



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:05 AM UTC

PDB ID : 3MED / pdb_00003med
Title : HIV-1 K103N Reverse Transcriptase in Complex with TMC125
Authors : Lansdon, E.B.
Deposited on : 2010-03-31
Resolution : 2.50 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

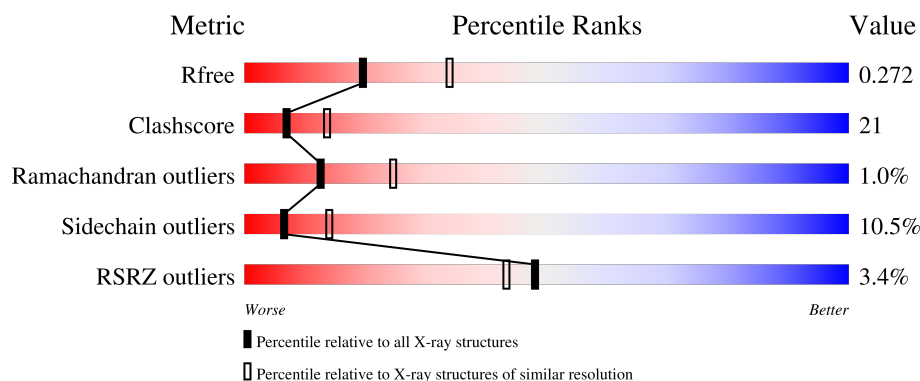
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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% 54% 39% 5%
2	B	440	3% 53% 32% 5% 9%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7967 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 p66 Reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	552	Total	C	N	O	S	0	0	0
			4501	2909	751	833	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	ASN	LYS	engineered mutation	UNP P04585

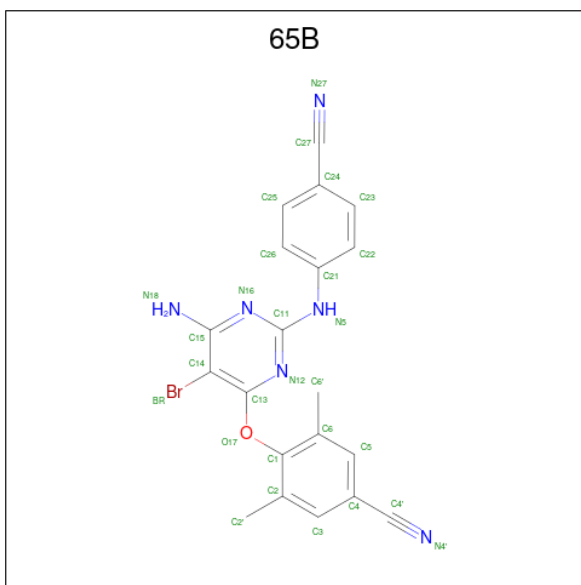
- Molecule 2 is a protein called p51 Reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	401	Total	C	N	O	S	0	0	0
			3317	2159	548	604	6			

There is a discrepancy between the modelled and reference sequences:

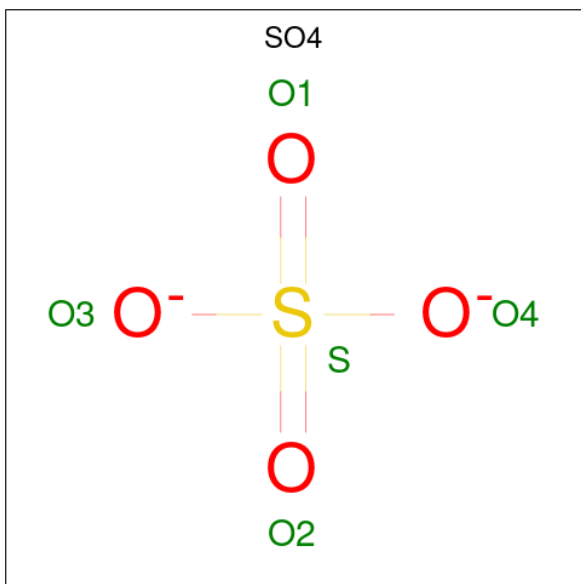
Chain	Residue	Modelled	Actual	Comment	Reference
B	103	ASN	LYS	engineered mutation	UNP P04585

- Molecule 3 is 4-({6-AMINO-5-BROMO-2-[(4-CYANOPHENYL)AMINO]PYRIMIDIN-4-YL}OXY)-3,5-DIMETHYLBENZONITRILE (CCD ID: 65B) (formula: C₂₀H₁₅BrN₆O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	Br	C	N	O	0	0
			28	1	20	6	1		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Cl	0	0
			1	1		

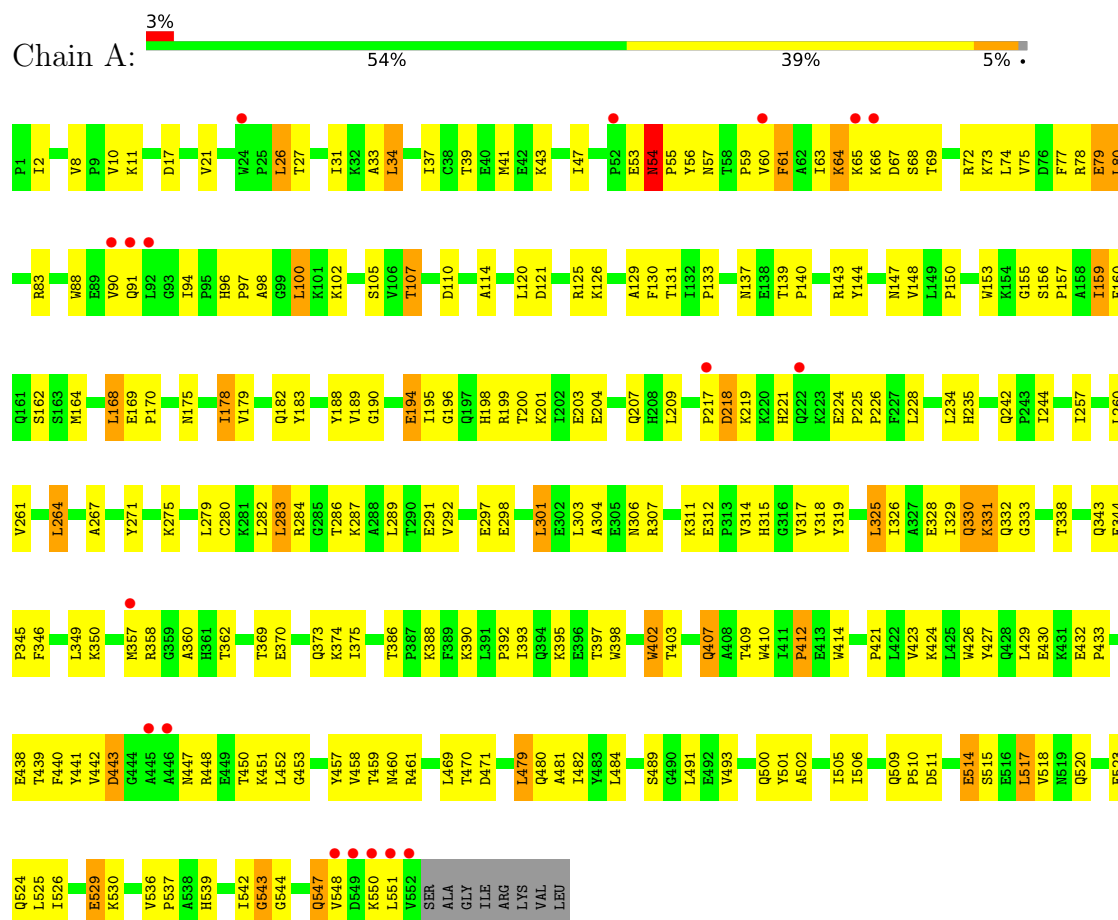
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	55	Total	O	0	0
			55	55		
6	B	35	Total	O	0	0
			35	35		

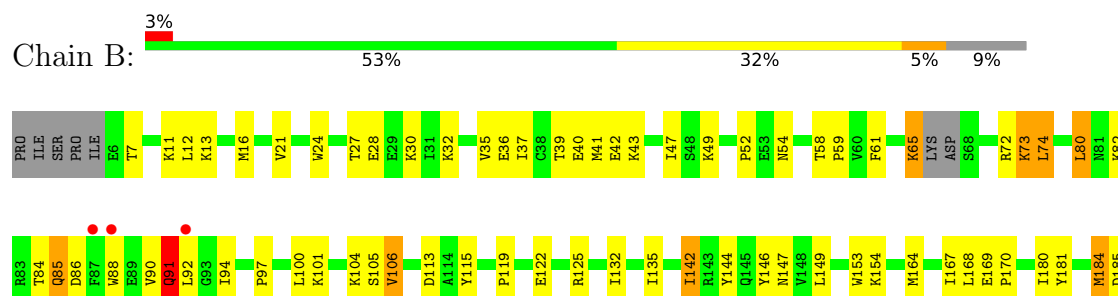
3 Residue-property plots

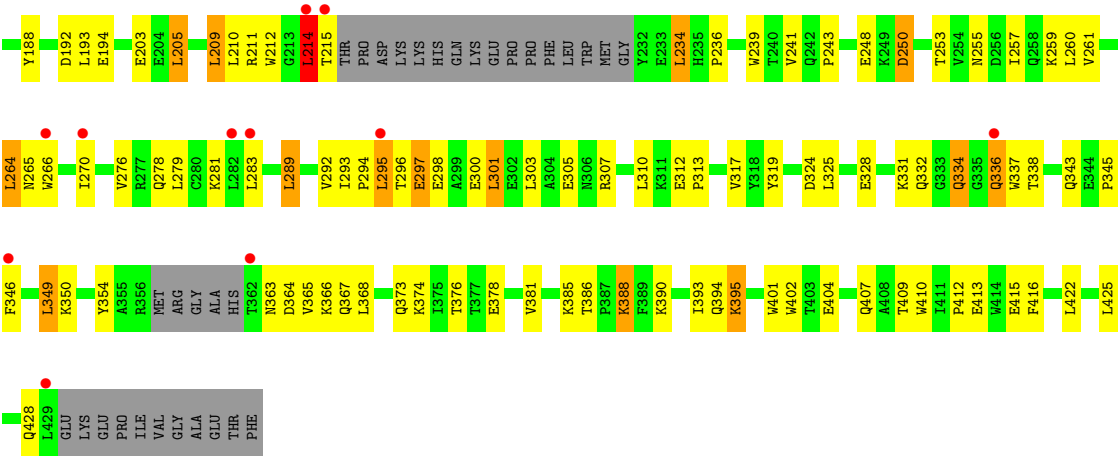
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: p66 Reverse transcriptase



• Molecule 2: p51 Reverse transcriptase





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	119.60Å 153.97Å 153.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.82 – 2.50 29.82 – 2.50	Depositor EDS
% Data completeness (in resolution range)	86.7 (29.82-2.50) 86.7 (29.82-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.11 (at 2.51Å)	Xtriage
Refinement program	CNX 2005	Depositor
R, R_{free}	0.224 , 0.277 0.220 , 0.272	Depositor DCC
R_{free} test set	2135 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.410	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7967	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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: SO4, 65B, CL

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	0.45	0/4618	0.80	2/6276 (0.0%)
2	B	0.45	0/3409	0.81	2/4633 (0.0%)
All	All	0.45	0/8027	0.81	4/10909 (0.0%)

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
2	B	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	54	ASN	CA-C-N	7.63	127.34	119.56
1	A	54	ASN	C-N-CA	7.63	127.34	119.56
2	B	54	ASN	CA-C-N	5.35	126.20	120.47
2	B	54	ASN	C-N-CA	5.35	126.20	120.47

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	91	GLN	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4501	0	4546	204	0
2	B	3317	0	3336	137	0
3	A	28	0	15	3	0
4	A	15	0	0	0	0
4	B	15	0	0	0	0
5	B	1	0	0	0	0
6	A	55	0	0	4	0
6	B	35	0	0	0	0
All	All	7967	0	7897	332	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 21.

All (332) 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:459:THR:HG22	1:A:461:ARG:H	1.23	1.01
2:B:334:GLN:HB2	2:B:336:GLN:HE21	1.29	0.93
1:A:195:ILE:O	1:A:199:ARG:HG3	1.69	0.91
1:A:459:THR:HG22	1:A:461:ARG:N	1.86	0.89
1:A:438:GLU:OE2	1:A:459:THR:HG21	1.77	0.84
1:A:175:ASN:HB3	1:A:178:ILE:HG23	1.61	0.83
1:A:542:ILE:HD11	2:B:261:VAL:HG11	1.61	0.81
1:A:79:GLU:HG3	1:A:83:ARG:NH1	1.98	0.79
1:A:407:GLN:HE21	1:A:407:GLN:HA	1.47	0.78
2:B:388:LYS:HE3	2:B:415:GLU:OE1	1.85	0.76
1:A:217:PRO:HB3	1:A:221:HIS:HE2	1.50	0.76
1:A:459:THR:CG2	1:A:461:ARG:H	1.97	0.76
1:A:8:VAL:HB	1:A:159:ILE:HD13	1.68	0.76
2:B:297:GLU:CD	2:B:298:GLU:H	1.94	0.75
1:A:131:THR:HG22	1:A:143:ARG:HG2	1.70	0.74
1:A:97:PRO:HA	1:A:100:LEU:HD22	1.70	0.74
1:A:199:ARG:HH21	1:A:219:LYS:HB3	1.52	0.74
1:A:175:ASN:HB3	1:A:178:ILE:CG2	2.19	0.73
1:A:120:LEU:HD12	1:A:125:ARG:HG2	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:ASP:O	1:A:83:ARG:HD3	1.89	0.73
1:A:430:GLU:OE2	1:A:530:LYS:HG2	1.89	0.72
2:B:293:ILE:HG23	2:B:294:PRO:HD2	1.73	0.71
2:B:106:VAL:HG13	2:B:234:LEU:HB2	1.73	0.70
1:A:330:GLN:HE21	1:A:338:THR:HG23	1.55	0.69
2:B:295:LEU:H	2:B:295:LEU:HD12	1.57	0.69
1:A:107:THR:HG22	1:A:198:HIS:NE2	2.07	0.68
1:A:26:LEU:HD23	1:A:133:PRO:HG3	1.74	0.68
1:A:162:SER:HB2	2:B:52:PRO:HG3	1.76	0.67
2:B:82:LYS:HD2	2:B:413:GLU:OE1	1.95	0.67
2:B:278:GLN:HG2	2:B:298:GLU:HB3	1.76	0.67
1:A:178:ILE:HD11	1:A:189:VAL:HG13	1.76	0.66
2:B:376:THR:HG23	2:B:386:THR:HG23	1.76	0.66
2:B:91:GLN:HE21	2:B:91:GLN:C	2.04	0.66
1:A:54:ASN:ND2	1:A:56:TYR:H	1.94	0.66
2:B:115:TYR:HB3	2:B:149:LEU:HB2	1.77	0.65
2:B:122:GLU:HA	2:B:125:ARG:HG3	1.78	0.65
1:A:217:PRO:HB3	1:A:221:HIS:NE2	2.12	0.65
2:B:270:ILE:HG12	2:B:346:PHE:HB3	1.79	0.65
1:A:412:PRO:HG3	2:B:401:TRP:CZ2	2.32	0.65
2:B:319:TYR:OH	2:B:385:LYS:HD3	1.97	0.64
1:A:287:LYS:HD2	1:A:291:GLU:CD	2.21	0.64
1:A:224:GLU:HG3	1:A:225:PRO:HD2	1.79	0.64
1:A:412:PRO:HG3	2:B:401:TRP:HZ2	1.61	0.64
1:A:386:THR:HG22	6:A:574:HOH:O	1.98	0.64
2:B:35:VAL:HG23	2:B:36:GLU:N	2.13	0.64
1:A:343:GLN:HG3	1:A:349:LEU:HD11	1.81	0.63
1:A:547:GLN:H	1:A:547:GLN:HE21	1.45	0.63
1:A:395:LYS:HD2	1:A:414:TRP:CH2	2.34	0.62
2:B:88:TRP:CZ2	2:B:154:LYS:HD2	2.35	0.62
2:B:345:PRO:O	2:B:346:PHE:HB2	1.99	0.62
1:A:441:TYR:CE2	1:A:544:GLY:HA3	2.35	0.62
1:A:100:LEU:O	1:A:318:TYR:HB3	1.99	0.61
2:B:241:VAL:O	2:B:243:PRO:HD3	1.99	0.61
2:B:350:LYS:HE2	2:B:378:GLU:OE1	2.00	0.61
2:B:7:THR:HG22	2:B:119:PRO:HB2	1.81	0.61
1:A:547:GLN:HE21	1:A:547:GLN:N	1.99	0.61
1:A:529:GLU:O	1:A:530:LYS:HG3	2.01	0.61
2:B:334:GLN:HB2	2:B:336:GLN:NE2	2.10	0.61
1:A:244:ILE:HD12	1:A:267:ALA:HB2	1.83	0.60
2:B:214:LEU:HD22	2:B:215:THR:N	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:LEU:HD22	1:A:121:ASP:H	1.66	0.60
1:A:520:GLN:O	1:A:523:GLU:HG2	2.02	0.60
1:A:257:ILE:O	1:A:261:VAL:HG23	2.01	0.60
1:A:69:THR:O	1:A:69:THR:HG22	2.02	0.59
1:A:393:ILE:HB	1:A:423:VAL:CG2	2.32	0.59
1:A:451:LYS:HB3	1:A:471:ASP:HA	1.84	0.59
1:A:131:THR:CG2	1:A:143:ARG:HE	2.15	0.59
1:A:2:ILE:HG13	6:A:572:HOH:O	2.02	0.59
2:B:80:LEU:HD22	2:B:84:THR:HG23	1.84	0.59
1:A:330:GLN:NE2	1:A:338:THR:HG23	2.16	0.59
2:B:214:LEU:HD22	2:B:215:THR:H	1.67	0.59
2:B:167:ILE:HG12	2:B:212:TRP:CD2	2.37	0.59
1:A:199:ARG:HH21	1:A:219:LYS:CB	2.16	0.58
1:A:275:LYS:H	1:A:306:ASN:HD21	1.51	0.58
1:A:57:ASN:OD1	1:A:131:THR:HG23	2.04	0.58
1:A:506:ILE:HD12	1:A:506:ILE:N	2.19	0.58
1:A:114:ALA:HB1	1:A:160:PHE:CE1	2.38	0.58
1:A:360:ALA:HA	1:A:514:GLU:OE2	2.04	0.58
1:A:536:VAL:HG13	1:A:542:ILE:HG13	1.85	0.58
2:B:395:LYS:HG2	2:B:416:PHE:CE2	2.39	0.58
1:A:200:THR:O	1:A:204:GLU:HG3	2.03	0.58
2:B:11:LYS:HG2	2:B:12:LEU:O	2.04	0.58
1:A:450:THR:O	1:A:451:LYS:HB2	2.04	0.57
1:A:500:GLN:HG3	2:B:422:LEU:HD12	1.86	0.57
1:A:164:MET:HG3	1:A:168:LEU:HD22	1.86	0.57
1:A:429:LEU:HD11	1:A:506:ILE:HG22	1.86	0.57
1:A:228:LEU:HD22	1:A:242:GLN:HG2	1.86	0.57
2:B:35:VAL:CG2	2:B:36:GLU:N	2.68	0.57
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.87	0.56
2:B:278:GLN:HG2	2:B:298:GLU:CB	2.34	0.56
1:A:224:GLU:HG3	1:A:225:PRO:CD	2.35	0.56
2:B:32:LYS:O	2:B:35:VAL:HG22	2.06	0.56
2:B:301:LEU:HD22	2:B:305:GLU:HG3	1.86	0.56
2:B:13:LYS:HG2	2:B:86:ASP:HB2	1.86	0.56
1:A:129:ALA:HA	1:A:144:TYR:O	2.05	0.56
1:A:402:TRP:CD1	2:B:331:LYS:HZ1	2.24	0.56
2:B:386:THR:CG2	2:B:412:PRO:HB3	2.36	0.56
1:A:315:HIS:HB3	6:A:599:HOH:O	2.04	0.56
2:B:373:GLN:NE2	2:B:407:GLN:H	2.04	0.56
1:A:536:VAL:HG13	1:A:537:PRO:HD2	1.88	0.55
1:A:66:LYS:C	1:A:68:SER:H	2.14	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:TRP:CE3	1:A:403:THR:HG23	2.42	0.55
2:B:332:GLN:HG3	2:B:338:THR:HG23	1.88	0.55
1:A:479:LEU:HB3	1:A:517:LEU:HD13	1.88	0.55
1:A:457:TYR:HA	1:A:548:VAL:HG21	1.89	0.55
1:A:131:THR:HG22	1:A:143:ARG:HE	1.71	0.55
2:B:164:MET:HE2	2:B:168:LEU:HD11	1.89	0.55
1:A:61:PHE:CD1	1:A:61:PHE:N	2.75	0.55
2:B:104:LYS:HE2	2:B:192:ASP:HB3	1.89	0.55
1:A:175:ASN:HD21	1:A:201:LYS:NZ	2.05	0.54
2:B:373:GLN:HE22	2:B:407:GLN:H	1.53	0.54
2:B:401:TRP:O	2:B:404:GLU:HB2	2.07	0.54
2:B:210:LEU:HD12	2:B:211:ARG:HH11	1.72	0.54
2:B:297:GLU:OE2	2:B:298:GLU:HG3	2.07	0.54
1:A:426:TRP:HB3	1:A:526:ILE:HD12	1.88	0.54
2:B:97:PRO:HG2	2:B:181:TYR:HB2	1.88	0.54
1:A:226:PRO:HB3	1:A:235:HIS:CE1	2.41	0.54
1:A:156:SER:HB2	1:A:157:PRO:HD3	1.89	0.54
2:B:13:LYS:HE2	2:B:16:MET:HE1	1.90	0.54
1:A:178:ILE:HD11	1:A:189:VAL:CG1	2.38	0.54
1:A:388:LYS:HD2	1:A:388:LYS:N	2.21	0.54
1:A:447:ASN:HB3	1:A:450:THR:HB	1.90	0.54
1:A:517:LEU:HA	1:A:520:GLN:HE21	1.73	0.53
1:A:307:ARG:O	1:A:311:LYS:HG2	2.09	0.53
2:B:65:LYS:HG2	2:B:72:ARG:HB2	1.91	0.53
2:B:125:ARG:HD3	2:B:147:ASN:HA	1.91	0.53
1:A:54:ASN:HD22	1:A:56:TYR:H	1.56	0.53
1:A:469:LEU:HD22	1:A:480:GLN:HG3	1.90	0.53
2:B:100:LEU:HG	2:B:381:VAL:HG13	1.90	0.53
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.89	0.53
1:A:26:LEU:CD2	1:A:133:PRO:HG3	2.38	0.53
1:A:260:LEU:CD1	1:A:279:LEU:HD13	2.39	0.52
1:A:27:THR:O	1:A:31:ILE:HG13	2.09	0.52
2:B:24:TRP:CZ3	2:B:61:PHE:CD1	2.97	0.52
1:A:459:THR:CG2	1:A:460:ASN:N	2.72	0.52
1:A:509:GLN:N	1:A:510:PRO:HD3	2.24	0.52
2:B:317:VAL:HG12	2:B:349:LEU:HD13	1.91	0.52
2:B:303:LEU:O	2:B:307:ARG:HG3	2.10	0.52
1:A:501:TYR:CZ	1:A:505:ILE:HD11	2.45	0.52
1:A:550:LYS:HG3	1:A:551:LEU:N	2.24	0.52
2:B:61:PHE:CE2	2:B:74:LEU:HD13	2.45	0.52
1:A:139:THR:OG1	1:A:140:PRO:HD2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:LYS:HD2	1:A:426:TRP:CH2	2.45	0.52
1:A:182:GLN:HG2	6:A:577:HOH:O	2.11	0.51
1:A:224:GLU:HG3	1:A:225:PRO:N	2.25	0.51
1:A:542:ILE:O	1:A:543:GLY:C	2.51	0.51
1:A:77:PHE:O	1:A:78:ARG:C	2.54	0.51
1:A:91:GLN:NE2	1:A:183:TYR:CD1	2.78	0.51
1:A:178:ILE:HD12	1:A:190:GLY:O	2.10	0.51
2:B:61:PHE:CZ	2:B:402:TRP:HH2	2.29	0.51
1:A:100:LEU:HG	3:A:561:65B:C11	2.41	0.51
1:A:218:ASP:H	1:A:221:HIS:CE1	2.28	0.51
1:A:331:LYS:HB3	1:A:421:PRO:HG2	1.93	0.51
2:B:260:LEU:HD21	2:B:303:LEU:HD13	1.93	0.51
1:A:178:ILE:HD12	1:A:179:VAL:N	2.26	0.51
2:B:260:LEU:HG	2:B:279:LEU:HD21	1.92	0.51
1:A:439:THR:HG21	2:B:289:LEU:HD13	1.91	0.51
2:B:328:GLU:HG2	2:B:390:LYS:HD3	1.93	0.50
1:A:60:VAL:HG11	1:A:130:PHE:CD2	2.47	0.50
2:B:253:THR:O	2:B:257:ILE:HG13	2.11	0.50
2:B:61:PHE:CZ	2:B:402:TRP:CH2	3.00	0.50
1:A:188:TYR:HB3	3:A:561:65B:C3	2.42	0.50
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.44	0.50
2:B:257:ILE:HB	2:B:283:LEU:HD21	1.93	0.50
1:A:194:GLU:CD	1:A:194:GLU:H	2.18	0.49
2:B:324:ASP:O	2:B:343:GLN:HG2	2.12	0.49
2:B:91:GLN:C	2:B:91:GLN:NE2	2.70	0.49
1:A:369:THR:HG1	1:A:398:TRP:HZ3	1.60	0.49
2:B:13:LYS:HD2	2:B:85:GLN:HB3	1.95	0.49
1:A:291:GLU:HG3	1:A:292:VAL:N	2.28	0.49
1:A:303:LEU:HD12	1:A:303:LEU:O	2.12	0.49
1:A:502:ALA:O	1:A:506:ILE:HD13	2.12	0.49
1:A:114:ALA:HB1	1:A:160:PHE:CZ	2.48	0.48
2:B:61:PHE:CD1	2:B:61:PHE:N	2.81	0.48
2:B:334:GLN:N	2:B:334:GLN:CD	2.70	0.48
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.95	0.48
1:A:162:SER:CB	2:B:52:PRO:HG3	2.41	0.48
1:A:515:SER:HB3	1:A:518:VAL:HB	1.94	0.48
2:B:106:VAL:HG12	2:B:236:PRO:HD3	1.94	0.48
2:B:122:GLU:HG3	2:B:125:ARG:CZ	2.43	0.48
1:A:53:GLU:O	1:A:55:PRO:HD3	2.14	0.48
1:A:96:HIS:ND1	1:A:97:PRO:HD2	2.28	0.48
1:A:426:TRP:HB3	1:A:526:ILE:CD1	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:312:GLU:HB3	2:B:313:PRO:HD2	1.95	0.48
1:A:409:THR:O	2:B:364:ASP:HB2	2.14	0.48
2:B:185:ASP:OD2	2:B:409:THR:HG21	2.14	0.48
1:A:332:GLN:O	1:A:333:GLY:C	2.55	0.48
2:B:264:LEU:HB3	2:B:276:VAL:HG12	1.94	0.48
1:A:175:ASN:O	1:A:178:ILE:HG23	2.14	0.48
2:B:295:LEU:H	2:B:295:LEU:CD1	2.20	0.48
2:B:94:ILE:N	2:B:94:ILE:HD12	2.29	0.48
1:A:329:ILE:HD11	1:A:375:ILE:HD12	1.95	0.47
1:A:66:LYS:O	1:A:67:ASP:HB3	2.14	0.47
1:A:131:THR:HG22	1:A:143:ARG:CG	2.40	0.47
1:A:271:TYR:CZ	1:A:314:VAL:HG22	2.49	0.47
2:B:132:ILE:HB	2:B:142:ILE:HG12	1.96	0.47
2:B:255:ASN:HD21	2:B:259:LYS:NZ	2.12	0.47
2:B:312:GLU:HB3	2:B:313:PRO:CD	2.44	0.47
1:A:505:ILE:HB	1:A:506:ILE:HD12	1.96	0.47
1:A:345:PRO:HA	1:A:346:PHE:HA	1.54	0.47
2:B:80:LEU:HD13	2:B:153:TRP:CD1	2.49	0.47
1:A:287:LYS:HD2	1:A:291:GLU:OE1	2.14	0.47
2:B:293:ILE:CG2	2:B:294:PRO:HD2	2.42	0.47
1:A:298:GLU:H	1:A:298:GLU:CD	2.22	0.47
2:B:266:TRP:CZ3	2:B:346:PHE:CZ	3.02	0.47
1:A:194:GLU:O	1:A:196:GLY:N	2.48	0.47
1:A:319:TYR:CE1	1:A:325:LEU:HD11	2.50	0.47
1:A:91:GLN:NE2	1:A:183:TYR:CE1	2.83	0.47
1:A:98:ALA:HB2	1:A:350:LYS:HB3	1.97	0.47
1:A:369:THR:OG1	1:A:398:TRP:HZ3	1.97	0.47
2:B:94:ILE:HD12	2:B:94:ILE:H	1.79	0.47
2:B:236:PRO:HA	2:B:239:TRP:CE2	2.49	0.47
2:B:295:LEU:HD12	2:B:295:LEU:N	2.28	0.47
2:B:325:LEU:HD12	2:B:385:LYS:HG3	1.97	0.46
2:B:337:TRP:HE1	2:B:367:GLN:HE21	1.61	0.46
2:B:24:TRP:HZ3	2:B:61:PHE:CD1	2.33	0.46
1:A:228:LEU:HD22	1:A:242:GLN:CG	2.45	0.46
1:A:54:ASN:HD22	1:A:54:ASN:C	2.23	0.46
1:A:195:ILE:HD11	1:A:199:ARG:HD2	1.97	0.46
1:A:286:THR:HG23	1:A:286:THR:O	2.16	0.46
1:A:523:GLU:CG	1:A:524:GLN:N	2.78	0.46
2:B:27:THR:OG1	2:B:30:LYS:HG3	2.16	0.46
1:A:514:GLU:H	1:A:514:GLU:HG2	1.46	0.46
1:A:60:VAL:HG12	1:A:75:VAL:HG22	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:ILE:HD12	1:A:179:VAL:H	1.81	0.46
1:A:536:VAL:CG1	1:A:542:ILE:HG13	2.45	0.46
1:A:548:VAL:O	1:A:548:VAL:HG22	2.16	0.46
2:B:35:VAL:O	2:B:36:GLU:C	2.59	0.46
1:A:452:LEU:HD23	1:A:453:GLY:N	2.31	0.45
1:A:458:VAL:HG23	1:A:548:VAL:HB	1.98	0.45
3:A:561:65B:H26	3:A:561:65B:N12	2.32	0.45
2:B:301:LEU:HD21	2:B:305:GLU:OE1	2.17	0.45
1:A:169:GLU:HB3	1:A:170:PRO:HD3	1.97	0.45
1:A:397:THR:HG21	1:A:424:LYS:HA	1.98	0.45
2:B:35:VAL:CG2	2:B:36:GLU:H	2.29	0.45
1:A:164:MET:O	1:A:168:LEU:HB2	2.15	0.45
2:B:214:LEU:HD22	2:B:215:THR:HG22	1.97	0.45
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.51	0.45
1:A:452:LEU:HD23	1:A:452:LEU:C	2.42	0.45
2:B:214:LEU:HD13	2:B:214:LEU:C	2.41	0.45
2:B:393:ILE:HG12	2:B:394:GLN:N	2.32	0.45
1:A:301:LEU:O	1:A:304:ALA:HB3	2.17	0.45
1:A:79:GLU:HG3	1:A:83:ARG:HH12	1.78	0.45
1:A:442:VAL:HG21	1:A:482:ILE:HD13	1.97	0.45
1:A:65:LYS:CE	1:A:72:ARG:HH11	2.30	0.44
1:A:328:GLU:HG2	1:A:390:LYS:HB2	1.99	0.44
2:B:180:ILE:HA	2:B:188:TYR:O	2.17	0.44
1:A:319:TYR:HE1	1:A:325:LEU:HD11	1.82	0.44
2:B:260:LEU:CD2	2:B:279:LEU:HD21	2.47	0.44
1:A:433:PRO:HG3	2:B:255:ASN:OD1	2.17	0.44
2:B:154:LYS:HA	2:B:184:MET:HE3	1.99	0.44
2:B:205:LEU:HD22	2:B:209:LEU:HD22	2.00	0.44
2:B:61:PHE:CZ	2:B:74:LEU:HD13	2.53	0.44
1:A:260:LEU:HD13	1:A:264:LEU:HD22	1.99	0.44
1:A:10:VAL:HG12	1:A:11:LYS:N	2.32	0.44
1:A:34:LEU:HA	1:A:34:LEU:HD12	1.78	0.44
1:A:79:GLU:HG3	1:A:83:ARG:HH11	1.78	0.44
1:A:91:GLN:HE22	1:A:183:TYR:HD1	1.63	0.44
1:A:194:GLU:CD	1:A:194:GLU:N	2.76	0.44
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.99	0.44
1:A:442:VAL:O	1:A:443:ASP:HB2	2.16	0.44
1:A:459:THR:HG22	1:A:460:ASN:N	2.33	0.44
1:A:511:ASP:OD1	1:A:511:ASP:C	2.61	0.43
1:A:450:THR:HG22	1:A:452:LEU:HB2	2.00	0.43
1:A:484:LEU:HD23	1:A:484:LEU:HA	1.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:517:LEU:O	1:A:520:GLN:HB2	2.18	0.43
2:B:47:ILE:HD12	2:B:144:TYR:CD1	2.53	0.43
2:B:142:ILE:HG12	2:B:142:ILE:H	1.73	0.43
2:B:214:LEU:CD2	2:B:215:THR:HG22	2.48	0.43
1:A:41:MET:HE2	1:A:47:ILE:HG23	1.99	0.43
2:B:386:THR:HG21	2:B:412:PRO:HB3	2.00	0.43
1:A:80:LEU:HD13	1:A:153:TRP:CD1	2.53	0.43
1:A:63:ILE:CD1	1:A:74:LEU:HD12	2.48	0.43
1:A:440:PHE:CE1	1:A:489:SER:HB3	2.54	0.43
1:A:469:LEU:CD2	1:A:480:GLN:HG3	2.48	0.43
2:B:289:LEU:HD12	2:B:289:LEU:HA	1.71	0.43
1:A:121:ASP:OD2	1:A:121:ASP:C	2.62	0.43
1:A:64:LYS:HB3	1:A:64:LYS:HE2	1.74	0.43
1:A:169:GLU:OE1	1:A:169:GLU:HA	2.18	0.43
1:A:203:GLU:OE2	1:A:219:LYS:HG3	2.18	0.42
2:B:80:LEU:CD2	2:B:84:THR:HG23	2.47	0.42
2:B:346:PHE:N	2:B:346:PHE:HD1	2.17	0.42
2:B:85:GLN:HA	2:B:88:TRP:NE1	2.34	0.42
1:A:148:VAL:O	1:A:150:PRO:HD3	2.19	0.42
1:A:164:MET:HE2	1:A:168:LEU:HD22	2.01	0.42
2:B:376:THR:HG21	2:B:410:TRP:CZ3	2.53	0.42
1:A:441:TYR:CD2	1:A:544:GLY:HA3	2.53	0.42
2:B:279:LEU:C	2:B:281:LYS:N	2.78	0.42
2:B:346:PHE:N	2:B:346:PHE:CD1	2.87	0.42
2:B:363:ASN:HB3	2:B:366:LYS:HB3	2.01	0.42
1:A:39:THR:HG23	1:A:43:LYS:HE2	2.02	0.42
1:A:54:ASN:HA	1:A:55:PRO:HD3	1.78	0.42
1:A:283:LEU:O	1:A:284:ARG:C	2.63	0.42
2:B:28:GLU:HA	2:B:135:ILE:HD11	2.02	0.42
2:B:154:LYS:HA	2:B:184:MET:CE	2.50	0.42
2:B:35:VAL:O	2:B:39:THR:HG23	2.20	0.41
1:A:427:TYR:CE2	1:A:525:LEU:HD13	2.55	0.41
2:B:214:LEU:HD13	2:B:215:THR:C	2.45	0.41
2:B:332:GLN:HB2	2:B:336:GLN:O	2.19	0.41
1:A:283:LEU:HD12	1:A:283:LEU:HA	1.71	0.41
1:A:155:GLY:O	1:A:159:ILE:HG13	2.20	0.41
2:B:169:GLU:N	2:B:170:PRO:HD2	2.35	0.41
1:A:11:LYS:HB3	1:A:11:LYS:HE2	1.83	0.41
1:A:131:THR:HG22	1:A:143:ARG:NE	2.36	0.41
2:B:24:TRP:CZ3	2:B:61:PHE:CE1	3.08	0.41
1:A:199:ARG:NH2	1:A:219:LYS:HB3	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:GLU:CG	1:A:225:PRO:HD2	2.50	0.41
1:A:409:THR:OG1	1:A:410:TRP:N	2.53	0.41
2:B:354:TYR:HD2	2:B:374:LYS:HD2	1.84	0.41
2:B:425:LEU:HD12	2:B:428:GLN:NE2	2.36	0.41
1:A:326:ILE:HD12	1:A:326:ILE:N	2.35	0.41
1:A:392:PRO:O	1:A:423:VAL:HG22	2.21	0.41
1:A:547:GLN:N	1:A:547:GLN:NE2	2.67	0.41
2:B:37:ILE:O	2:B:41:MET:HG3	2.21	0.41
2:B:301:LEU:HD13	2:B:301:LEU:C	2.46	0.41
1:A:164:MET:HE2	1:A:168:LEU:CD2	2.50	0.41
1:A:33:ALA:O	1:A:37:ILE:HG12	2.20	0.40
1:A:66:LYS:C	1:A:68:SER:N	2.79	0.40
2:B:373:GLN:HE22	2:B:407:GLN:N	2.18	0.40
2:B:88:TRP:CE2	2:B:154:LYS:HD2	2.56	0.40
2:B:279:LEU:C	2:B:281:LYS:H	2.29	0.40
1:A:88:TRP:CE3	1:A:88:TRP:HA	2.57	0.40
2:B:13:LYS:HB2	2:B:16:MET:SD	2.61	0.40
1:A:139:THR:OG1	1:A:140:PRO:CD	2.69	0.40
1:A:358:ARG:HD3	1:A:370:GLU:CD	2.46	0.40
1:A:450:THR:CG2	1:A:452:LEU:HB2	2.51	0.40
1:A:470:THR:O	1:A:471:ASP:C	2.64	0.40
2:B:42:GLU:HG3	2:B:43:LYS:N	2.36	0.40
1:A:325:LEU:HD12	1:A:343:GLN:HG2	2.02	0.40
2:B:58:THR:HA	2:B:59:PRO:HD3	1.86	0.40
2:B:154:LYS:HG2	2:B:184:MET:CE	2.52	0.40
2:B:296:THR:O	2:B:300:GLU:HG3	2.21	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	550/560 (98%)	518 (94%)	27 (5%)	5 (1%)	14	27
2	B	393/440 (89%)	374 (95%)	15 (4%)	4 (1%)	12	24
All	All	943/1000 (94%)	892 (95%)	42 (4%)	9 (1%)	12	24

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	543	GLY
1	A	90	VAL
1	A	412	PRO
2	B	85	GLN
2	B	250	ASP
2	B	90	VAL
2	B	214	LEU
1	A	443	ASP
1	A	493	VAL

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	494/500 (99%)	442 (90%)	52 (10%)	6	14
2	B	365/400 (91%)	327 (90%)	38 (10%)	7	14
All	All	859/900 (95%)	769 (90%)	90 (10%)	6	14

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	34	LEU
1	A	54	ASN
1	A	61	PHE
1	A	64	LYS
1	A	73	LYS
1	A	79	GLU

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Mol	Chain	Res	Type
1	A	80	LEU
1	A	94	ILE
1	A	100	LEU
1	A	102	LYS
1	A	105	SER
1	A	107	THR
1	A	110	ASP
1	A	126	LYS
1	A	137	ASN
1	A	159	ILE
1	A	168	LEU
1	A	178	ILE
1	A	194	GLU
1	A	207	GLN
1	A	209	LEU
1	A	218	ASP
1	A	234	LEU
1	A	264	LEU
1	A	280	CYS
1	A	282	LEU
1	A	283	LEU
1	A	289	LEU
1	A	297	GLU
1	A	301	LEU
1	A	312	GLU
1	A	317	VAL
1	A	325	LEU
1	A	330	GLN
1	A	331	LYS
1	A	344	GLU
1	A	357	MET
1	A	362	THR
1	A	373	GLN
1	A	374	LYS
1	A	402	TRP
1	A	407	GLN
1	A	432	GLU
1	A	448	ARG
1	A	479	LEU
1	A	491	LEU
1	A	514	GLU
1	A	517	LEU

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Mol	Chain	Res	Type
1	A	529	GLU
1	A	539	HIS
1	A	547	GLN
2	B	40	GLU
2	B	49	LYS
2	B	65	LYS
2	B	73	LYS
2	B	74	LEU
2	B	80	LEU
2	B	91	GLN
2	B	92	LEU
2	B	101	LYS
2	B	105	SER
2	B	106	VAL
2	B	113	ASP
2	B	142	ILE
2	B	184	MET
2	B	193	LEU
2	B	194	GLU
2	B	203	GLU
2	B	205	LEU
2	B	209	LEU
2	B	214	LEU
2	B	234	LEU
2	B	248	GLU
2	B	250	ASP
2	B	264	LEU
2	B	265	ASN
2	B	289	LEU
2	B	292	VAL
2	B	295	LEU
2	B	297	GLU
2	B	301	LEU
2	B	310	LEU
2	B	334	GLN
2	B	336	GLN
2	B	349	LEU
2	B	365	VAL
2	B	368	LEU
2	B	388	LYS
2	B	395	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	151	GLN
1	A	161	GLN
1	A	174	GLN
1	A	175	ASN
1	A	222	GLN
1	A	242	GLN
1	A	258	GLN
1	A	306	ASN
1	A	330	GLN
1	A	340	GLN
1	A	373	GLN
1	A	464	GLN
1	A	474	ASN
1	A	480	GLN
1	A	512	GLN
1	A	520	GLN
1	A	547	GLN
2	B	85	GLN
2	B	91	GLN
2	B	147	ASN
2	B	151	GLN
2	B	161	GLN
2	B	242	GLN
2	B	255	ASN
2	B	258	GLN
2	B	269	GLN
2	B	336	GLN
2	B	348	ASN
2	B	367	GLN
2	B	373	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	563	-	4,4,4	0.40	0	6,6,6	0.15	0
4	SO4	B	441	-	4,4,4	0.38	0	6,6,6	0.10	0
4	SO4	A	564	-	4,4,4	0.37	0	6,6,6	0.07	0
4	SO4	A	562	-	4,4,4	0.35	0	6,6,6	0.28	0
4	SO4	B	442	-	4,4,4	0.36	0	6,6,6	0.13	0
4	SO4	B	443	-	4,4,4	1.17	0	6,6,6	0.51	0
3	65B	A	561	-	30,30,30	2.67	14 (46%)	40,42,42	1.84	5 (12%)

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	65B	A	561	-	-	0/12/12/12	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	561	65B	C15-N16	5.80	1.42	1.35
3	A	561	65B	C13-N12	5.23	1.39	1.32
3	A	561	65B	C1-C6	4.29	1.47	1.40
3	A	561	65B	C3-C2	4.02	1.45	1.39
3	A	561	65B	C1-C2	3.97	1.47	1.40
3	A	561	65B	C26-C21	3.97	1.45	1.39
3	A	561	65B	C13-C14	3.42	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	561	65B	C22-C21	3.13	1.44	1.39
3	A	561	65B	C26-C25	3.08	1.43	1.38
3	A	561	65B	C23-C22	2.92	1.43	1.38
3	A	561	65B	C6'-C6	2.33	1.55	1.51
3	A	561	65B	C15-C14	2.24	1.45	1.40
3	A	561	65B	C4-C4'	-2.23	1.39	1.44
3	A	561	65B	C11-N16	2.17	1.40	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	561	65B	C11-N16-C15	5.64	121.17	116.59
3	A	561	65B	O17-C13-C14	5.02	121.12	117.89
3	A	561	65B	N16-C11-N12	-4.75	118.47	126.26
3	A	561	65B	C11-N12-C13	4.22	122.64	115.38
3	A	561	65B	C14-C13-N12	-2.97	120.58	123.78

There are no chirality outliers.

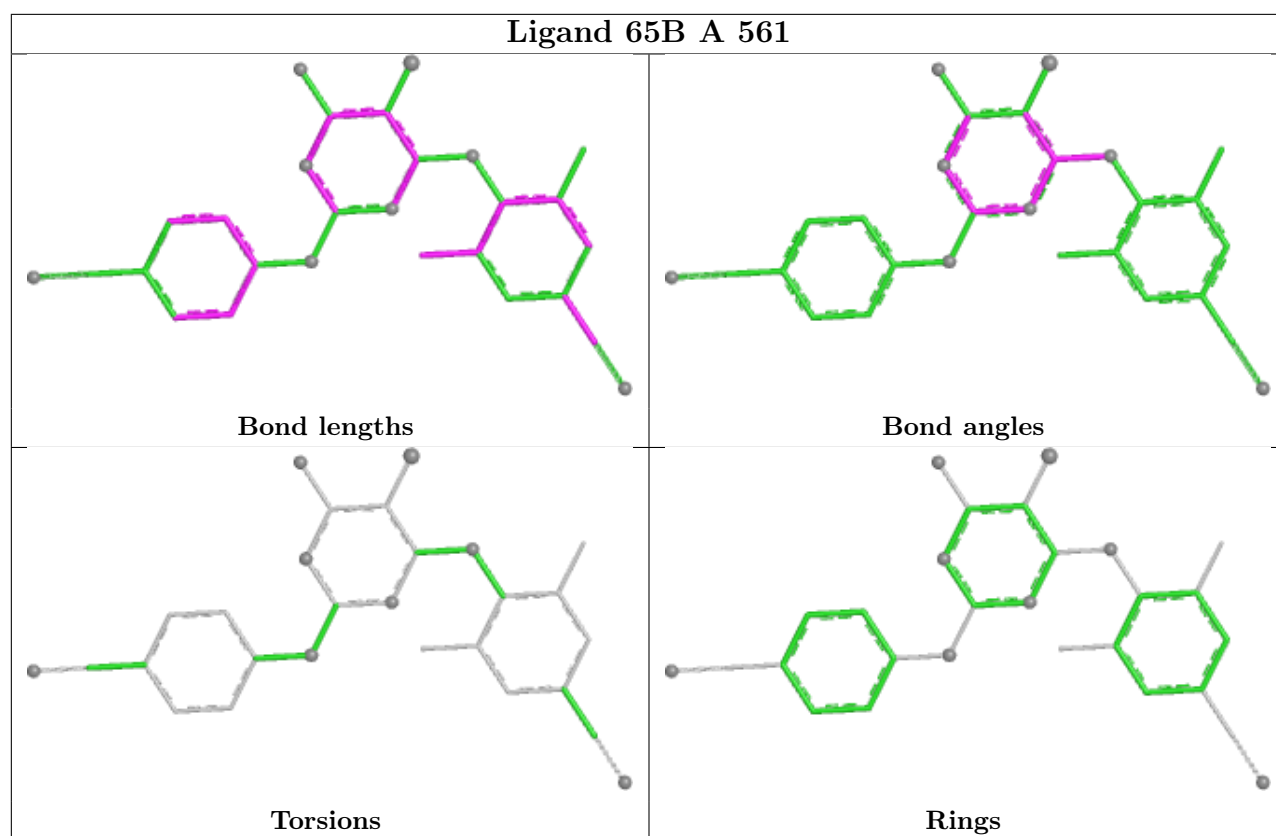
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	561	65B	3	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å ²)	Q < 0.9
1	A	552/560 (98%)	0.17	18 (3%)	49	45	31, 56, 93, 121	0
2	B	401/440 (91%)	0.10	14 (3%)	47	42	32, 53, 87, 108	0
All	All	953/1000 (95%)	0.14	32 (3%)	48	43	31, 55, 90, 121	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	551	LEU	5.1
1	A	92	LEU	4.6
2	B	295	LEU	4.1
2	B	215	THR	3.6
2	B	88	TRP	3.5
2	B	87	PHE	3.5
2	B	214	LEU	3.4
2	B	429	LEU	3.0
1	A	552	VAL	2.9
1	A	548	VAL	2.8
1	A	217	PRO	2.7
2	B	362	THR	2.7
2	B	282	LEU	2.6
2	B	283	LEU	2.6
1	A	222	GLN	2.6
1	A	549	ASP	2.6
2	B	266	TRP	2.5
1	A	90	VAL	2.5
2	B	92	LEU	2.5
1	A	24	TRP	2.5
1	A	66	LYS	2.4
1	A	446	ALA	2.4
1	A	550	LYS	2.4
2	B	336	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	270	ILE	2.3
2	B	346	PHE	2.3
1	A	65	LYS	2.2
1	A	91	GLN	2.2
1	A	357	MET	2.2
1	A	52	PRO	2.1
1	A	445	ALA	2.0
1	A	60	VAL	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

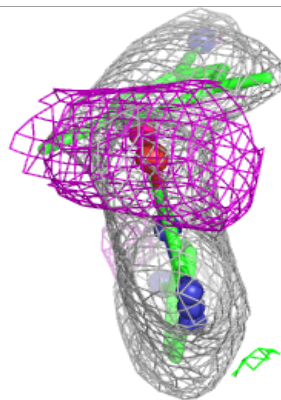
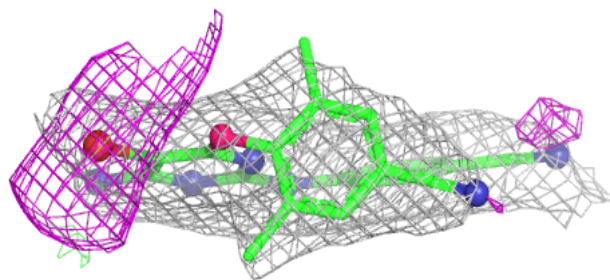
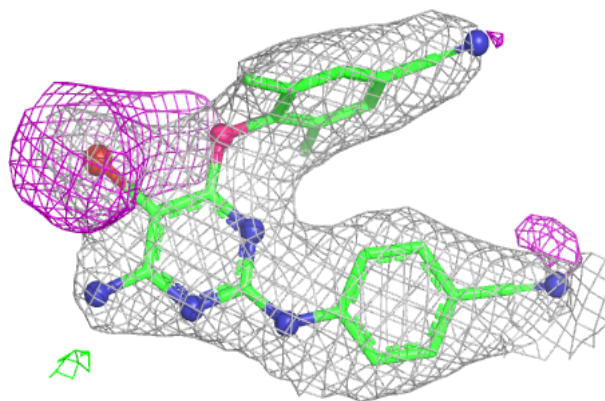
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	B	441	5/5	0.74	0.14	134,135,135,135	0
4	SO4	A	564	5/5	0.77	0.11	123,123,124,124	0
4	SO4	B	443	5/5	0.81	0.19	95,95,96,96	0
3	65B	A	561	28/28	0.82	0.14	42,46,58,89	0
4	SO4	A	563	5/5	0.89	0.12	70,71,73,73	0
5	CL	B	444	1/1	0.90	0.10	68,68,68,68	0
4	SO4	B	442	5/5	0.91	0.09	92,93,93,94	0
4	SO4	A	562	5/5	0.94	0.08	71,72,73,76	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 65B A 561:

$2mF_o-DF_c$ (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.