:424:LEU:O	1:A:425:GLN:C	2.60	0.42
1:A:101:LEU:HD23	1:A:101:LEU:HA	1.83	0.42
1:A:407:ASP:OD2	1:A:407:ASP:C	2.63	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:B:427:MET:HE2	1:B:442:MET:HG2	2.01	0.42
1:B:120:ILE:O	1:B:121:GLU:C	2.61	0.42
1:B:334:ALA:O	1:B:335:ASN:C	2.61	0.42
1:B:365:ASN:OD1	1:B:367:TRP:HE3	2.02	0.42
1:A:362:ASN:HD22	1:A:368:PHE:HB2	1.85	0.42
1:A:383:HIS:C	1:A:385:LEU:N	2.76	0.42
1:B:358:ARG:HB2	1:B:361:THR:OG1	2.20	0.42
1:A:120:ILE:HD11	1:B:123:ILE:CD1	2.49	0.42
1:A:375:ARG:HH11	1:A:375:ARG:CG	2.32	0.42
1:A:417:ILE:O	1:A:420:MET:N	2.45	0.42
1:B:58:PRO:HD2	1:B:61:LYS:HB2	2.01	0.42
1:B:191:ASP:C	1:B:193:SER:N	2.78	0.42
1:A:355:LEU:HD22	1:A:401:GLU:HG2	2.01	0.42
1:B:229:ALA:HB1	1:B:241:MET:CE	2.49	0.42
1:A:233:GLU:HG3	1:A:262:TYR:CD1	2.55	0.42
1:A:243:ALA:O	1:A:247:LEU:HG	2.20	0.42
1:B:191:ASP:O	1:B:193:SER:N	2.52	0.42
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:397:ASN:O	1:A:398:GLU:C	2.63	0.42
1:A:213:ARG:CZ	1:A:217:ASP:OD1	2.68	0.41
1:A:348:ARG:O	1:A:349:SER:C	2.63	0.41
1:A:475:ALA:HB1	1:A:476:PRO:HD2	2.02	0.41
1:B:38:VAL:HG12	1:B:39:ALA:O	2.20	0.41
1:B:318:ASP:O	1:B:319:GLY:C	2.62	0.41
1:B:360:ASP:OD1	1:B:360:ASP:N	2.53	0.41
1:A:296:VAL:O	1:A:297:ARG:C	2.63	0.41
1:A:383:HIS:C	1:A:385:LEU:H	2.29	0.41
1:B:83:PHE:HB3	1:B:364:ARG:NH2	2.36	0.41
1:B:201:PHE:C	1:B:202:LEU:HD23	2.44	0.41
1:B:383:HIS:C	1:B:385:LEU:N	2.78	0.41
1:B:120:ILE:HD13	1:B:120:ILE:HA	1.72	0.41
1:B:259:ASP:OD1	1:B:260:LYS:N	2.45	0.41
1:B:413:VAL:O	1:B:414:ILE:C	2.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:HIS:HE1	1:A:385:LEU:HD12	1.86	0.41
1:B:343:GLN:H	1:B:479:TYR:HA	1.86	0.41
1:B:410:MET:O	1:B:411:GLY:C	2.63	0.41
1:A:75:GLY:O	1:A:78:ARG:N	2.53	0.41
1:A:120:ILE:CD1	1:B:123:ILE:HD11	2.50	0.41
1:A:240:GLY:HA3	1:A:290:PHE:CZ	2.54	0.41
1:A:334:ALA:O	1:A:335:ASN:C	2.64	0.41
1:A:481:ILE:HD12	1:A:481:ILE:HG23	1.83	0.41
1:A:340:ILE:HG22	1:A:479:TYR:CD2	2.56	0.41
1:B:126:SER:C	1:B:128:ILE:N	2.78	0.41
1:B:427:MET:HA	1:B:453:PHE:CE1	2.56	0.41
1:A:50:LEU:HA	1:A:50:LEU:HD23	1.82	0.41
1:A:201:PHE:HE2	1:A:203:ARG:HD3	1.85	0.41
1:B:84:HIS:O	1:B:87:ASP:N	2.54	0.41
1:B:231:HIS:O	1:B:260:LYS:HA	2.21	0.41
1:B:431:LEU:O	1:B:439:CYS:SG	2.79	0.41
1:A:487:THR:C	1:A:489:ALA:N	2.78	0.41
1:A:45:VAL:HB	1:A:101:LEU:CD2	2.51	0.40
1:B:174:LEU:O	1:B:174:LEU:HD12	2.21	0.40
1:B:226:TYR:CE2	1:B:256:ALA:HB2	2.55	0.40
1:B:419:ALA:HA	1:B:459:PHE:CE2	2.56	0.40
1:A:455:ILE:C	1:A:457:SER:N	2.78	0.40
1:B:53:VAL:HB	1:B:107:ASP:CG	2.46	0.40
1:B:383:HIS:ND1	1:B:384:LEU:N	2.70	0.40
1:B:424:LEU:O	1:B:425:GLN:C	2.64	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:A:443:LYS:HA	1:A:444:PRO:HA	1.91	0.40
1:A:486:TYR:HD1	1:A:492:TYR:CE1	2.39	0.40
1:B:70:ILE:CG1	1:B:71:ARG:N	2.84	0.40
1:B:76:ILE:HD13	1:B:76:ILE:HA	1.98	0.40
1:B:264:ASN:O	1:B:265:ALA:C	2.64	0.40
1:A:234:GLY:C	1:A:236:TYR:N	2.78	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 ⓘ

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	448/490 (91%)	352 (79%)	79 (18%)	17 (4%)	2	16
1	B	448/490 (91%)	353 (79%)	78 (17%)	17 (4%)	2	16
All	All	896/980 (91%)	705 (79%)	157 (18%)	34 (4%)	2	16

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
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

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Mol	Chain	Res	Type
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%)	349 (93%)	27 (7%)	13	40
1	B	376/422 (89%)	341 (91%)	35 (9%)	8	30
All	All	752/844 (89%)	690 (92%)	62 (8%)	10	35

All (62) 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
1	A	85	THR
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	211	GLN
1	A	277	LEU

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Mol	Chain	Res	Type
1	A	289	CYS
1	A	324	ASP
1	A	333	GLU
1	A	341	LYS
1	A	342	LEU
1	A	360	ASP
1	A	369	PRO
1	A	387	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	94	VAL
1	B	116	LEU
1	B	120	ILE
1	B	155	PRO
1	B	170	GLN
1	B	197	LEU
1	B	202	LEU
1	B	211	GLN
1	B	217	ASP
1	B	232	THR
1	B	254	CYS
1	B	261	ILE
1	B	277	LEU
1	B	289	CYS
1	B	324	ASP
1	B	327	ILE
1	B	333	GLU
1	B	335	ASN
1	B	339	THR
1	B	342	LEU
1	B	360	ASP
1	B	363	THR
1	B	369	PRO
1	B	387	ASN
1	B	410	MET
1	B	436	VAL

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Mol	Chain	Res	Type
1	B	463	SER
1	B	465	GLU
1	B	471	GLU
1	B	488	GLU
1	B	493	ASP
1	B	501	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) 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	377	GLN
1	A	389	ASN
1	A	403	ASN
1	A	483	ASN
1	A	485	GLN
1	B	73	GLN
1	B	84	HIS
1	B	173	ASN
1	B	176	GLN
1	B	211	GLN
1	B	231	HIS
1	B	250	GLN
1	B	257	HIS
1	B	335	ASN
1	B	403	ASN
1	B	406	GLN
1	B	425	GLN
1	B	483	ASN
1	B	485	GLN

5.3.3 RNA ⓘ

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](#)

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	-	14,15,15	1.45	1 (7%)	16,22,22	0.82	0
2	MCG	B	2001	-	14,15,15	1.52	2 (14%)	16,22,22	0.86	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	-	-	6/15/16/16	0/1/1/1
2	MCG	B	2001	-	-	7/15/16/16	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2001	MCG	CA-CB	-3.11	1.50	1.53
2	A	1001	MCG	CE-CZ	-2.44	1.44	1.49
2	B	2001	MCG	CE-CZ	-2.14	1.44	1.49

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	MCG	CD2-CE-CZ-OH1
2	B	2001	MCG	CD2-CE-CZ-OH1
2	A	1001	MCG	CD1-CE-CZ-OH1
2	B	2001	MCG	CD1-CE-CZ-OH1
2	B	2001	MCG	CD1-CE-CZ-OH2
2	A	1001	MCG	CD1-CE-CZ-OH2
2	B	2001	MCG	CD2-CE-CZ-OH2
2	A	1001	MCG	CD2-CE-CZ-OH2
2	B	2001	MCG	C-CA-CB-CG1
2	B	2001	MCG	C-CA-CB-CG2
2	B	2001	MCG	N-CA-CB-CG1
2	A	1001	MCG	C-CA-CB-CG1
2	A	1001	MCG	C-CA-CB-CG2

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 [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%)	-0.15	4 (0%) 81 65	10, 65, 119, 164	0
1	B	452/490 (92%)	-0.09	6 (1%) 75 56	14, 67, 123, 162	0
All	All	904/980 (92%)	-0.12	10 (1%) 78 60	10, 66, 120, 164	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	490	ASN	4.3
1	B	224	TRP	2.8
1	B	385	LEU	2.6
1	A	381	PRO	2.5
1	B	389	ASN	2.4
1	B	390	PHE	2.4
1	A	255	ILE	2.3
1	A	226	TYR	2.3
1	B	263	SER	2.2
1	A	501	HIS	2.1

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($\text{\AA}^2$)	Q<0.9
2	MCG	B	2001	15/15	0.90	0.09	56,70,75,76	0
2	MCG	A	1001	15/15	0.95	0.08	50,59,67,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.