



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:53 PM UTC

PDB ID : 1ARH / pdb_00001arh
Title : ASPARTATE AMINOTRANSFERASE, Y225R/R386A MUTANT
Authors : Malashkevich, V.N.; Jansonius, J.N.
Deposited on : 1995-08-23
Resolution : 2.30 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

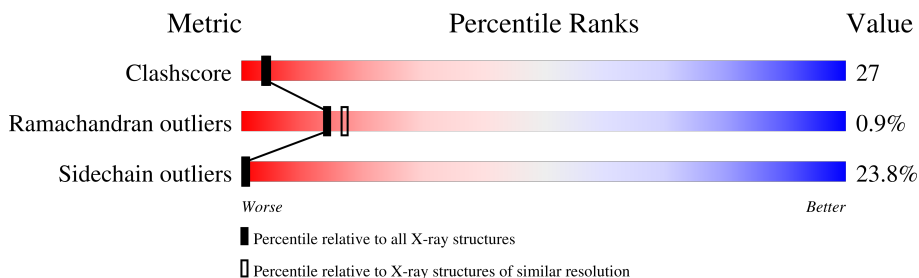
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	396	
1	B	396	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6543 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.

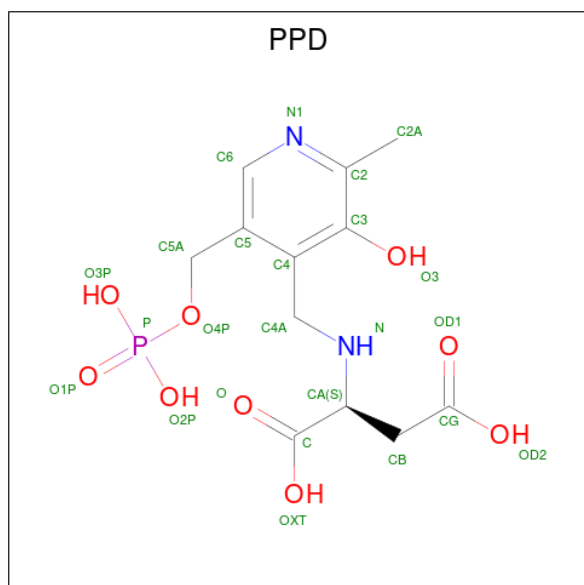
- Molecule 1 is a protein called ASPARTATE AMINOTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	396	Total	C	N	O	S	0	0	0
			3062	1930	536	583	13			
1	B	396	Total	C	N	O	S	0	0	0
			3062	1930	536	583	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	225	ARG	TYR	engineered mutation	UNP P00509
A	386	ALA	ARG	engineered mutation	UNP P00509
B	225	ARG	TYR	engineered mutation	UNP P00509
B	386	ALA	ARG	engineered mutation	UNP P00509

- Molecule 2 is 2-[(3-HYDROXY-2-METHYL-5-PHOSPHONOOXYMETHYL-PYRIDIN-4-YLMETHYLENE)-AMINO]-SUCCINIC ACID (CCD ID: PPD) (formula: C₁₂H₁₇N₂O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 24	C 12	N 2	O 9	P 1	0	0
2	B	1	Total 24	C 12	N 2	O 9	P 1	0	0

- Molecule 3 is water.

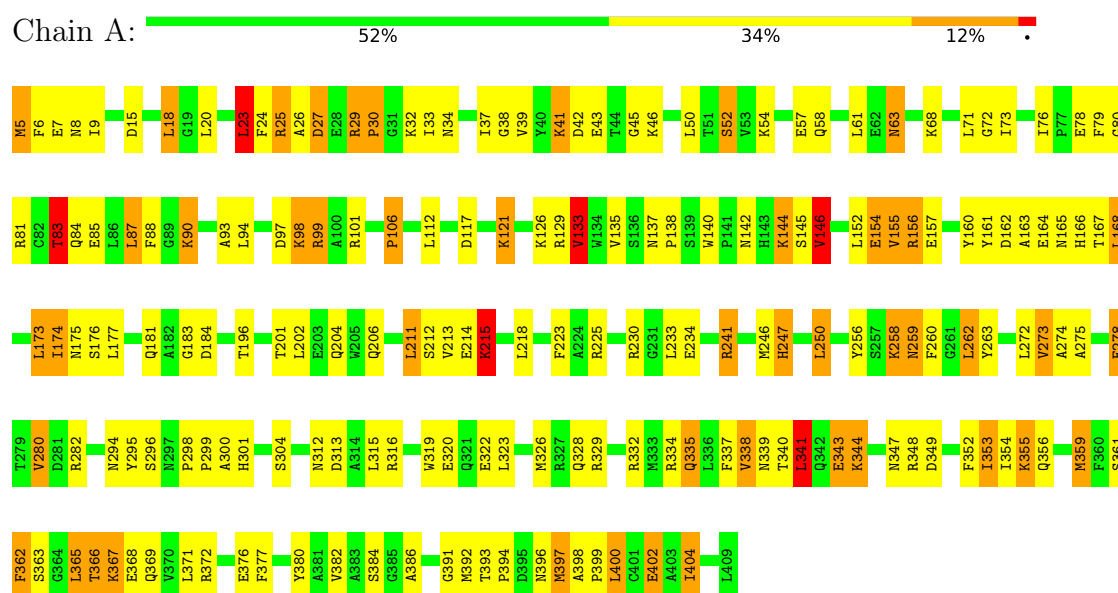
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	192	Total 192	O 192	0	0
3	B	179	Total 179	O 179	0	0

3 Residue-property plots

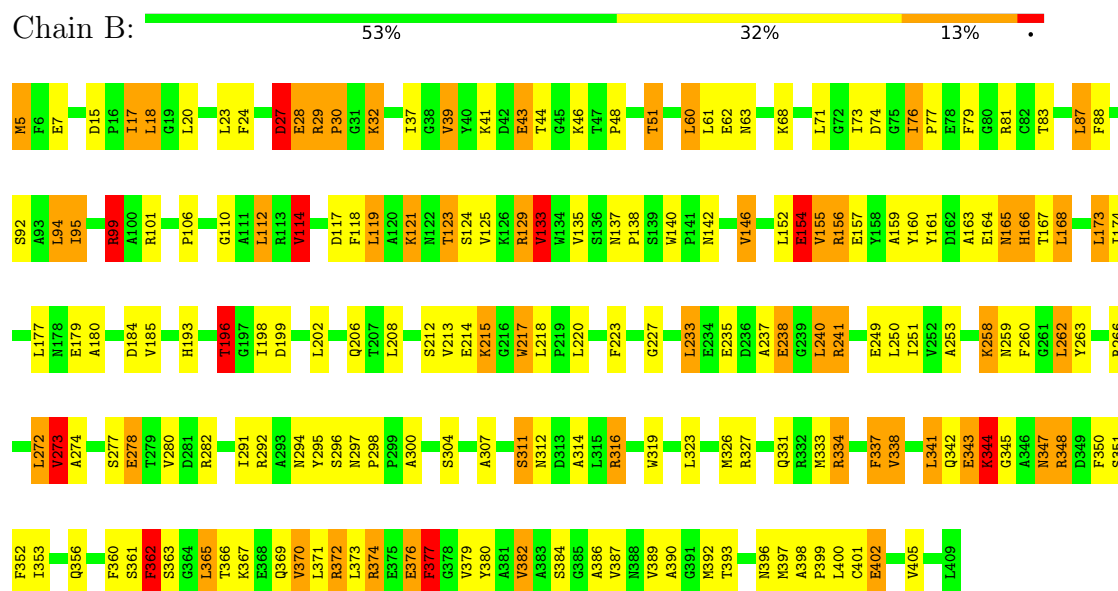
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: ASPARTATE AMINOTRANSFERASE



• Molecule 1: ASPARTATE AMINOTRANSFERASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.12Å 79.61Å 89.85Å 90.00° 117.91° 90.00°	Depositor
Resolution (Å)	8.00 – 2.30	Depositor
% Data completeness (in resolution range)	96.2 (8.00-2.30)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT 4C	Depositor
R, R_{free}	0.219 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6543	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PPD

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	0.98	0/3122	1.49	32/4229 (0.8%)
1	B	0.99	0/3122	1.46	25/4229 (0.6%)
All	All	0.98	0/6244	1.48	57/8458 (0.7%)

There are no bond length outliers.

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	376	GLU	CB-CA-C	-9.53	94.79	110.79
1	B	27	ASP	CA-CB-CG	9.06	121.66	112.60
1	A	377	PHE	N-CA-C	8.04	123.44	112.90
1	A	404	ILE	N-CA-CB	7.97	121.37	110.54
1	A	273	VAL	N-CA-CB	7.55	121.83	111.41
1	B	300	ALA	N-CA-C	7.38	118.97	111.07
1	A	300	ALA	N-CA-C	7.26	118.98	111.14
1	A	298	PRO	N-CA-C	7.14	119.41	110.70
1	B	377	PHE	CB-CA-C	-6.93	98.81	110.44
1	A	377	PHE	N-CA-CB	6.89	120.66	110.33
1	B	106	PRO	N-CA-CB	6.87	107.32	102.65
1	B	199	ASP	CA-CB-CG	6.86	119.45	112.60
1	A	250	LEU	N-CA-CB	-6.80	100.20	111.69
1	A	146	VAL	N-CA-CB	6.77	118.47	110.55
1	B	337	PHE	CA-CB-CG	6.49	120.29	113.80
1	B	114	VAL	N-CA-CB	6.33	120.07	110.58
1	A	63	ASN	N-CA-C	6.19	121.11	113.50
1	B	362	PHE	CA-CB-CG	6.16	119.96	113.80
1	B	166	HIS	CA-CB-CG	-6.15	107.65	113.80
1	B	27	ASP	CB-CA-C	6.01	118.63	110.94
1	A	88	PHE	N-CA-C	5.97	120.64	113.23
1	A	71	LEU	N-CA-C	-5.97	102.83	110.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	273	VAL	N-CA-CB	5.95	119.62	111.41
1	B	99	ARG	N-CA-CB	-5.95	101.34	110.44
1	A	83	THR	N-CA-CB	5.84	118.47	110.01
1	B	154	GLU	N-CA-CB	5.83	120.13	110.63
1	B	29	ARG	N-CA-C	-5.83	102.55	110.36
1	A	42	ASP	CA-CB-CG	5.82	118.42	112.60
1	A	312	ASN	CA-CB-CG	-5.81	106.79	112.60
1	B	88	PHE	N-CA-C	5.75	120.43	113.41
1	A	133	VAL	N-CA-CB	5.73	119.32	111.41
1	B	217	TRP	CA-CB-CG	5.71	124.46	113.60
1	A	341	LEU	N-CA-C	-5.69	104.98	111.07
1	A	196	THR	N-CA-C	5.61	119.30	112.23
1	A	247	HIS	CA-CB-CG	-5.60	108.20	113.80
1	A	280	VAL	N-CA-CB	5.57	118.11	110.54
1	A	106	PRO	N-CA-CB	5.54	106.42	102.65
1	B	63	ASN	N-CA-C	5.54	120.16	113.41
1	B	259	ASN	N-CA-C	5.47	119.46	112.34
1	B	196	THR	N-CA-C	5.47	119.13	112.23
1	B	133	VAL	N-CA-CB	5.47	118.96	111.41
1	B	146	VAL	N-CA-CB	5.36	116.82	110.55
1	B	298	PRO	N-CA-C	5.33	117.21	110.70
1	A	348	ARG	N-CA-C	-5.30	100.05	109.06
1	B	297	ASN	CB-CA-C	5.30	118.18	109.97
1	A	259	ASN	N-CA-C	5.29	117.79	111.71
1	A	27	ASP	N-CA-C	-5.28	101.55	109.15
1	B	71	LEU	N-CA-C	-5.26	102.73	110.52
1	A	58	GLN	N-CA-C	-5.24	105.48	111.14
1	A	215	LYS	N-CA-C	5.22	119.70	113.23
1	A	175	ASN	N-CA-CB	5.20	117.85	110.16
1	A	313	ASP	N-CA-C	5.10	117.50	111.33
1	A	397	MET	N-CA-C	5.09	116.52	111.07
1	A	23	LEU	N-CA-CB	5.09	118.17	110.28
1	B	51	THR	N-CA-CB	5.05	118.08	110.30
1	A	72	GLY	N-CA-C	-5.03	105.88	112.82
1	A	280	VAL	CB-CA-C	-5.03	105.35	112.14

There are no chirality outliers.

There are no planarity outliers.

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	3062	0	3014	163	0
1	B	3062	0	3014	180	0
2	A	24	0	12	0	0
2	B	24	0	12	2	0
3	A	192	0	0	10	0
3	B	179	0	0	7	0
All	All	6543	0	6052	333	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 (333) 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:344:LYS:HD2	1:B:402:GLU:HG3	1.24	1.16
1:A:183:GLY:HA2	1:B:5:MET:HE1	1.37	1.06
1:B:260:PHE:HB3	1:B:262:LEU:HD22	1.40	1.02
1:A:201:THR:H	1:A:204:GLN:HE21	1.08	1.01
1:A:201:THR:H	1:A:204:GLN:NE2	1.69	0.89
1:B:344:LYS:CD	1:B:402:GLU:HG3	2.03	0.88
1:B:24:PHE:CZ	1:B:32:LYS:HE3	2.10	0.87
1:A:352:PHE:HA	1:A:355:LYS:HD3	1.60	0.83
1:A:260:PHE:HB3	1:A:262:LEU:HD22	1.58	0.83
1:A:397:MET:HE3	1:A:400:LEU:HD23	1.62	0.82
1:A:41:LYS:HD2	1:A:45:GLY:C	2.04	0.82
1:B:29:ARG:HB3	1:B:30:PRO:HD2	1.62	0.81
1:A:183:GLY:CA	1:B:5:MET:HE1	2.11	0.80
1:B:123:THR:CG2	1:B:125:VAL:H	1.94	0.79
1:A:156:ARG:NH1	1:A:156:ARG:HA	1.96	0.79
1:A:41:LYS:HD2	1:A:45:GLY:HA2	1.65	0.79
1:B:331:GLN:NE2	3:B:571:HOH:O	2.16	0.78
1:A:24:PHE:CE1	1:A:34:ASN:HB2	2.18	0.78
1:A:202:LEU:O	1:A:206:GLN:HG3	1.83	0.77
1:B:196:THR:CG2	1:B:198:ILE:H	1.97	0.77
1:B:164:GLU:C	1:B:165:ASN:HD22	1.94	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:ILE:HD13	1:A:211:LEU:CD2	2.17	0.75
1:B:344:LYS:HE2	1:B:344:LYS:O	1.87	0.74
1:A:398:ALA:HB3	1:A:399:PRO:HD3	1.70	0.74
1:A:174:ILE:HD13	1:A:211:LEU:HD23	1.70	0.74
1:A:398:ALA:O	1:A:402:GLU:HG2	1.88	0.73
1:A:162:ASP:OD1	1:A:164:GLU:HG2	1.88	0.72
1:A:41:LYS:HD2	1:A:45:GLY:CA	2.17	0.72
1:B:123:THR:HG22	1:B:125:VAL:H	1.54	0.72
1:B:344:LYS:HD2	1:B:402:GLU:CG	2.14	0.72
1:B:94:LEU:N	1:B:94:LEU:HD23	2.05	0.71
1:A:41:LYS:NZ	1:A:41:LYS:HB3	2.05	0.71
1:B:202:LEU:O	1:B:206:GLN:HG3	1.89	0.71
1:B:196:THR:HG22	1:B:198:ILE:H	1.54	0.71
1:B:185:VAL:HG22	1:B:218:LEU:HD23	1.72	0.70
1:B:196:THR:CG2	1:B:198:ILE:HB	2.21	0.70
1:B:333:MET:HE2	1:B:392:MET:C	2.16	0.70
1:B:334:ARG:HH12	1:B:361:SER:HG	1.35	0.70
1:B:165:ASN:HD22	1:B:165:ASN:N	1.89	0.69
1:A:328:GLN:O	1:A:332:ARG:HD3	1.92	0.69
1:A:164:GLU:HG3	1:A:165:ASN:OD1	1.93	0.69
1:A:23:LEU:HD12	1:A:380:TYR:HE2	1.58	0.69
1:A:41:LYS:HE3	1:A:391:GLY:HA2	1.74	0.69
1:A:201:THR:N	1:A:204:GLN:HE21	1.86	0.69
1:B:161:TYR:CE2	1:B:163:ALA:HA	2.28	0.69
1:B:123:THR:CG2	1:B:125:VAL:HG23	2.22	0.69
1:A:98:LYS:HE3	1:A:101:ARG:HD3	1.73	0.68
1:A:294:ASN:HD21	1:B:294:ASN:HD21	1.39	0.68
1:B:161:TYR:HH	1:B:166:HIS:HD1	1.40	0.68
1:A:79:PHE:O	1:A:83:THR:HG23	1.94	0.68
1:B:99:ARG:HH11	1:B:99:ARG:HG2	1.56	0.68
1:A:98:LYS:CE	1:A:101:ARG:HD3	2.23	0.67
1:A:29:ARG:HD2	1:A:30:PRO:HD2	1.75	0.67
1:A:24:PHE:CE1	1:A:32:LYS:HD2	2.30	0.66
1:A:384:SER:HB3	3:A:440:HOH:O	1.96	0.66
1:A:211:LEU:CD1	1:A:215:LYS:HD3	2.26	0.66
1:B:382:VAL:HG23	1:B:386:ALA:O	1.95	0.65
1:A:8:ASN:ND2	3:A:599:HOH:O	2.30	0.65
1:B:99:ARG:HG2	1:B:99:ARG:NH1	2.11	0.65
1:A:137:ASN:ND2	1:A:157:GLU:OE1	2.29	0.65
1:A:29:ARG:O	1:A:32:LYS:HG2	1.96	0.65
1:B:154:GLU:OE2	1:B:156:ARG:NH1	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:312:ASN:O	1:B:316:ARG:HB2	1.96	0.65
1:A:24:PHE:CZ	1:A:34:ASN:HB2	2.32	0.64
1:A:117:ASP:O	1:A:121:LYS:HG2	1.98	0.64
1:A:211:LEU:HD12	1:A:215:LYS:HD3	1.78	0.64
1:A:382:VAL:HG23	1:A:386:ALA:O	1.98	0.64
1:B:99:ARG:NH1	1:B:274:ALA:O	2.30	0.64
1:B:160:TYR:O	1:B:168:LEU:HD23	1.97	0.63
1:A:41:LYS:NZ	1:A:45:GLY:HA2	2.13	0.63
1:A:154:GLU:OE2	1:A:156:ARG:NH2	2.30	0.63
1:A:25:ARG:NH2	3:A:547:HOH:O	2.30	0.63
1:B:333:MET:HE2	1:B:392:MET:O	1.99	0.63
1:A:340:THR:O	1:A:344:LYS:HB2	1.99	0.62
1:A:366:THR:HG22	1:A:369:GLN:H	1.64	0.62
1:B:237:ALA:O	1:B:241:ARG:HD3	1.99	0.62
1:A:263:TYR:HB2	1:B:68:LYS:O	1.99	0.62
1:B:23:LEU:HD23	1:B:23:LEU:O	2.00	0.62
1:B:398:ALA:HB3	1:B:399:PRO:HD3	1.80	0.61
1:A:97:ASP:OD1	1:A:97:ASP:N	2.31	0.61
1:A:225:ARG:HE	1:A:359:MET:HE3	1.65	0.61
1:A:41:LYS:CD	1:A:45:GLY:HA2	2.30	0.61
1:B:238:GLU:HA	1:B:238:GLU:OE1	2.00	0.60
1:A:316:ARG:O	1:A:320:GLU:HG3	2.01	0.60
1:A:41:LYS:HE2	3:A:578:HOH:O	2.02	0.60
1:A:87:LEU:O	1:A:241:ARG:HD2	2.02	0.60
1:A:352:PHE:CA	1:A:355:LYS:HD3	2.32	0.60
1:B:123:THR:HG21	1:B:125:VAL:HG23	1.84	0.60
1:A:29:ARG:CG	1:A:29:ARG:HH11	2.15	0.60
1:A:98:LYS:NZ	1:A:101:ARG:HD3	2.17	0.59
1:A:78:GLU:HB3	3:A:543:HOH:O	2.02	0.59
1:B:123:THR:HG23	1:B:125:VAL:H	1.68	0.59
1:B:356:GLN:NE2	1:B:361:SER:OG	2.35	0.59
1:A:397:MET:HE3	1:A:400:LEU:CD2	2.33	0.59
1:A:33:ILE:CD1	1:A:400:LEU:HB2	2.32	0.58
1:B:292:ARG:HA	1:B:296:SER:HA	1.85	0.58
1:A:173:LEU:HD12	1:A:173:LEU:C	2.28	0.58
1:B:372:ARG:HG3	1:B:376:GLU:HG2	1.85	0.58
1:B:278:GLU:CD	1:B:282:ARG:HH12	2.11	0.58
1:B:24:PHE:HB2	1:B:380:TYR:CD2	2.39	0.58
1:B:258:LYS:HZ3	2:B:411:PPD:H4A2	1.68	0.58
1:B:334:ARG:NH1	1:B:361:SER:OG	2.31	0.57
1:B:212:SER:HA	1:B:217:TRP:CD1	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:LEU:HD13	1:B:401:CYS:HB3	1.85	0.57
1:B:129:ARG:HH11	1:B:129:ARG:CG	2.18	0.57
1:B:397:MET:HE3	1:B:400:LEU:HD13	1.85	0.57
1:A:29:ARG:CG	1:A:30:PRO:HD2	2.34	0.57
1:B:323:LEU:HA	1:B:326:MET:HE3	1.86	0.57
1:A:278:GLU:OE1	1:A:282:ARG:NH1	2.30	0.57
1:B:334:ARG:HG2	1:B:334:ARG:HH11	1.69	0.57
1:A:29:ARG:HG3	1:A:30:PRO:HD2	1.87	0.57
1:B:401:CYS:O	1:B:405:VAL:HG23	2.04	0.57
1:A:85:GLU:OE1	1:A:90:LYS:HD2	2.05	0.56
1:B:112:LEU:HD13	1:B:253:ALA:CB	2.36	0.56
1:B:334:ARG:NH2	1:B:360:PHE:O	2.38	0.56
1:B:352:PHE:CE1	1:B:353:ILE:HD12	2.40	0.56
1:B:117:ASP:O	1:B:121:LYS:HD2	2.06	0.56
1:B:196:THR:HG23	1:B:198:ILE:H	1.70	0.56
1:A:41:LYS:CE	1:A:45:GLY:HA2	2.36	0.56
1:B:94:LEU:HD23	1:B:94:LEU:H	1.68	0.56
1:A:99:ARG:NH1	1:A:274:ALA:O	2.39	0.56
1:A:234:GLU:OE1	1:A:241:ARG:NH2	2.39	0.56
1:B:344:LYS:HD2	1:B:402:GLU:HA	1.86	0.56
1:A:6:PHE:HB3	1:A:9:ILE:HD12	1.88	0.56
1:A:29:ARG:CD	1:A:30:PRO:HD2	2.36	0.55
1:A:73:ILE:HD11	1:B:18:LEU:HD23	1.86	0.55
1:B:43:GLU:CD	1:B:43:GLU:H	2.14	0.55
1:B:99:ARG:HH11	1:B:99:ARG:CG	2.19	0.55
1:B:28:GLU:OE1	1:B:28:GLU:HA	2.07	0.55
1:B:196:THR:HG23	1:B:198:ILE:HB	1.87	0.55
1:A:29:ARG:HH11	1:A:29:ARG:HG3	1.70	0.55
1:A:161:TYR:CZ	1:A:163:ALA:HA	2.41	0.55
1:B:240:LEU:O	1:B:240:LEU:HD22	2.06	0.55
1:B:333:MET:HE2	1:B:393:THR:CA	2.37	0.55
1:A:156:ARG:CB	1:A:156:ARG:HH11	2.20	0.54
1:B:73:ILE:HD13	1:B:292:ARG:HB2	1.89	0.54
1:B:369:GLN:O	1:B:373:LEU:HB2	2.06	0.54
1:B:334:ARG:HH11	1:B:334:ARG:CG	2.21	0.54
1:A:323:LEU:HA	1:A:326:MET:HE2	1.90	0.54
1:B:5:MET:N	1:B:7:GLU:OE1	2.41	0.54
1:A:25:ARG:HG2	1:A:26:ALA:N	2.21	0.54
1:B:77:PRO:O	1:B:81:ARG:HD3	2.08	0.54
1:A:335:GLN:HA	1:A:354:ILE:HD11	1.90	0.54
1:A:392:MET:SD	1:A:397:MET:HE1	2.49	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:46:LYS:O	1:B:48:PRO:HD3	2.08	0.53
1:B:374:ARG:HB2	1:B:379:VAL:O	2.09	0.53
1:B:180:ALA:HB3	1:B:217:TRP:CZ3	2.44	0.53
1:B:294:ASN:C	1:B:294:ASN:HD22	2.16	0.53
1:B:389:VAL:HG13	1:B:392:MET:HE2	1.91	0.53
1:B:291:ILE:HG23	1:B:295:TYR:CZ	2.44	0.53
1:A:258:LYS:HG2	1:A:359:MET:CE	2.39	0.52
1:B:337:PHE:HD1	1:B:397:MET:HE2	1.75	0.52
1:A:32:LYS:O	1:A:32:LYS:HG3	2.09	0.52
1:A:247:HIS:HD2	3:A:502:HOH:O	1.92	0.52
1:B:129:ARG:HH11	1:B:129:ARG:HG3	1.75	0.52
1:B:196:THR:HG23	1:B:198:ILE:HD12	1.91	0.52
1:A:33:ILE:HG22	1:A:34:ASN:N	2.22	0.52
1:A:46:LYS:HD2	3:A:559:HOH:O	2.10	0.52
1:B:333:MET:HE2	1:B:393:THR:HA	1.91	0.52
1:B:396:ASN:O	1:B:400:LEU:HB2	2.10	0.52
1:A:33:ILE:HD12	1:A:400:LEU:HB2	1.92	0.52
1:B:133:VAL:O	1:B:155:VAL:HA	2.09	0.52
1:B:249:GLU:HA	1:B:273:VAL:O	2.09	0.52
1:B:24:PHE:HD1	1:B:380:TYR:CD1	2.27	0.51
1:B:260:PHE:CB	1:B:262:LEU:HD22	2.29	0.51
1:B:352:PHE:CD1	1:B:353:ILE:HD12	2.44	0.51
1:A:337:PHE:HD1	1:A:397:MET:HE2	1.75	0.51
1:B:258:LYS:NZ	2:B:411:PPD:H4A2	2.26	0.51
1:B:27:ASP:O	1:B:32:LYS:NZ	2.35	0.51
1:B:344:LYS:CE	1:B:402:GLU:HG3	2.40	0.51
1:A:106:PRO:HD3	1:A:295:TYR:CZ	2.46	0.51
1:B:382:VAL:HG12	3:B:435:HOH:O	2.10	0.51
1:A:366:THR:HG23	1:A:368:GLU:OE1	2.12	0.50
1:A:156:ARG:HA	1:A:156:ARG:HH11	1.73	0.50
1:A:41:LYS:HZ3	1:A:45:GLY:HA2	1.76	0.50
1:A:68:LYS:HD3	1:B:262:LEU:HD12	1.94	0.50
1:A:234:GLU:CD	1:A:241:ARG:HH22	2.20	0.50
1:A:352:PHE:HB2	1:A:355:LYS:HZ2	1.77	0.50
1:B:337:PHE:HD1	1:B:397:MET:CE	2.24	0.50
1:B:341:LEU:CD1	1:B:401:CYS:HB3	2.42	0.50
1:A:8:ASN:HB3	3:A:544:HOH:O	2.12	0.50
1:A:299:PRO:HA	1:B:266:ARG:HG2	1.93	0.49
1:A:398:ALA:N	1:A:399:PRO:HD2	2.27	0.49
1:B:327:ARG:O	1:B:331:GLN:HG3	2.11	0.49
1:A:362:PHE:HD1	1:A:386:ALA:HB2	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:398:ALA:N	1:B:399:PRO:HD2	2.26	0.49
1:A:258:LYS:HG2	1:A:359:MET:HE3	1.95	0.49
1:A:201:THR:N	1:A:204:GLN:NE2	2.49	0.49
1:B:397:MET:HE2	1:B:401:CYS:SG	2.52	0.49
1:A:99:ARG:HG2	1:A:274:ALA:O	2.13	0.49
1:B:101:ARG:HD3	3:B:499:HOH:O	2.12	0.49
1:A:362:PHE:CD1	1:A:386:ALA:HB2	2.48	0.49
1:A:398:ALA:HB3	1:A:399:PRO:CD	2.40	0.49
1:A:366:THR:HG23	1:A:368:GLU:H	1.78	0.49
1:B:344:LYS:CD	1:B:402:GLU:HA	2.43	0.49
1:A:57:GLU:OE2	1:A:301:HIS:NE2	2.35	0.48
1:B:377:PHE:N	1:B:377:PHE:CD1	2.79	0.48
1:B:334:ARG:O	1:B:338:VAL:HG13	2.14	0.48
1:B:161:TYR:OH	1:B:166:HIS:ND1	2.31	0.48
1:A:140:TRP:CZ2	1:A:142:ASN:HB3	2.48	0.48
1:B:193:HIS:ND1	1:B:196:THR:HB	2.28	0.48
1:B:337:PHE:HB2	1:B:392:MET:HE1	1.96	0.48
1:A:41:LYS:HB3	1:A:41:LYS:HZ2	1.75	0.48
1:A:352:PHE:HB2	1:A:355:LYS:NZ	2.28	0.48
1:B:129:ARG:HG3	1:B:129:ARG:NH1	2.27	0.48
1:B:165:ASN:N	1:B:165:ASN:ND2	2.59	0.48
1:B:398:ALA:HB3	1:B:399:PRO:CD	2.44	0.48
1:A:142:ASN:O	1:A:146:VAL:HG13	2.14	0.48
1:A:339:ASN:O	1:A:343:GLU:HG2	2.13	0.48
1:A:400:LEU:HD12	1:A:400:LEU:O	2.13	0.48
1:B:123:THR:HG23	1:B:124:SER:N	2.28	0.48
1:A:27:ASP:HB2	1:A:380:TYR:OH	2.14	0.48
1:A:76:ILE:O	1:A:79:PHE:HB3	2.14	0.48
1:A:99:ARG:HG2	1:A:99:ARG:HH11	1.78	0.48
1:A:174:ILE:CD1	1:A:211:LEU:HD23	2.42	0.48
1:B:110:GLY:O	1:B:114:VAL:HG13	2.13	0.48
1:B:362:PHE:CE1	1:B:384:SER:HB2	2.49	0.47
1:A:29:ARG:HG3	1:A:30:PRO:CD	2.44	0.47
1:B:343:GLU:O	1:B:345:GLY:N	2.47	0.47
1:B:41:LYS:HB2	1:B:390:ALA:O	2.14	0.47
1:B:159:ALA:O	1:B:173:LEU:HB2	2.14	0.47
1:B:304:SER:HB3	3:B:568:HOH:O	2.14	0.47
1:A:367:LYS:NZ	1:A:368:GLU:OE2	2.40	0.47
1:B:118:PHE:HD1	1:B:119:LEU:HD13	1.78	0.47
1:B:24:PHE:CE1	1:B:32:LYS:HE3	2.49	0.47
1:B:333:MET:HE1	1:B:393:THR:C	2.39	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:SER:OG	1:A:322:GLU:OE1	2.31	0.47
1:A:161:TYR:CE2	1:A:163:ALA:HA	2.49	0.47
1:B:92:SER:HB3	1:B:95:ILE:HD12	1.96	0.47
1:A:341:LEU:HD12	1:A:341:LEU:HA	1.83	0.46
1:A:161:TYR:HE1	1:A:166:HIS:HA	1.80	0.46
1:A:365:LEU:HD12	1:A:365:LEU:HA	1.72	0.46
1:A:99:ARG:NH1	1:A:99:ARG:HG2	2.29	0.46
1:A:329:ARG:NH2	1:A:392:MET:O	2.44	0.46
1:A:225:ARG:NE	1:A:359:MET:HE3	2.29	0.46
1:B:333:MET:HE2	1:B:393:THR:N	2.31	0.46
1:B:135:VAL:O	1:B:157:GLU:HA	2.15	0.45
1:B:129:ARG:HH11	1:B:129:ARG:CB	2.28	0.45
1:B:333:MET:HB3	1:B:392:MET:CE	2.45	0.45
1:A:218:LEU:HD13	3:A:506:HOH:O	2.14	0.45
1:B:23:LEU:HD23	1:B:23:LEU:C	2.40	0.45
1:A:7:GLU:H	1:A:7:GLU:CD	2.25	0.45
1:B:83:THR:HG22	1:B:87:LEU:HD22	1.99	0.45
1:B:180:ALA:O	1:B:217:TRP:HZ3	1.99	0.45
1:B:251:ILE:HG12	1:B:272:LEU:HD23	1.98	0.45
1:B:365:LEU:HD12	1:B:365:LEU:HA	1.77	0.45
1:A:93:ALA:O	1:A:97:ASP:OD1	2.35	0.45
1:B:250:LEU:HD12	1:B:250:LEU:C	2.41	0.45
1:B:382:VAL:HG13	3:B:513:HOH:O	2.16	0.45
1:A:164:GLU:CG	1:A:165:ASN:N	2.80	0.45
1:A:173:LEU:HD12	1:A:173:LEU:O	2.17	0.45
1:B:347:ASN:HD22	1:B:348:ARG:H	1.64	0.45
1:A:18:LEU:HD22	1:B:292:ARG:CZ	2.47	0.45
1:B:123:THR:CG2	1:B:124:SER:N	2.80	0.45
1:B:15:ASP:OD1	1:B:17:ILE:N	2.45	0.44
1:B:352:PHE:CE1	1:B:353:ILE:CD1	3.00	0.44
1:A:138:PRO:HG3	1:A:362:PHE:CE2	2.52	0.44
1:A:5:MET:HA	1:A:5:MET:HE3	1.99	0.44
1:A:355:LYS:HE2	1:A:355:LYS:HB2	1.45	0.44
1:B:258:LYS:N	1:B:258:LYS:CD	2.81	0.44
1:B:348:ARG:HB2	1:B:350:PHE:CE1	2.52	0.44
1:A:338:VAL:HG11	1:A:354:ILE:HG12	2.00	0.44
1:B:376:GLU:HA	1:B:376:GLU:OE1	2.16	0.44
1:A:356:GLN:OE1	1:A:361:SER:OG	2.29	0.44
1:B:220:LEU:HD13	1:B:251:ILE:HB	1.99	0.44
1:B:343:GLU:HG2	1:B:344:LYS:N	2.33	0.43
1:A:15:ASP:HB3	1:A:18:LEU:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:VAL:HG22	1:B:263:TYR:CE1	2.53	0.43
1:B:77:PRO:HB2	1:B:81:ARG:NH1	2.33	0.43
1:A:144:LYS:HB2	1:A:144:LYS:HE3	1.50	0.43
1:A:80:GLY:O	1:A:84:GLN:HG3	2.18	0.43
1:A:161:TYR:OH	1:A:166:HIS:HD2	2.02	0.43
1:B:46:LYS:C	1:B:48:PRO:HD3	2.43	0.43
1:B:214:GLU:HG3	1:B:215:LYS:HD3	2.01	0.43
1:A:177:LEU:HA	1:A:177:LEU:HD23	1.72	0.43
1:A:366:THR:HB	1:A:369:GLN:OE1	2.18	0.43
1:A:393:THR:HB	1:A:394:PRO:HD2	2.00	0.43
1:B:129:ARG:HH11	1:B:129:ARG:HB2	1.84	0.42
1:A:211:LEU:HD11	1:A:215:LYS:HD3	1.98	0.42
1:A:315:LEU:HA	1:A:315:LEU:HD23	1.81	0.42
1:B:233:LEU:HD21	1:B:319:TRP:CH2	2.54	0.42
1:B:294:ASN:ND2	3:B:519:HOH:O	2.52	0.42
1:A:63:ASN:ND2	3:A:562:HOH:O	2.47	0.42
1:A:260:PHE:CE1	1:A:319:TRP:CZ2	3.07	0.42
1:A:99:ARG:HD2	1:A:275:ALA:O	2.19	0.42
1:B:123:THR:HG23	1:B:125:VAL:HG23	1.99	0.42
1:B:382:VAL:HG12	3:B:459:HOH:O	2.18	0.42
1:A:20:LEU:HA	1:A:20:LEU:HD23	1.70	0.42
1:A:396:ASN:O	1:A:400:LEU:HB3	2.18	0.42
1:B:196:THR:HG23	1:B:198:ILE:CB	2.48	0.42
1:B:215:LYS:HA	1:B:215:LYS:HD2	1.77	0.42
1:B:129:ARG:NH1	1:B:184:ASP:OD1	2.52	0.42
1:B:312:ASN:OD1	1:B:314:ALA:HB3	2.19	0.42
1:B:208:LEU:HD23	1:B:208:LEU:HA	1.82	0.42
1:B:177:LEU:HA	1:B:177:LEU:HD23	1.64	0.42
1:B:337:PHE:CD1	1:B:397:MET:HE1	2.55	0.42
1:A:164:GLU:HG3	1:A:165:ASN:N	2.33	0.41
1:A:161:TYR:CD1	1:A:162:ASP:N	2.88	0.41
1:B:154:GLU:CD	1:B:156:ARG:HH12	2.26	0.41
1:B:307:ALA:O	1:B:311:SER:OG	2.29	0.41
1:B:140:TRP:CH2	1:B:142:ASN:HB3	2.56	0.41
1:B:366:THR:O	1:B:370:VAL:HG13	2.21	0.41
1:B:334:ARG:HG2	1:B:353:ILE:CG2	2.51	0.41
1:B:397:MET:CE	1:B:400:LEU:HD13	2.51	0.41
1:A:5:MET:HB3	1:A:5:MET:HE2	1.64	0.41
1:A:83:THR:HG22	1:A:256:TYR:OH	2.20	0.41
1:B:227:GLY:O	1:B:327:ARG:HD3	2.20	0.41
1:B:123:THR:HG21	1:B:125:VAL:CG2	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:GLU:CD	1:B:156:ARG:NH1	2.79	0.41
1:B:347:ASN:HD22	1:B:348:ARG:N	2.19	0.41
1:A:29:ARG:CG	1:A:29:ARG:NH1	2.79	0.41
1:A:352:PHE:CD1	1:A:352:PHE:C	2.99	0.41
1:B:76:ILE:O	1:B:79:PHE:HB3	2.21	0.41
1:B:294:ASN:C	1:B:294:ASN:ND2	2.79	0.41
1:A:156:ARG:HH11	1:A:156:ARG:HB3	1.85	0.40
1:B:137:ASN:HA	1:B:138:PRO:HA	1.75	0.40
1:B:235:GLU:O	1:B:238:GLU:HB2	2.21	0.40
1:A:41:LYS:HD2	1:A:45:GLY:O	2.17	0.40
1:A:165:ASN:O	1:A:167:THR:HG23	2.21	0.40
1:B:118:PHE:CD1	1:B:119:LEU:HD13	2.55	0.40
1:B:196:THR:HG21	1:B:198:ILE:HB	1.97	0.40
1:A:133:VAL:O	1:A:155:VAL:HA	2.21	0.40
1:A:181:GLN:O	1:A:184:ASP:HB2	2.22	0.40
1:A:202:LEU:HD13	1:A:206:GLN:CD	2.46	0.40
1:A:352:PHE:CE1	1:A:353:ILE:HG13	2.57	0.40
1:A:160:TYR:CE1	1:A:168:LEU:HD21	2.55	0.40
1:B:74:ASP:OD1	1:B:74:ASP:N	2.47	0.40
1:B:212:SER:HG	1:B:217:TRP:CD1	2.39	0.40
1:A:18:LEU:CD2	1:B:292:ARG:CZ	3.00	0.40
1:A:29:ARG:HG3	1:A:30:PRO:N	2.37	0.40
1:A:183:GLY:HA2	1:B:5:MET:CE	2.28	0.40
1:A:316:ARG:O	1:A:316:ARG:HG2	2.22	0.40
1:B:60:LEU:HD12	1:B:60:LEU:HA	1.79	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	394/396 (100%)	367 (93%)	22 (6%)	5 (1%)	9 10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	394/396 (100%)	368 (93%)	24 (6%)	2 (0%)	24	31
All	All	788/792 (100%)	735 (93%)	46 (6%)	7 (1%)	14	17

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	30	PRO
1	A	30	PRO
1	B	344	LYS
1	A	296	SER
1	A	43	GLU
1	A	38	GLY
1	A	37	ILE

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	319/319 (100%)	244 (76%)	75 (24%)	1	1
1	B	319/319 (100%)	242 (76%)	77 (24%)	1	0
All	All	638/638 (100%)	486 (76%)	152 (24%)	1	0

All (152) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	MET
1	A	18	LEU
1	A	23	LEU
1	A	25	ARG
1	A	29	ARG
1	A	39	VAL
1	A	41	LYS
1	A	50	LEU
1	A	52	SER

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Mol	Chain	Res	Type
1	A	54	LYS
1	A	61	LEU
1	A	81	ARG
1	A	83	THR
1	A	87	LEU
1	A	90	LYS
1	A	94	LEU
1	A	98	LYS
1	A	99	ARG
1	A	112	LEU
1	A	121	LYS
1	A	126	LYS
1	A	129	ARG
1	A	133	VAL
1	A	135	VAL
1	A	144	LYS
1	A	145	SER
1	A	146	VAL
1	A	152	LEU
1	A	154	GLU
1	A	155	VAL
1	A	156	ARG
1	A	168	LEU
1	A	173	LEU
1	A	174	ILE
1	A	176	SER
1	A	211	LEU
1	A	212	SER
1	A	213	VAL
1	A	214	GLU
1	A	215	LYS
1	A	223	PHE
1	A	230	ARG
1	A	233	LEU
1	A	241	ARG
1	A	246	MET
1	A	250	LEU
1	A	258	LYS
1	A	259	ASN
1	A	262	LEU
1	A	272	LEU
1	A	273	VAL

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Mol	Chain	Res	Type
1	A	278	GLU
1	A	280	VAL
1	A	304	SER
1	A	334	ARG
1	A	335	GLN
1	A	338	VAL
1	A	341	LEU
1	A	343	GLU
1	A	344	LYS
1	A	347	ASN
1	A	349	ASP
1	A	353	ILE
1	A	355	LYS
1	A	359	MET
1	A	362	PHE
1	A	363	SER
1	A	365	LEU
1	A	366	THR
1	A	367	LYS
1	A	371	LEU
1	A	372	ARG
1	A	400	LEU
1	A	402	GLU
1	A	404	ILE
1	B	5	MET
1	B	17	ILE
1	B	18	LEU
1	B	20	LEU
1	B	27	ASP
1	B	28	GLU
1	B	32	LYS
1	B	37	ILE
1	B	39	VAL
1	B	43	GLU
1	B	44	THR
1	B	51	THR
1	B	60	LEU
1	B	61	LEU
1	B	62	GLU
1	B	76	ILE
1	B	87	LEU
1	B	94	LEU

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Mol	Chain	Res	Type
1	B	95	ILE
1	B	99	ARG
1	B	112	LEU
1	B	114	VAL
1	B	119	LEU
1	B	121	LYS
1	B	123	THR
1	B	129	ARG
1	B	133	VAL
1	B	146	VAL
1	B	152	LEU
1	B	154	GLU
1	B	155	VAL
1	B	156	ARG
1	B	165	ASN
1	B	167	THR
1	B	168	LEU
1	B	173	LEU
1	B	174	ILE
1	B	179	GLU
1	B	196	THR
1	B	213	VAL
1	B	215	LYS
1	B	223	PHE
1	B	233	LEU
1	B	238	GLU
1	B	240	LEU
1	B	241	ARG
1	B	258	LYS
1	B	262	LEU
1	B	272	LEU
1	B	273	VAL
1	B	277	SER
1	B	278	GLU
1	B	280	VAL
1	B	311	SER
1	B	316	ARG
1	B	334	ARG
1	B	338	VAL
1	B	341	LEU
1	B	342	GLN
1	B	343	GLU

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Mol	Chain	Res	Type
1	B	344	LYS
1	B	347	ASN
1	B	348	ARG
1	B	351	SER
1	B	362	PHE
1	B	363	SER
1	B	365	LEU
1	B	367	LYS
1	B	370	VAL
1	B	371	LEU
1	B	372	ARG
1	B	374	ARG
1	B	376	GLU
1	B	377	PHE
1	B	382	VAL
1	B	387	VAL
1	B	402	GLU

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

Mol	Chain	Res	Type
1	A	63	ASN
1	A	96	ASN
1	A	122	ASN
1	A	166	HIS
1	A	204	GLN
1	A	259	ASN
1	A	297	ASN
1	A	328	GLN
1	A	342	GLN
1	B	69	ASN
1	B	165	ASN
1	B	178	ASN
1	B	226	GLN
1	B	247	HIS
1	B	286	GLN
1	B	294	ASN
1	B	328	GLN
1	B	347	ASN
1	B	356	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PPD	A	411	-	24,24,24	1.37	1 (4%)	31,34,34	1.79	6 (19%)
2	PPD	B	411	-	24,24,24	1.62	1 (4%)	31,34,34	1.71	9 (29%)

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	PPD	A	411	-	-	11/19/19/19	0/1/1/1
2	PPD	B	411	-	-	9/19/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	411	PPD	C4A-C4	-5.85	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	411	PPD	C4A-C4	-4.59	1.45	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	411	PPD	C6-C5-C4	4.53	121.49	118.06
2	A	411	PPD	C4A-N-CA	4.15	121.63	113.84
2	B	411	PPD	C6-C5-C4	4.02	121.10	118.06
2	B	411	PPD	C4A-N-CA	3.21	119.87	113.84
2	A	411	PPD	C5-C6-N1	-3.21	118.61	123.83
2	A	411	PPD	C2A-C2-C3	3.06	124.37	120.80
2	B	411	PPD	C3-C2-N1	-3.03	117.14	120.96
2	A	411	PPD	C3-C2-N1	-2.94	117.25	120.96
2	A	411	PPD	C6-N1-C2	2.84	124.34	119.20
2	B	411	PPD	C5-C6-N1	-2.49	119.78	123.83
2	B	411	PPD	C2A-C2-C3	2.46	123.67	120.80
2	B	411	PPD	C6-N1-C2	2.42	123.59	119.20
2	B	411	PPD	O3P-P-O1P	2.22	119.47	110.83
2	B	411	PPD	C4A-C4-C5	2.04	121.97	119.75
2	B	411	PPD	C3-C4-C5	-2.01	116.91	118.73

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	411	PPD	C5A-O4P-P-O2P
2	A	411	PPD	C5A-O4P-P-O3P
2	A	411	PPD	C-CA-N-C4A
2	B	411	PPD	C5-C4-C4A-N
2	B	411	PPD	C5A-O4P-P-O2P
2	B	411	PPD	C5A-O4P-P-O3P
2	B	411	PPD	C-CA-N-C4A
2	A	411	PPD	C5-C4-C4A-N
2	B	411	PPD	C3-C4-C4A-N
2	A	411	PPD	C5A-O4P-P-O1P
2	B	411	PPD	C5A-O4P-P-O1P
2	A	411	PPD	C3-C4-C4A-N
2	B	411	PPD	O-C-CA-CB
2	B	411	PPD	OXT-C-CA-CB
2	A	411	PPD	C-CA-CB-CG
2	A	411	PPD	N-CA-CB-CG
2	A	411	PPD	OXT-C-CA-CB

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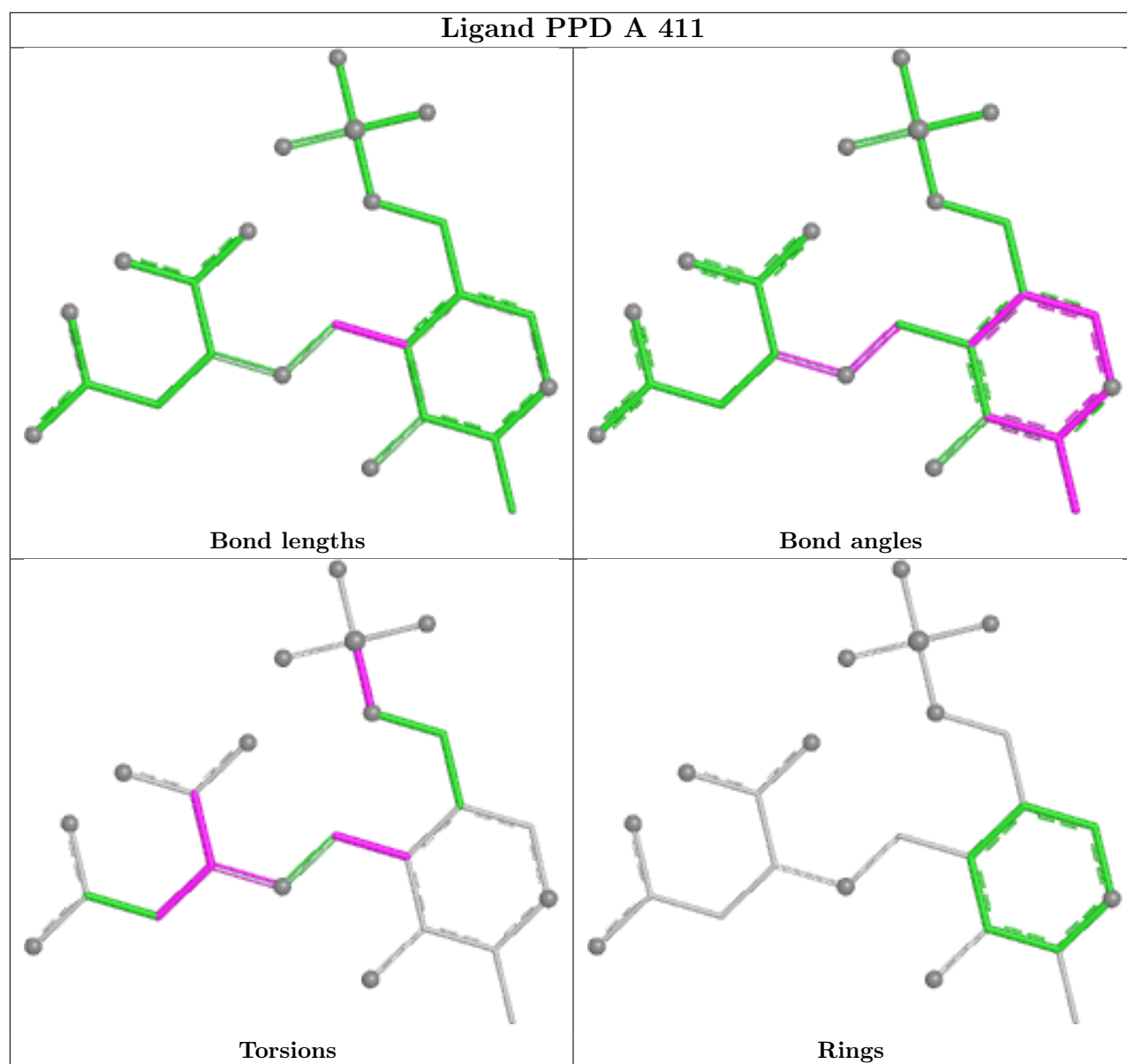
Mol	Chain	Res	Type	Atoms
2	A	411	PPD	O-C-CA-CB
2	A	411	PPD	CB-CA-N-C4A
2	B	411	PPD	CB-CA-N-C4A

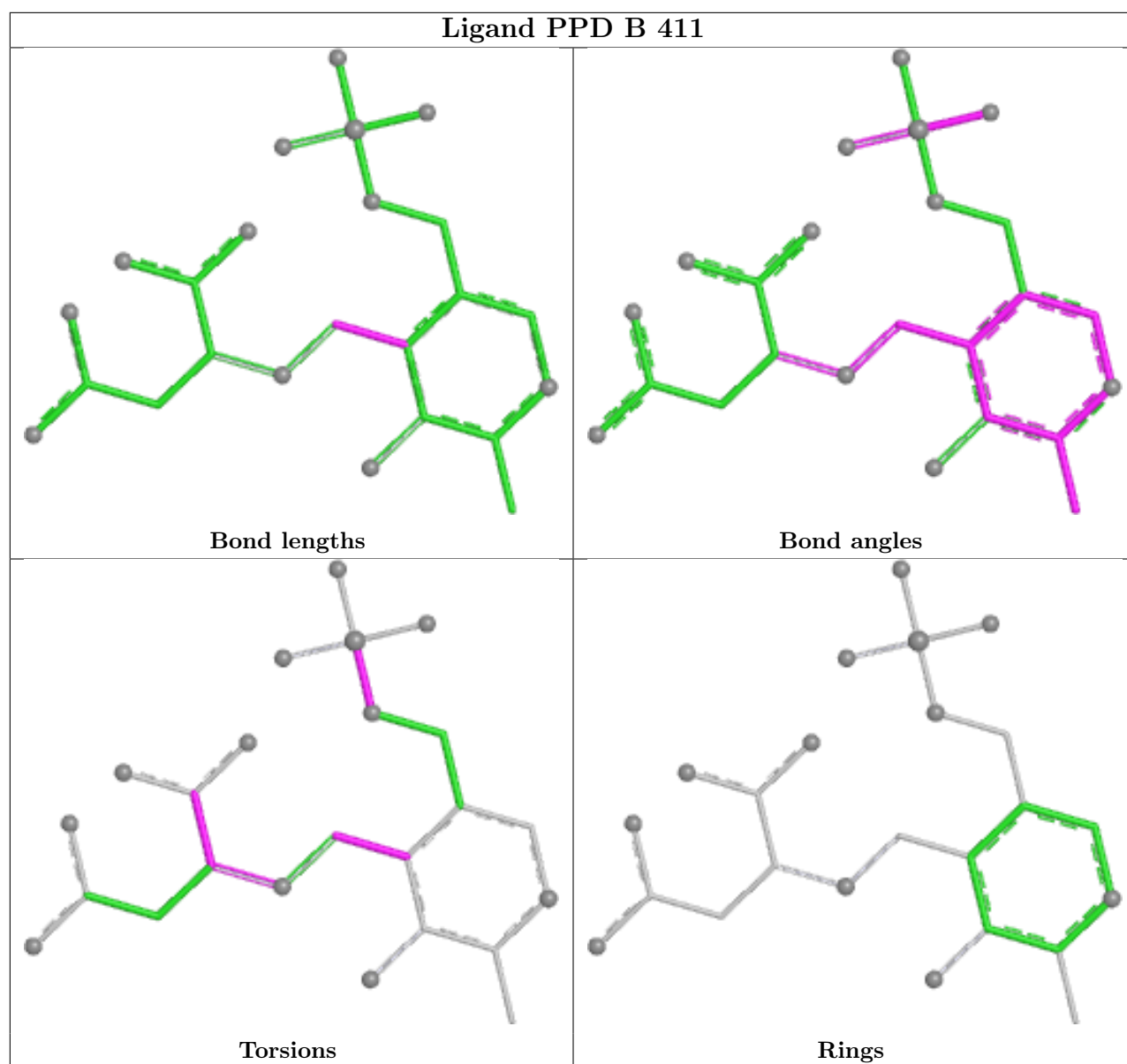
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	411	PPD	2	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.