



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:55 AM UTC

PDB ID : 1C0U / pdb_00001c0u
Title : CRYSTAL STRUCTURE OF HIV-1 REVERSE TRANSCRIPTASE IN
COMPLEX WITH BM+50.0934
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Deposited on : 1999-07-19
Resolution : 2.52 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

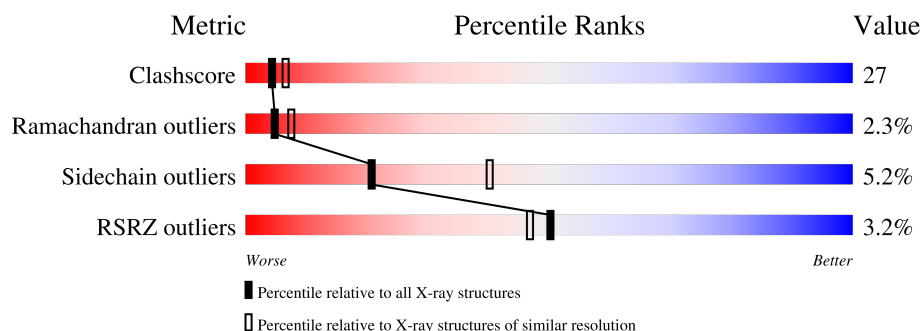
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.52 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))
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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	560	3% 46% 44% 6% .
2	B	440	3% 46% 43% . 6%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7938 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.

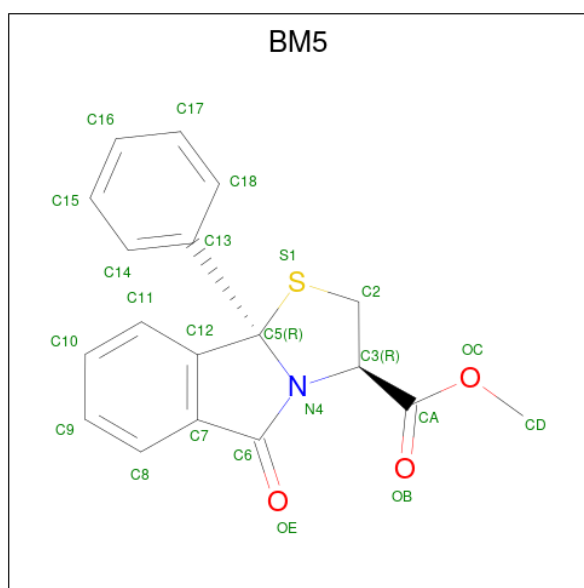
- Molecule 1 is a protein called HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	539	Total	C	N	O	S	0	0	0
			4410	2853	734	815	8			

- Molecule 2 is a protein called HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	414	Total	C	N	O	S	0	0	0
			3415	2219	566	623	7			

- Molecule 3 is (R)-(+)-5(9BH)-OXO-9B-PHENYL-2,3-DIHYDROTHIAZOLO[2,3-A]ISOINDOL-3-CARBOXYLIC ACID METHYL ESTER (CCD ID: BM5) (formula: C₁₈H₁₅NO₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			23	18	1	3	1		

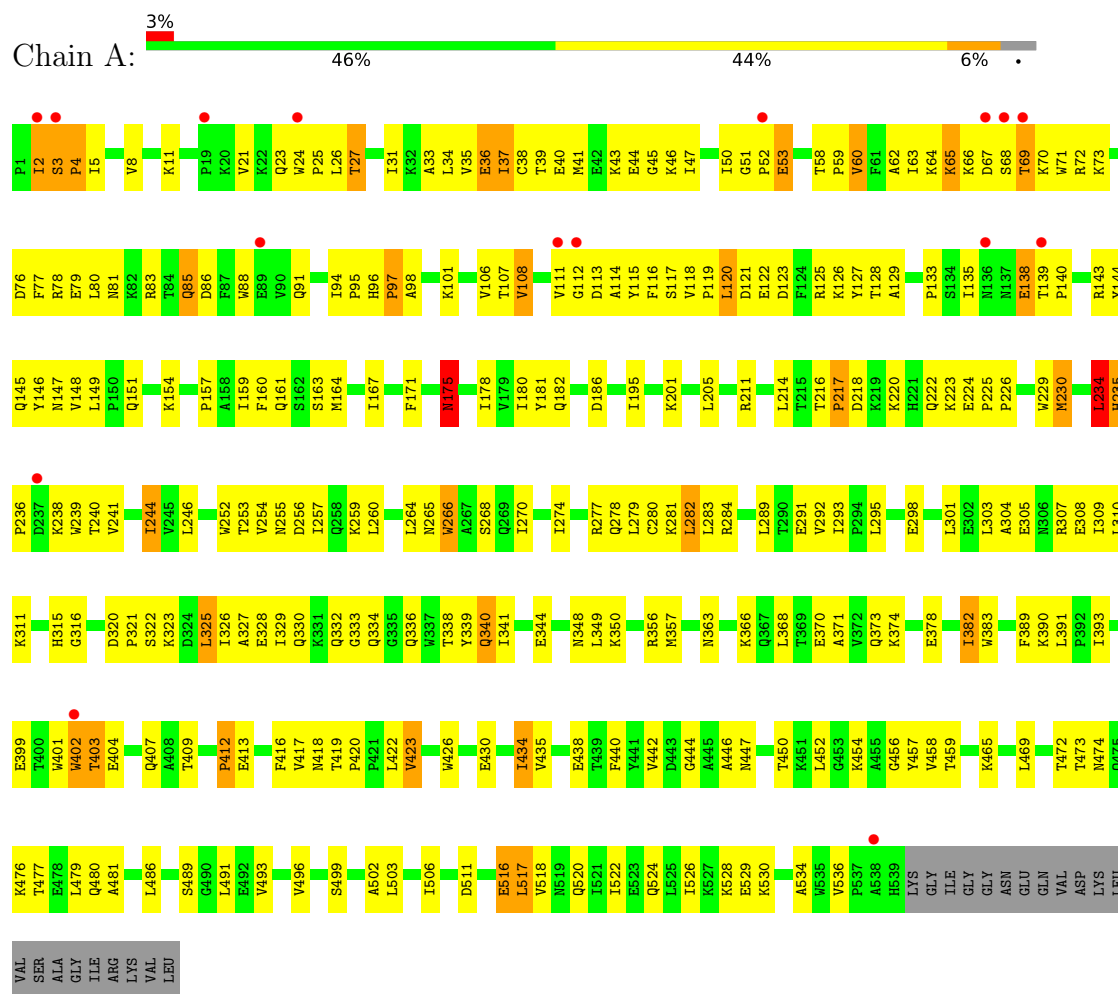
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total 57	O 57	0	0
4	B	33	Total 33	O 33	0	0

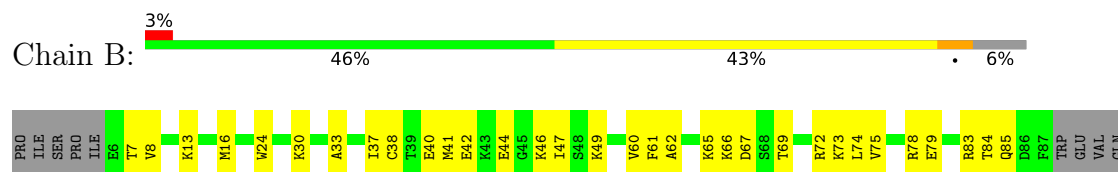
3 Residue-property plots

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: HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN)



• Molecule 2: HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN)





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	137.30Å 108.50Å 72.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.52 15.00 – 2.52	Depositor EDS
% Data completeness (in resolution range)	88.8 (15.00-2.52) 88.2 (15.00-2.52)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.232 , 0.298 0.243 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.387	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 62.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7938	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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: CSD, BM5

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	0/4518	1.00	23/6140 (0.4%)
2	B	0.49	0/3509	0.97	12/4763 (0.3%)
All	All	0.48	0/8027	0.99	35/10903 (0.3%)

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	349	LEU	N-CA-C	-10.00	101.58	113.88
2	B	69	THR	N-CA-C	-9.69	101.57	113.97
2	B	382	ILE	N-CA-C	9.43	119.97	110.82
1	A	3	SER	N-CA-C	9.12	116.33	108.13
2	B	428	GLN	N-CA-C	-8.62	102.93	113.19
2	B	147	ASN	N-CA-C	-6.94	105.09	113.97
1	A	382	ILE	N-CA-C	6.93	117.72	110.72
1	A	282	LEU	N-CA-C	6.63	120.24	111.75
1	A	175	ASN	CA-C-N	6.52	126.46	119.28
1	A	175	ASN	C-N-CA	6.52	126.46	119.28
2	B	186	ASP	N-CA-C	6.03	119.48	110.14
1	A	402	TRP	N-CA-C	6.03	117.52	111.07
2	B	388	LYS	N-CA-C	-5.98	100.25	109.76
1	A	234	LEU	N-CA-C	5.73	117.63	108.41
1	A	371	ALA	N-CA-C	-5.71	104.97	111.07
2	B	250	ASP	N-CA-C	-5.69	104.99	111.14
1	A	147	ASN	N-CA-C	-5.68	106.70	113.97
1	A	3	SER	CA-C-N	5.65	126.90	119.84
1	A	3	SER	C-N-CA	5.65	126.90	119.84
2	B	391	LEU	N-CA-C	5.58	117.72	109.62
2	B	349	LEU	N-CA-C	-5.54	105.64	112.90
1	A	419	THR	CA-C-N	5.54	123.71	119.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	419	THR	C-N-CA	5.54	123.71	119.66
1	A	235	HIS	N-CA-C	-5.43	102.82	110.31
2	B	131	THR	N-CA-C	5.37	117.18	108.26
1	A	348	ASN	N-CA-C	5.36	118.06	110.50
1	A	180	ILE	N-CA-C	5.35	115.60	108.11
1	A	420	PRO	N-CA-C	5.28	115.54	110.47
1	A	458	VAL	N-CA-C	-5.22	100.00	107.78
1	A	53	GLU	N-CA-C	-5.21	106.70	113.16
1	A	195	ILE	N-CA-C	5.20	116.55	110.62
2	B	417	VAL	N-CA-C	5.15	116.11	108.65
1	A	186	ASP	N-CA-C	5.12	118.41	110.17
2	B	401	TRP	N-CA-C	5.10	121.79	114.39
1	A	434	ILE	N-CA-C	5.02	114.98	107.51

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	4410	0	4452	253	0
2	B	3415	0	3445	178	0
3	A	23	0	14	1	0
4	A	57	0	0	4	0
4	B	33	0	0	4	0
All	All	7938	0	7911	422	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 27.

All (422) 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:A:503:LEU:HA	1:A:506:ILE:HD12	1.43	0.99
2:B:125:ARG:HE	2:B:147:ASN:HA	1.33	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ILE:HD13	1:A:244:ILE:H	1.32	0.93
1:A:244:ILE:HD11	1:A:310:LEU:HD22	1.50	0.93
2:B:111:VAL:HB	2:B:214:LEU:HD23	1.50	0.91
2:B:168:LEU:HD13	2:B:180:ILE:HG21	1.56	0.88
2:B:209:LEU:HG	2:B:214:LEU:HB2	1.56	0.87
1:A:65:LYS:HE3	1:A:67:ASP:H	1.40	0.87
1:A:476:LYS:HG2	1:A:517:LEU:HD12	1.55	0.87
2:B:332:GLN:NE2	2:B:424:LYS:HE2	1.94	0.83
1:A:64:LYS:H	1:A:64:LYS:HD3	1.43	0.83
1:A:239:TRP:CE2	1:A:316:GLY:HA3	2.13	0.83
2:B:114:ALA:HB2	2:B:214:LEU:HG	1.63	0.81
1:A:79:GLU:O	1:A:83:ARG:HG3	1.80	0.80
2:B:164:MET:SD	2:B:167:ILE:HD11	2.23	0.78
2:B:106:VAL:HB	2:B:234:LEU:HD12	1.66	0.78
1:A:401:TRP:CZ3	1:A:409:THR:HG21	2.18	0.78
2:B:178:ILE:HG12	2:B:191:SER:HB3	1.66	0.77
1:A:239:TRP:CZ2	1:A:316:GLY:HA3	2.22	0.75
2:B:65:LYS:HA	2:B:407:GLN:HE21	1.51	0.75
2:B:209:LEU:HD11	2:B:214:LEU:HD22	1.70	0.74
1:A:450:THR:HB	1:A:452:LEU:HD23	1.70	0.74
1:A:65:LYS:O	1:A:69:THR:HA	1.88	0.73
1:A:238:LYS:HG3	1:A:316:GLY:O	1.88	0.73
1:A:308:GLU:O	1:A:311:LYS:HB2	1.89	0.72
1:A:36:GLU:O	1:A:39:THR:HG22	1.90	0.71
2:B:46:LYS:HE2	2:B:116:PHE:CG	2.26	0.71
1:A:446:ALA:HB2	1:A:477:THR:HG21	1.73	0.71
1:A:171:PHE:O	1:A:175:ASN:ND2	2.24	0.70
1:A:289:LEU:H	1:A:289:LEU:HD22	1.57	0.70
1:A:308:GLU:HA	1:A:311:LYS:HD2	1.74	0.70
2:B:434:ILE:HD12	2:B:434:ILE:H	1.54	0.70
1:A:96:HIS:HD2	1:A:98:ALA:H	1.39	0.69
2:B:277:ARG:HH22	2:B:281:LYS:HZ2	1.39	0.69
1:A:330:GLN:HB2	1:A:338:THR:HG1	1.56	0.69
2:B:423:VAL:HG21	4:B:1043:HOH:O	1.94	0.68
2:B:94:ILE:HD13	2:B:94:ILE:H	1.59	0.68
2:B:214:LEU:HD12	2:B:214:LEU:N	2.08	0.68
1:A:114:ALA:HB1	1:A:160:PHE:CZ	2.29	0.68
1:A:516:GLU:O	1:A:520:GLN:HG3	1.94	0.68
1:A:244:ILE:CD1	1:A:310:LEU:HD22	2.25	0.67
1:A:330:GLN:HB2	1:A:338:THR:OG1	1.95	0.67
2:B:30:LYS:HG2	2:B:62:ALA:HB3	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:194:GLU:CD	2:B:196:GLY:H	2.02	0.66
1:A:469:LEU:HD11	1:A:480:GLN:HG2	1.78	0.65
2:B:191:SER:HG	2:B:198:HIS:HD1	1.44	0.65
1:A:86:ASP:HA	1:A:154:LYS:NZ	2.11	0.64
1:A:123:ASP:O	1:A:126:LYS:HE2	1.96	0.64
2:B:139:THR:HG22	2:B:140:PRO:O	1.98	0.64
2:B:106:VAL:HB	2:B:234:LEU:CD1	2.27	0.64
2:B:136:ASN:HB3	2:B:138:GLU:HG3	1.80	0.64
2:B:244:ILE:HG13	2:B:426:TRP:CZ2	2.33	0.64
2:B:369:THR:HG22	2:B:398:TRP:CH2	2.33	0.64
2:B:194:GLU:OE2	2:B:195:ILE:HG22	1.99	0.63
1:A:308:GLU:HA	1:A:311:LYS:CD	2.28	0.63
1:A:235:HIS:HB2	1:A:238:LYS:O	1.99	0.63
2:B:125:ARG:NE	2:B:147:ASN:HA	2.12	0.63
2:B:206:ARG:O	2:B:210:LEU:N	2.31	0.62
1:A:139:THR:HB	1:A:140:PRO:HD2	1.81	0.62
2:B:350:LYS:HE3	2:B:378:GLU:OE2	1.99	0.62
2:B:356:ARG:CB	2:B:367:GLN:HG2	2.30	0.62
2:B:171:PHE:CG	2:B:205:LEU:HD23	2.33	0.62
1:A:96:HIS:CD2	1:A:98:ALA:H	2.18	0.62
2:B:105:SER:HB3	2:B:235:HIS:CD2	2.35	0.62
2:B:114:ALA:HB2	2:B:214:LEU:CG	2.30	0.62
2:B:368:LEU:HD13	2:B:398:TRP:CZ3	2.35	0.62
1:A:8:VAL:O	1:A:121:ASP:HB2	2.00	0.61
1:A:218:ASP:O	1:A:222:GLN:HG2	2.00	0.61
1:A:24:TRP:CD1	1:A:25:PRO:HD2	2.36	0.61
1:A:46:LYS:HD3	1:A:116:PHE:HD1	1.66	0.61
1:A:69:THR:O	1:A:69:THR:HG22	2.00	0.61
2:B:270:ILE:HG12	2:B:346:PHE:HB3	1.81	0.61
1:A:112:GLY:C	1:A:114:ALA:H	2.09	0.60
1:A:161:GLN:HG3	1:A:182:GLN:NE2	2.15	0.60
1:A:50:ILE:HD13	1:A:145:GLN:HB3	1.82	0.60
1:A:161:GLN:HA	1:A:182:GLN:OE1	2.01	0.60
2:B:232:TYR:CE1	2:B:234:LEU:HD23	2.36	0.60
1:A:260:LEU:HG	1:A:264:LEU:HD23	1.83	0.60
1:A:21:VAL:CG1	1:A:59:PRO:HD3	2.32	0.59
1:A:280:CSD:C	1:A:281:LYS:N	2.65	0.59
2:B:332:GLN:HE21	2:B:424:LYS:HE2	1.67	0.59
1:A:135:ILE:O	1:A:138:GLU:HG2	2.03	0.59
2:B:60:VAL:HG12	2:B:75:VAL:HG22	1.83	0.59
2:B:111:VAL:CB	2:B:214:LEU:HD23	2.27	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ILE:HD13	1:A:244:ILE:N	2.12	0.59
1:A:266:TRP:CD1	1:A:266:TRP:C	2.81	0.59
1:A:114:ALA:HB1	1:A:160:PHE:CE2	2.38	0.58
1:A:46:LYS:HD3	1:A:116:PHE:CD1	2.37	0.58
1:A:265:ASN:O	1:A:268:SER:HB3	2.03	0.58
1:A:37:ILE:HG22	1:A:41:MET:HE3	1.85	0.58
1:A:211:ARG:HG2	1:A:211:ARG:HH11	1.67	0.58
2:B:7:THR:HG22	2:B:119:PRO:HG2	1.84	0.58
1:A:175:ASN:N	1:A:175:ASN:HD22	2.00	0.58
1:A:503:LEU:CA	1:A:506:ILE:HD12	2.27	0.58
2:B:40:GLU:HG3	2:B:44:GLU:OE2	2.04	0.58
2:B:112:GLY:O	2:B:115:TYR:HD2	1.87	0.58
2:B:434:ILE:HD12	2:B:434:ILE:N	2.18	0.58
1:A:106:VAL:HG23	1:A:236:PRO:HB3	1.85	0.58
2:B:111:VAL:HG12	2:B:209:LEU:HD21	1.85	0.58
2:B:116:PHE:HA	2:B:148:VAL:HG21	1.84	0.58
1:A:534:ALA:HB1	4:B:1113:HOH:O	2.04	0.58
1:A:373:GLN:NE2	2:B:396:GLU:HB3	2.19	0.57
2:B:354:TYR:OH	2:B:370:GLU:HB3	2.04	0.57
1:A:2:ILE:HG13	1:A:3:SER:H	1.69	0.57
1:A:111:VAL:O	1:A:114:ALA:HB2	2.04	0.57
1:A:330:GLN:NE2	1:A:340:GLN:OE1	2.37	0.57
1:A:107:THR:HG22	1:A:108:VAL:H	1.68	0.57
1:A:33:ALA:HB1	1:A:71:TRP:HB2	1.86	0.57
2:B:171:PHE:CD2	2:B:205:LEU:HD23	2.39	0.57
2:B:287:LYS:HD2	2:B:293:ILE:HD11	1.85	0.57
1:A:341:ILE:HG21	1:A:383:TRP:CH2	2.40	0.57
1:A:489:SER:OG	1:A:493:VAL:HG21	2.05	0.57
1:A:76:ASP:OD2	1:A:78:ARG:HG3	2.05	0.57
1:A:138:GLU:HG3	1:A:139:THR:H	1.69	0.57
1:A:31:ILE:O	1:A:35:VAL:HG23	2.05	0.56
1:A:125:ARG:HG2	1:A:146:TYR:O	2.04	0.56
1:A:366:LYS:O	1:A:370:GLU:HG3	2.05	0.56
2:B:209:LEU:CD1	2:B:214:LEU:HD22	2.35	0.56
1:A:373:GLN:HG2	4:A:1013:HOH:O	2.04	0.56
2:B:298:GLU:CD	2:B:298:GLU:H	2.13	0.56
2:B:213:GLY:C	2:B:214:LEU:HD12	2.30	0.56
1:A:260:LEU:HG	1:A:264:LEU:CD2	2.35	0.56
2:B:344:GLU:HB3	2:B:347:LYS:HE3	1.87	0.56
1:A:211:ARG:HG2	1:A:211:ARG:NH1	2.20	0.56
2:B:178:ILE:HG12	2:B:191:SER:CB	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:332:GLN:HE22	2:B:424:LYS:HE2	1.70	0.56
1:A:164:MET:HE1	1:A:214:LEU:HD13	1.86	0.56
1:A:389:PHE:HB3	1:A:391:LEU:HD21	1.86	0.56
1:A:336:GLN:HG3	1:A:356:ARG:HG2	1.86	0.56
1:A:163:SER:O	1:A:167:ILE:HG13	2.06	0.55
1:A:175:ASN:ND2	1:A:175:ASN:N	2.52	0.55
1:A:21:VAL:HG11	1:A:59:PRO:HD3	1.87	0.55
1:A:118:VAL:HB	1:A:149:LEU:HD22	1.89	0.55
2:B:94:ILE:HD13	2:B:94:ILE:N	2.20	0.55
1:A:129:ALA:HA	1:A:144:TYR:O	2.07	0.55
1:A:33:ALA:HB1	1:A:71:TRP:CB	2.36	0.55
1:A:434:ILE:HD11	1:A:530:LYS:HB3	1.88	0.55
1:A:307:ARG:O	1:A:311:LYS:HG3	2.07	0.55
2:B:413:GLU:OE1	2:B:413:GLU:HA	2.04	0.55
1:A:2:ILE:HG13	1:A:3:SER:N	2.22	0.55
1:A:254:VAL:HB	1:A:289:LEU:O	2.06	0.55
2:B:108:VAL:HG22	2:B:188:TYR:CD2	2.42	0.55
1:A:328:GLU:HG3	1:A:390:LYS:HB2	1.88	0.55
2:B:106:VAL:N	2:B:234:LEU:O	2.39	0.55
2:B:78:ARG:HD2	2:B:413:GLU:OE1	2.07	0.54
1:A:11:LYS:O	1:A:85:GLN:HB3	2.07	0.54
1:A:34:LEU:HD21	1:A:62:ALA:HB2	1.89	0.54
1:A:244:ILE:H	1:A:244:ILE:CD1	2.13	0.54
2:B:427:TYR:C	2:B:429:LEU:H	2.15	0.54
1:A:326:ILE:HG22	1:A:327:ALA:N	2.22	0.54
1:A:81:ASN:C	1:A:83:ARG:H	2.16	0.54
2:B:353:LYS:NZ	2:B:353:LYS:HB3	2.23	0.54
1:A:33:ALA:O	1:A:36:GLU:HB3	2.08	0.54
1:A:181:TYR:HB2	3:A:999:BM5:OB	2.08	0.54
2:B:356:ARG:HB2	2:B:367:GLN:HG2	1.89	0.54
1:A:450:THR:CB	1:A:452:LEU:HD23	2.35	0.53
2:B:120:LEU:O	2:B:121:ASP:C	2.51	0.53
2:B:356:ARG:HB3	2:B:367:GLN:HG2	1.90	0.53
1:A:499:SER:O	1:A:502:ALA:HB3	2.08	0.53
2:B:47:ILE:HG22	2:B:146:TYR:HA	1.90	0.53
2:B:115:TYR:CE1	2:B:156:SER:HB3	2.44	0.53
2:B:167:ILE:O	2:B:208:HIS:NE2	2.42	0.53
2:B:171:PHE:CZ	2:B:205:LEU:HB2	2.44	0.53
1:A:430:GLU:HG3	1:A:434:ILE:HD11	1.91	0.53
2:B:252:TRP:CZ3	2:B:260:LEU:HD22	2.44	0.53
1:A:64:LYS:H	1:A:64:LYS:CD	2.18	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:TYR:CD1	1:A:457:TYR:C	2.86	0.53
2:B:213:GLY:H	2:B:214:LEU:HD12	1.73	0.53
1:A:320:ASP:OD1	1:A:323:LYS:HG3	2.10	0.52
1:A:65:LYS:HE3	1:A:66:LYS:H	1.74	0.52
1:A:403:THR:HG23	1:A:404:GLU:HG2	1.92	0.52
1:A:36:GLU:O	1:A:37:ILE:C	2.53	0.52
1:A:332:GLN:O	1:A:332:GLN:HG2	2.10	0.52
1:A:417:VAL:O	1:A:417:VAL:HG13	2.09	0.52
2:B:97:PRO:HG3	2:B:181:TYR:HB2	1.91	0.52
2:B:387:PRO:HG2	2:B:389:PHE:CE1	2.45	0.52
1:A:536:VAL:HG12	2:B:258:GLN:HB3	1.92	0.52
1:A:68:SER:CB	1:A:70:LYS:HZ2	2.23	0.52
2:B:111:VAL:CG1	2:B:209:LEU:HD21	2.40	0.52
1:A:27:THR:O	1:A:31:ILE:HG13	2.10	0.52
1:A:86:ASP:HA	1:A:154:LYS:HZ2	1.74	0.52
1:A:434:ILE:CD1	1:A:530:LYS:HB3	2.40	0.52
1:A:447:ASN:HB3	1:A:450:THR:OG1	2.09	0.52
2:B:46:LYS:HE2	2:B:116:PHE:CD1	2.45	0.52
1:A:115:TYR:CD1	1:A:151:GLN:HA	2.46	0.51
2:B:13:LYS:HB2	2:B:16:MET:HG3	1.91	0.51
2:B:332:GLN:NE2	2:B:424:LYS:CE	2.71	0.51
1:A:3:SER:HB3	1:A:5:ILE:HG13	1.92	0.51
1:A:447:ASN:HB3	1:A:450:THR:HG1	1.76	0.51
2:B:116:PHE:HA	2:B:148:VAL:CG2	2.41	0.51
2:B:172:ARG:HE	2:B:180:ILE:HB	1.75	0.51
2:B:207:GLN:O	2:B:210:LEU:HB3	2.10	0.51
1:A:149:LEU:HD21	1:A:159:ILE:HG22	1.92	0.51
1:A:293:ILE:N	1:A:293:ILE:HD12	2.24	0.51
1:A:401:TRP:HZ3	1:A:409:THR:HG21	1.72	0.51
2:B:239:TRP:CH2	2:B:378:GLU:HG2	2.46	0.51
1:A:138:GLU:HG3	1:A:139:THR:N	2.26	0.51
1:A:444:GLY:HA2	1:A:454:LYS:O	2.11	0.51
1:A:252:TRP:NE1	1:A:295:LEU:HD11	2.25	0.50
1:A:38:CYS:HB3	1:A:144:TYR:CE1	2.46	0.50
2:B:379:SER:OG	2:B:387:PRO:HD3	2.11	0.50
1:A:3:SER:HB2	1:A:119:PRO:HD3	1.93	0.50
1:A:225:PRO:HA	1:A:226:PRO:C	2.36	0.50
1:A:373:GLN:HG3	1:A:374:LYS:N	2.26	0.50
2:B:79:GLU:O	2:B:83:ARG:HG3	2.10	0.50
2:B:438:GLU:HG2	2:B:438:GLU:O	2.12	0.50
1:A:51:GLY:C	1:A:53:GLU:H	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.37	0.50
2:B:30:LYS:HE3	2:B:62:ALA:O	2.12	0.50
2:B:246:LEU:HB2	2:B:307:ARG:NH1	2.27	0.50
2:B:180:ILE:HD13	2:B:189:VAL:HG22	1.93	0.50
2:B:376:THR:HG21	2:B:410:TRP:CZ3	2.47	0.50
1:A:374:LYS:O	1:A:378:GLU:HG3	2.12	0.49
1:A:120:LEU:CD2	1:A:121:ASP:H	2.25	0.49
2:B:195:ILE:HD11	2:B:199:ARG:HH21	1.76	0.49
2:B:431:LYS:HG2	2:B:432:GLU:N	2.27	0.49
1:A:35:VAL:O	1:A:39:THR:HB	2.12	0.49
1:A:246:LEU:HD22	1:A:260:LEU:HD11	1.95	0.49
2:B:357:MET:HE2	2:B:357:MET:HA	1.95	0.49
2:B:427:TYR:C	2:B:429:LEU:N	2.69	0.49
1:A:34:LEU:HD22	1:A:73:LYS:HG3	1.93	0.49
1:A:255:ASN:CG	1:A:289:LEU:HB3	2.38	0.49
1:A:116:PHE:O	1:A:148:VAL:HG11	2.13	0.49
1:A:122:GLU:H	1:A:122:GLU:CD	2.21	0.49
2:B:134:SER:OG	2:B:139:THR:HB	2.12	0.48
1:A:65:LYS:CE	1:A:66:LYS:H	2.25	0.48
1:A:94:ILE:HD11	4:A:1054:HOH:O	2.13	0.48
1:A:259:LYS:HG2	4:A:1007:HOH:O	2.13	0.48
1:A:486:LEU:HB3	1:A:524:GLN:HB3	1.95	0.48
2:B:164:MET:HG2	2:B:182:GLN:NE2	2.28	0.48
2:B:332:GLN:HE21	2:B:332:GLN:HA	1.78	0.48
1:A:68:SER:HB3	1:A:70:LYS:HZ2	1.78	0.48
2:B:163:SER:O	2:B:167:ILE:HG23	2.13	0.48
2:B:276:VAL:O	2:B:280:CYS:HB2	2.12	0.48
1:A:41:MET:HE1	1:A:73:LYS:HE2	1.94	0.48
1:A:241:VAL:HG21	1:A:270:ILE:HG21	1.95	0.48
2:B:393:ILE:O	2:B:416:PHE:HB3	2.13	0.48
1:A:255:ASN:ND2	1:A:289:LEU:HB3	2.29	0.48
1:A:399:GLU:OE1	1:A:399:GLU:HA	2.14	0.48
2:B:164:MET:HA	2:B:167:ILE:HG12	1.94	0.48
1:A:2:ILE:CG1	1:A:3:SER:H	2.26	0.48
1:A:240:THR:HA	1:A:315:HIS:HA	1.95	0.48
1:A:86:ASP:HA	1:A:154:LYS:HZ1	1.78	0.48
2:B:211:ARG:HG3	2:B:212:TRP:CD1	2.49	0.48
2:B:332:GLN:NE2	2:B:424:LYS:HG2	2.29	0.48
1:A:503:LEU:HG	2:B:421:PRO:HB2	1.96	0.47
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.54	0.47
1:A:260:LEU:HD21	1:A:303:LEU:HD13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:LEU:HD23	1:A:121:ASP:H	1.79	0.47
1:A:393:ILE:HB	1:A:423:VAL:HG22	1.97	0.47
2:B:103:LYS:HE3	2:B:179:VAL:HG23	1.95	0.47
2:B:205:LEU:HD13	2:B:205:LEU:C	2.39	0.47
1:A:402:TRP:CZ2	2:B:362:THR:HA	2.50	0.47
1:A:426:TRP:HB3	1:A:526:ILE:HG12	1.95	0.47
1:A:117:SER:HB3	1:A:214:LEU:HD23	1.95	0.47
1:A:216:THR:HG23	1:A:217:PRO:HD2	1.96	0.47
1:A:473:THR:O	1:A:477:THR:HG23	2.15	0.47
1:A:79:GLU:HG3	1:A:83:ARG:HD2	1.97	0.47
1:A:63:ILE:O	1:A:72:ARG:HB2	2.15	0.47
1:A:305:GLU:O	1:A:309:ILE:HG13	2.14	0.47
1:A:292:VAL:C	1:A:293:ILE:HD12	2.40	0.47
2:B:287:LYS:HD2	2:B:291:GLU:HG2	1.97	0.46
1:A:77:PHE:CD2	1:A:80:LEU:HD23	2.50	0.46
2:B:328:GLU:O	2:B:339:TYR:HA	2.14	0.46
1:A:254:VAL:HG13	1:A:283:LEU:HD12	1.96	0.46
1:A:402:TRP:CH2	2:B:362:THR:HA	2.50	0.46
1:A:50:ILE:HG23	1:A:145:GLN:HG2	1.98	0.46
1:A:161:GLN:HG3	1:A:182:GLN:HE22	1.79	0.46
2:B:266:TRP:HB2	2:B:422:LEU:HD13	1.96	0.46
1:A:412:PRO:O	1:A:413:GLU:C	2.58	0.46
2:B:104:LYS:HA	2:B:237:ASP:OD1	2.16	0.46
2:B:169:GLU:N	2:B:170:PRO:HD2	2.31	0.46
2:B:319:TYR:OH	2:B:385:LYS:HE2	2.16	0.46
2:B:434:ILE:H	2:B:434:ILE:CD1	2.23	0.46
1:A:491:LEU:HD13	1:A:529:GLU:OE1	2.16	0.46
2:B:7:THR:CG2	2:B:119:PRO:HG2	2.46	0.46
2:B:118:VAL:HB	2:B:149:LEU:CD1	2.46	0.46
1:A:50:ILE:HG13	1:A:143:ARG:HB3	1.97	0.46
1:A:418:ASN:HA	1:A:422:LEU:HD21	1.98	0.45
2:B:175:ASN:ND2	2:B:201:LYS:HD2	2.31	0.45
1:A:246:LEU:HD22	1:A:260:LEU:CD1	2.46	0.45
2:B:72:ARG:CZ	2:B:409:THR:HG22	2.46	0.45
1:A:115:TYR:OH	1:A:157:PRO:HG3	2.17	0.45
1:A:518:VAL:O	1:A:522:ILE:HG13	2.17	0.45
2:B:61:PHE:CE1	2:B:74:LEU:HD23	2.52	0.45
2:B:122:GLU:HA	2:B:125:ARG:NH1	2.31	0.45
1:A:117:SER:CB	1:A:214:LEU:HD23	2.46	0.45
1:A:323:LYS:HZ2	1:A:344:GLU:HG2	1.81	0.45
2:B:342:TYR:CD1	2:B:342:TYR:C	2.95	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:333:GLY:O	1:A:334:GLN:C	2.59	0.45
1:A:402:TRP:C	1:A:404:GLU:N	2.73	0.45
2:B:252:TRP:CD1	2:B:295:LEU:HD11	2.51	0.45
1:A:116:PHE:N	1:A:116:PHE:CD2	2.83	0.45
1:A:178:ILE:HD11	1:A:201:LYS:HG3	1.99	0.45
1:A:325:LEU:HD23	1:A:325:LEU:HA	1.87	0.45
1:A:95:PRO:HA	2:B:136:ASN:O	2.17	0.45
1:A:244:ILE:CG1	1:A:310:LEU:HD22	2.46	0.45
2:B:74:LEU:HD12	2:B:75:VAL:N	2.32	0.45
2:B:254:VAL:O	2:B:258:GLN:HG3	2.16	0.45
2:B:41:MET:HE2	2:B:47:ILE:HG23	2.00	0.44
2:B:42:GLU:OE1	2:B:49:LYS:NZ	2.47	0.44
2:B:239:TRP:CZ2	2:B:378:GLU:HG2	2.52	0.44
2:B:437:ALA:CB	2:B:439:THR:HG23	2.46	0.44
1:A:115:TYR:HD1	1:A:151:GLN:HA	1.81	0.44
1:A:230:MET:HE3	1:A:230:MET:HA	1.99	0.44
1:A:34:LEU:C	1:A:36:GLU:N	2.72	0.44
2:B:210:LEU:C	2:B:212:TRP:H	2.25	0.44
2:B:267:ALA:HB2	2:B:426:TRP:CZ3	2.51	0.44
2:B:319:TYR:CD2	2:B:383:TRP:CD1	3.05	0.44
1:A:229:TRP:HB2	1:A:234:LEU:HD22	1.99	0.44
1:A:435:VAL:HG22	2:B:290:THR:HG21	1.99	0.44
2:B:195:ILE:HD11	2:B:199:ARG:NH2	2.33	0.44
1:A:108:VAL:CG1	1:A:223:LYS:HB2	2.47	0.44
1:A:255:ASN:O	1:A:259:LYS:HG3	2.18	0.44
2:B:303:LEU:O	2:B:307:ARG:HG3	2.17	0.44
2:B:61:PHE:CZ	2:B:74:LEU:HG	2.52	0.44
1:A:226:PRO:HB3	1:A:235:HIS:CE1	2.52	0.44
2:B:173:LYS:HD2	2:B:173:LYS:N	2.33	0.44
1:A:404:GLU:OE1	2:B:334:GLN:HG2	2.18	0.44
2:B:168:LEU:O	2:B:169:GLU:C	2.61	0.44
1:A:21:VAL:HG13	1:A:59:PRO:HD3	2.00	0.43
1:A:281:LYS:O	1:A:284:ARG:HG3	2.18	0.43
2:B:115:TYR:CD1	2:B:156:SER:HB3	2.53	0.43
1:A:47:ILE:HD12	1:A:144:TYR:CG	2.53	0.43
1:A:238:LYS:HG2	1:A:239:TRP:N	2.32	0.43
1:A:280:CSD:C	1:A:281:LYS:CA	2.96	0.43
2:B:338:THR:HG22	2:B:353:LYS:HG3	2.00	0.43
2:B:353:LYS:HD3	4:B:1049:HOH:O	2.17	0.43
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.18	0.43
2:B:332:GLN:NE2	2:B:332:GLN:HA	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:ASN:C	1:A:83:ARG:N	2.75	0.43
1:A:253:THR:HG22	1:A:292:VAL:HG22	2.01	0.43
1:A:320:ASP:OD2	1:A:322:SER:HB3	2.18	0.43
1:A:357:MET:HE1	1:A:370:GLU:HB2	1.99	0.43
2:B:368:LEU:HB3	2:B:398:TRP:HZ3	1.84	0.43
2:B:398:TRP:O	2:B:402:TRP:HD1	2.02	0.43
1:A:23:GLN:OE1	1:A:60:VAL:HG12	2.17	0.43
1:A:402:TRP:CG	1:A:403:THR:N	2.85	0.43
1:A:407:GLN:NE2	4:A:1047:HOH:O	2.51	0.43
2:B:67:ASP:OD1	2:B:67:ASP:O	2.36	0.43
1:A:291:GLU:CD	1:A:293:ILE:HD11	2.44	0.43
2:B:98:ALA:O	2:B:101:LYS:NZ	2.41	0.43
2:B:172:ARG:HH21	2:B:180:ILE:CG2	2.31	0.43
1:A:435:VAL:CG2	2:B:290:THR:HG21	2.48	0.43
2:B:40:GLU:O	2:B:44:GLU:HG3	2.18	0.43
2:B:120:LEU:HD21	2:B:124:PHE:HD2	1.84	0.43
1:A:115:TYR:C	1:A:117:SER:H	2.27	0.43
1:A:120:LEU:CD2	1:A:121:ASP:N	2.82	0.43
1:A:112:GLY:C	1:A:114:ALA:N	2.76	0.42
1:A:280:CSD:O	1:A:281:LYS:C	2.63	0.42
2:B:350:LYS:HE3	2:B:378:GLU:CD	2.44	0.42
1:A:328:GLU:O	1:A:339:TYR:HA	2.18	0.42
1:A:416:PHE:HE1	1:A:422:LEU:HD22	1.84	0.42
2:B:94:ILE:C	2:B:96:HIS:H	2.27	0.42
1:A:116:PHE:HA	1:A:148:VAL:CG2	2.49	0.42
1:A:329:ILE:HA	1:A:338:THR:O	2.19	0.42
2:B:146:TYR:CD2	2:B:150:PRO:HB3	2.54	0.42
2:B:366:LYS:HG2	2:B:370:GLU:OE2	2.19	0.42
1:A:40:GLU:OE2	1:A:44:GLU:HG3	2.19	0.42
1:A:96:HIS:CD2	1:A:97:PRO:N	2.88	0.42
2:B:156:SER:N	2:B:157:PRO:HD2	2.34	0.42
1:A:334:GLN:OE1	1:A:356:ARG:NH2	2.53	0.42
1:A:472:THR:OG1	1:A:473:THR:N	2.52	0.42
2:B:125:ARG:HB3	2:B:145:GLN:NE2	2.34	0.42
1:A:479:LEU:HB2	1:A:517:LEU:HD13	2.02	0.42
1:A:138:GLU:CG	1:A:139:THR:H	2.29	0.42
2:B:384:GLY:O	2:B:385:LYS:HB3	2.20	0.42
2:B:402:TRP:CG	2:B:403:THR:N	2.87	0.42
1:A:88:TRP:CE3	1:A:88:TRP:HA	2.55	0.42
1:A:389:PHE:HB3	1:A:391:LEU:CD2	2.50	0.42
2:B:61:PHE:CZ	2:B:74:LEU:HD23	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:307:ARG:O	2:B:311:LYS:HG3	2.19	0.42
1:A:260:LEU:HD21	1:A:303:LEU:CD1	2.49	0.41
2:B:84:THR:HB	2:B:154:LYS:HE2	2.02	0.41
1:A:253:THR:OG1	1:A:256:ASP:OD2	2.33	0.41
1:A:442:VAL:HB	1:A:481:ALA:HB1	2.01	0.41
1:A:96:HIS:CD2	1:A:97:PRO:HD2	2.56	0.41
1:A:101:LYS:HD3	1:A:321:PRO:HG2	2.02	0.41
1:A:101:LYS:HD3	1:A:321:PRO:CG	2.50	0.41
1:A:224:GLU:HA	1:A:225:PRO:HD3	1.96	0.41
2:B:208:HIS:O	2:B:211:ARG:HG2	2.21	0.41
2:B:354:TYR:HD1	2:B:374:LYS:NZ	2.19	0.41
1:A:26:LEU:HD12	1:A:133:PRO:HG3	2.03	0.41
1:A:58:THR:HG23	1:A:76:ASP:O	2.21	0.41
1:A:116:PHE:HA	1:A:148:VAL:HG21	2.03	0.41
1:A:143:ARG:HG2	1:A:143:ARG:NH1	2.36	0.41
1:A:216:THR:CG2	1:A:217:PRO:HD2	2.51	0.41
1:A:257:ILE:HD13	1:A:282:LEU:HD23	2.03	0.41
1:A:303:LEU:O	1:A:307:ARG:HG3	2.21	0.41
1:A:438:GLU:OE1	1:A:459:THR:HG21	2.21	0.41
2:B:33:ALA:O	2:B:37:ILE:HG13	2.21	0.41
2:B:103:LYS:HE3	2:B:190:GLY:O	2.20	0.41
2:B:151:GLN:HB3	2:B:185:ASP:OD1	2.21	0.41
2:B:161:GLN:HB3	4:B:1115:HOH:O	2.20	0.41
1:A:293:ILE:N	1:A:293:ILE:CD1	2.83	0.41
1:A:301:LEU:O	1:A:304:ALA:N	2.53	0.41
1:A:457:TYR:C	1:A:457:TYR:HD1	2.27	0.41
2:B:46:LYS:HA	2:B:148:VAL:HG13	2.03	0.41
1:A:37:ILE:HD11	1:A:71:TRP:O	2.21	0.40
1:A:239:TRP:O	1:A:316:GLY:N	2.43	0.40
1:A:282:LEU:HD21	1:A:295:LEU:HD23	2.03	0.40
1:A:309:ILE:C	1:A:311:LYS:H	2.30	0.40
2:B:169:GLU:HB3	2:B:173:LYS:NZ	2.36	0.40
2:B:245:VAL:O	2:B:245:VAL:HG23	2.21	0.40
2:B:273:GLY:O	2:B:275:LYS:HG3	2.21	0.40
1:A:98:ALA:HB2	1:A:350:LYS:HB2	2.03	0.40
1:A:456:GLY:HA3	1:A:465:LYS:O	2.21	0.40
1:A:489:SER:O	1:A:528:LYS:NZ	2.54	0.40
2:B:100:LEU:C	2:B:102:LYS:H	2.30	0.40
1:A:43:LYS:C	1:A:45:GLY:H	2.29	0.40
1:A:378:GLU:O	1:A:382:ILE:HG12	2.20	0.40
1:A:402:TRP:O	1:A:404:GLU:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:106:VAL:HG22	2:B:190:GLY:HA3	2.04	0.40
2:B:424:LYS:HD3	2:B:424:LYS:C	2.46	0.40
1:A:97:PRO:HG3	1:A:234:LEU:HD11	2.02	0.40
1:A:126:LYS:HE3	1:A:127:TYR:CZ	2.57	0.40
1:A:128:THR:OG1	1:A:146:TYR:HB2	2.22	0.40
1:A:264:LEU:HD12	1:A:274:ILE:CG2	2.51	0.40
1:A:336:GLN:CG	1:A:356:ARG:HG2	2.52	0.40
1:A:440:PHE:CE1	1:A:489:SER:HB3	2.56	0.40
1:A:278:GLN:HG3	1:A:298:GLU:HB3	2.03	0.40
2:B:332:GLN:HE21	2:B:332:GLN:CA	2.34	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	535/560 (96%)	474 (89%)	48 (9%)	13 (2%)	4	7
2	B	408/440 (93%)	360 (88%)	39 (10%)	9 (2%)	5	8
All	All	943/1000 (94%)	834 (88%)	87 (9%)	22 (2%)	5	7

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	138	GLU
2	B	360	ALA
1	A	36	GLU
1	A	37	ILE
1	A	113	ASP
2	B	66	LYS
2	B	96	HIS

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Mol	Chain	Res	Type
1	A	4	PRO
1	A	69	THR
1	A	85	GLN
1	A	91	GLN
2	B	98	ALA
2	B	101	LYS
2	B	136	ASN
2	B	211	ARG
2	B	85	GLN
1	A	52	PRO
1	A	412	PRO
1	A	108	VAL
2	B	213	GLY
1	A	217	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	483/499 (97%)	459 (95%)	24 (5%)	22	42
2	B	375/400 (94%)	354 (94%)	21 (6%)	19	37
All	All	858/899 (95%)	813 (95%)	45 (5%)	21	40

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	PRO
1	A	27	THR
1	A	60	VAL
1	A	65	LYS
1	A	97	PRO
1	A	120	LEU
1	A	175	ASN
1	A	205	LEU
1	A	220	LYS

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Mol	Chain	Res	Type
1	A	230	MET
1	A	234	LEU
1	A	244	ILE
1	A	266	TRP
1	A	277	ARG
1	A	279	LEU
1	A	325	LEU
1	A	340	GLN
1	A	368	LEU
1	A	403	THR
1	A	423	VAL
1	A	474	ASN
1	A	496	VAL
1	A	516	GLU
1	A	517	LEU
2	B	8	VAL
2	B	24	TRP
2	B	94	ILE
2	B	148	VAL
2	B	187	LEU
2	B	214	LEU
2	B	234	LEU
2	B	250	ASP
2	B	265	ASN
2	B	280	CYS
2	B	283	LEU
2	B	287	LYS
2	B	289	LEU
2	B	291	GLU
2	B	298	GLU
2	B	325	LEU
2	B	353	LYS
2	B	361	HIS
2	B	368	LEU
2	B	413	GLU
2	B	425	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	HIS
1	A	161	GLN

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Mol	Chain	Res	Type
1	A	174	GLN
1	A	175	ASN
1	A	197	GLN
1	A	208	HIS
1	A	222	GLN
1	A	235	HIS
1	A	255	ASN
1	A	278	GLN
1	A	373	GLN
1	A	394	GLN
1	A	407	GLN
1	A	428	GLN
1	A	487	GLN
1	A	500	GLN
1	A	507	GLN
1	A	520	GLN
2	B	147	ASN
2	B	175	ASN
2	B	182	GLN
2	B	197	GLN
2	B	235	HIS
2	B	269	GLN
2	B	278	GLN
2	B	332	GLN
2	B	348	ASN
2	B	407	GLN
2	B	418	ASN
2	B	428	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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	$\# Z > 2$
1	CSD	A	280	1	4,7,8	1.00	0	1,8,10	1.79	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
1	CSD	A	280	1	-	2/2/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	280	CSD	N-CA-CB-SG
1	A	280	CSD	CA-CB-SG-OD1

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	280	CSD	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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	BM5	A	999	-	24,26,26	2.53	4 (16%)	29,39,39	2.17	3 (10%)

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	BM5	A	999	-	-	2/12/42/42	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	999	BM5	C2-C3	-8.80	1.38	1.53
3	A	999	BM5	C3-N4	4.47	1.52	1.46
3	A	999	BM5	C5-C13	3.49	1.58	1.53
3	A	999	BM5	C2-S1	-3.12	1.76	1.80

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	999	BM5	C2-C3-CA	10.34	128.54	111.42
3	A	999	BM5	CA-C3-N4	2.75	117.39	111.60
3	A	999	BM5	C2-C3-N4	-2.55	103.02	106.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

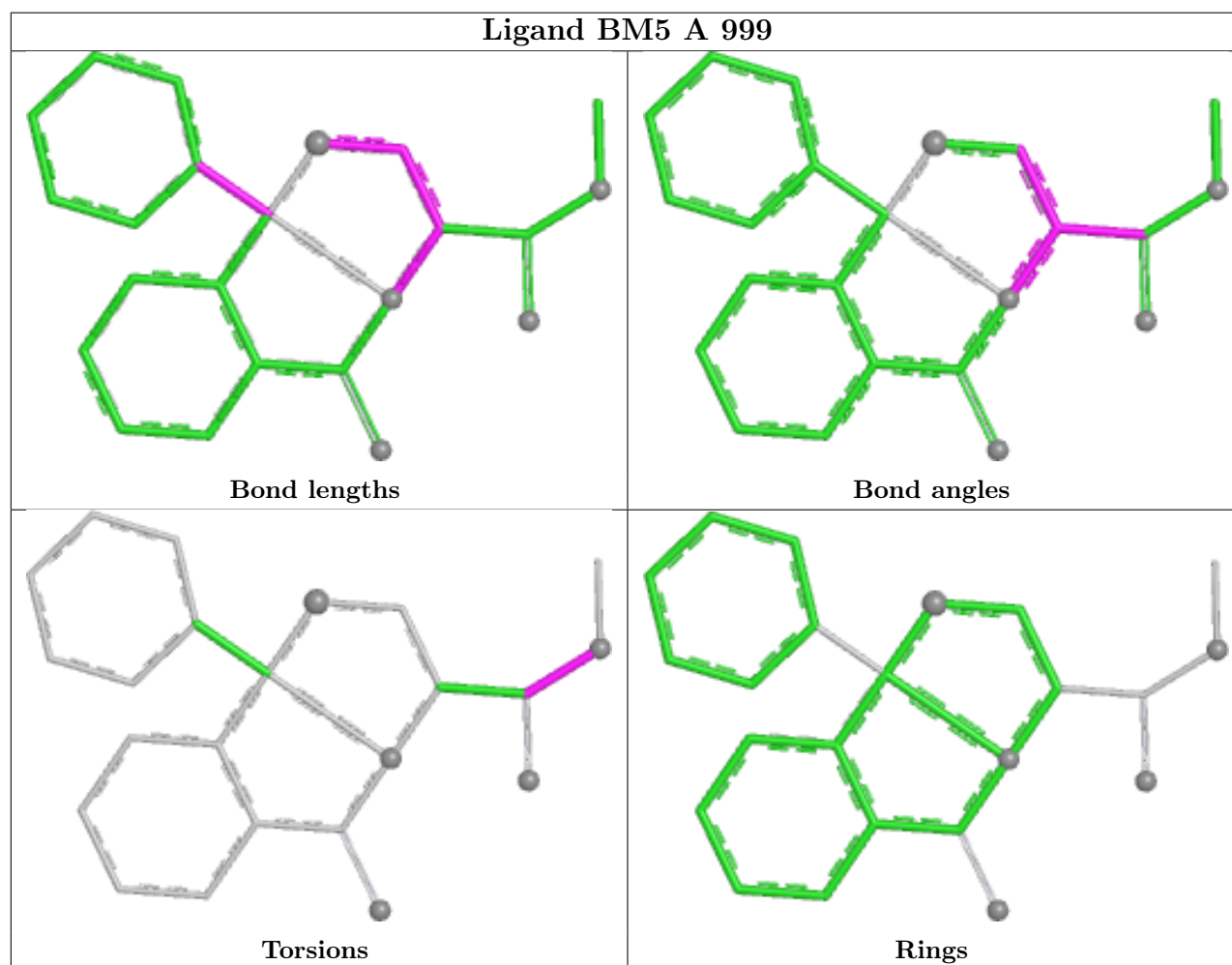
Mol	Chain	Res	Type	Atoms
3	A	999	BM5	OB-CA-OC-CD
3	A	999	BM5	C3-CA-OC-CD

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	999	BM5	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	280:CSD	C	281:LYS	N	2.65

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	538/560 (96%)	0.14	16 (2%)	52	49	19, 51, 97, 150	0
2	B	414/440 (94%)	0.11	14 (3%)	48	44	20, 47, 102, 148	0
All	All	952/1000 (95%)	0.12	30 (3%)	50	47	19, 49, 101, 150	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	68	SER	4.7
2	B	436	GLY	4.5
2	B	435	VAL	4.0
2	B	437	ALA	3.5
1	A	136	ASN	3.4
1	A	3	SER	3.1
2	B	241	VAL	2.9
1	A	52	PRO	2.9
2	B	214	LEU	2.8
2	B	240	THR	2.8
2	B	232	TYR	2.7
1	A	112	GLY	2.6
1	A	24	TRP	2.5
1	A	237	ASP	2.5
1	A	67	ASP	2.5
2	B	434	ILE	2.5
1	A	69	THR	2.4
1	A	2	ILE	2.4
2	B	200	THR	2.3
2	B	439	THR	2.3
2	B	208	HIS	2.3
1	A	139	THR	2.3
1	A	19	PRO	2.3
1	A	89	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	402	TRP	2.2
2	B	215	THR	2.2
1	A	111	VAL	2.0
1	A	538	ALA	2.0
2	B	361	HIS	2.0
2	B	174	GLN	2.0

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
1	CSD	A	280	8/9	0.90	0.09	40,46,64,64	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

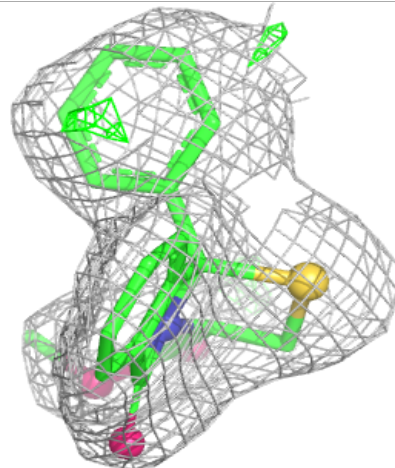
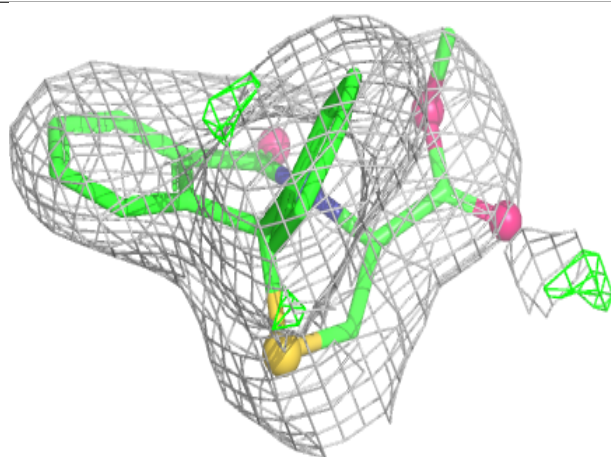
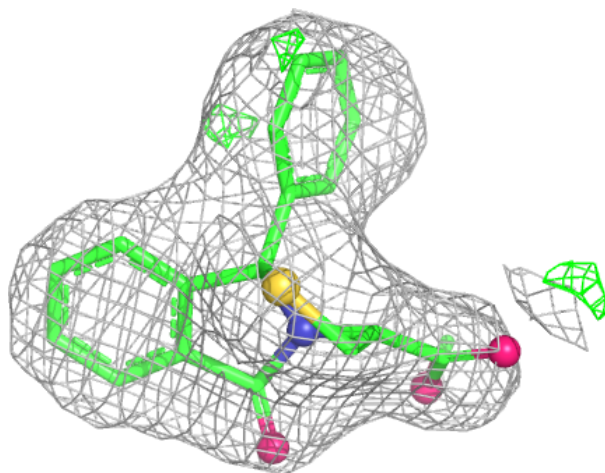
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BM5	A	999	23/23	0.90	0.10	25,47,57,61	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around BM5 A 999:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.