



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:54 AM GMT

PDB ID : 2J9Y
Title : TRYPTOPHAN SYNTHASE Q114N MUTANT IN COMPLEX WITH COMPOUND II
Authors : Blumenstein, L.; Domratcheva, T.; Niks, D.; Ngo, H.; Seidel, R.; Dunn, M.F.; Schlichting, I.
Deposited on : 2006-11-16
Resolution : 1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

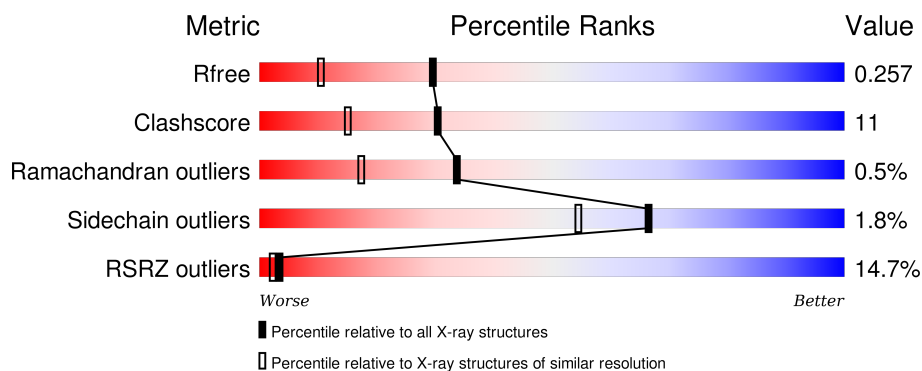
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	268	
2	B	397	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5448 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 TRYPTOPHAN SYNTHASE ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	1
			1902	1211	329	355	7			

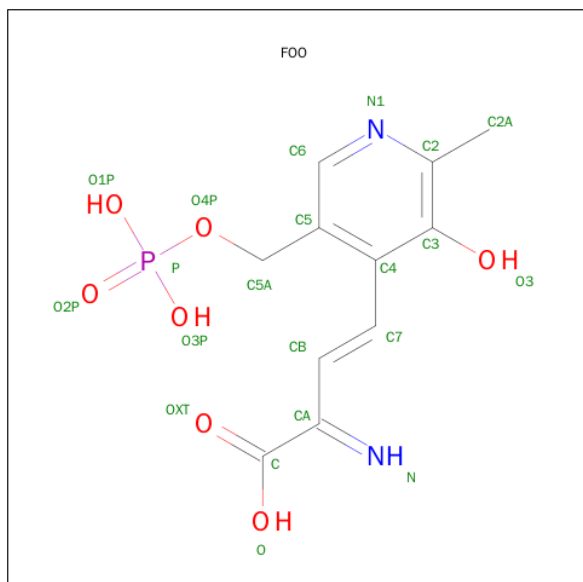
- Molecule 2 is a protein called TRYPTOPHAN SYNTHASE BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	394	Total	C	N	O	S	0	0	1
			2973	1867	523	564	19			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	114	ASN	GLN	ENGINEERED MUTATION	UNP P0A2K1

- Molecule 3 is (3E)-4-{3-HYDROXY-2-METHYL-5-[(PHOSPHONOXY)METHYL]PYRIDIN-4-YL}-2-IMINO BUT-3-ENOIC ACID (three-letter code: FOO) (formula: C₁₁H₁₃N₂O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			21	11	2	7	1		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Na	0	0
			1	1		

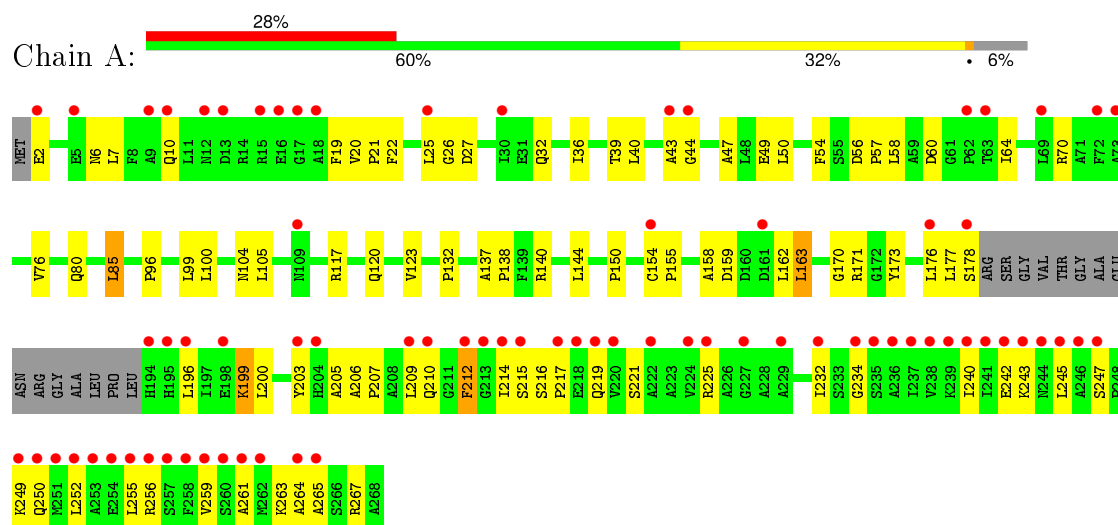
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	183	Total	O	0	0
			183	183		
5	B	368	Total	O	0	0
			368	368		

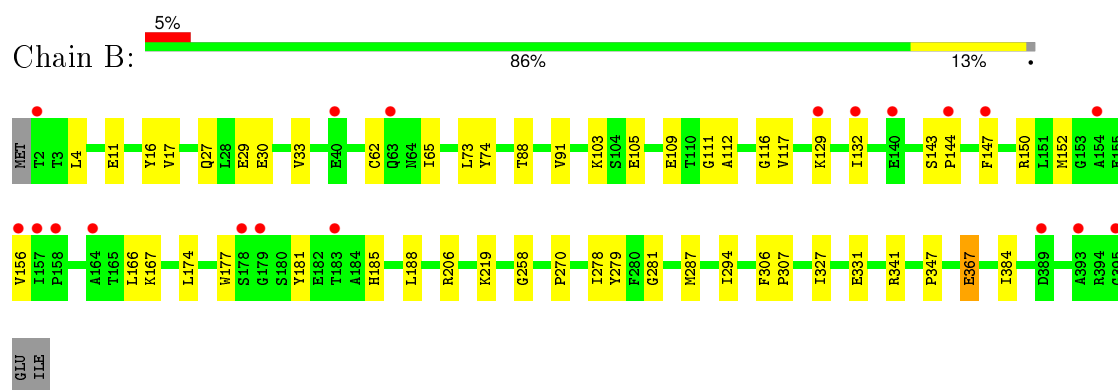
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: TRYPTOPHAN SYNTHASE ALPHA CHAIN



• Molecule 2: TRYPTOPHAN SYNTHASE BETA CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	182.74 Å 60.70 Å 67.41 Å 90.00° 94.83° 90.00°	Depositor
Resolution (Å)	19.45 – 1.80 19.45 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.45-1.80) 98.8 (19.45-1.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 1.70 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.263 0.224 , 0.257	Depositor DCC
R_{free} test set	3381 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	21.0	Xtriage
Anisotropy	0.845	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 80054 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5448	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.41	0/1940	0.55	0/2636
2	B	0.39	0/3031	0.62	0/4097
All	All	0.40	0/4971	0.59	0/6733

There are no bond length outliers.

There are no bond angle outliers.

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	1902	0	1903	72	0
2	B	2973	0	2943	40	0
3	B	21	0	8	2	0
4	B	1	0	0	0	0
5	A	183	0	0	2	0
5	B	368	0	0	10	2
All	All	5448	0	4854	107	2

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 11.

All (107) 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:242:GLU:HA	1:A:245:LEU:HD13	1.47	0.94
2:B:167:LYS:HD3	2:B:307:PRO:HG3	1.50	0.93
1:A:155:PRO:HA	1:A:177:LEU:HD12	1.62	0.80
2:B:27:GLN:HB3	5:B:2065:HOH:O	1.86	0.76
1:A:159:ASP:O	1:A:163:LEU:HD22	1.87	0.74
1:A:210:GLN:HE21	1:A:214:ILE:HD11	1.51	0.74
1:A:264:ALA:HA	1:A:267:ARG:NH1	2.05	0.72
1:A:249:LYS:O	5:A:2174:HOH:O	2.12	0.68
1:A:263:LYS:HD3	1:A:263:LYS:O	1.92	0.68
2:B:74:TYR:HE2	5:B:2110:HOH:O	1.76	0.68
1:A:36:ILE:O	1:A:40:LEU:HD13	1.94	0.67
2:B:65:ILE:HD11	2:B:73:LEU:HD23	1.75	0.67
2:B:62:CYS:SG	2:B:65:ILE:HD11	2.35	0.66
1:A:6:ASN:O	1:A:10:GLN:HG3	1.96	0.66
1:A:196:LEU:HD23	1:A:196:LEU:O	1.96	0.65
1:A:137:ALA:HB3	1:A:138:PRO:HD3	1.79	0.65
1:A:20:VAL:HG22	1:A:47:ALA:HB3	1.81	0.63
1:A:22:PHE:HD2	1:A:49:GLU:HG3	1.64	0.63
1:A:176:LEU:HB3	1:A:210:GLN:HA	1.80	0.62
1:A:140:ARG:O	1:A:144:LEU:HD13	2.00	0.62
1:A:39:THR:HG23	1:A:256:ARG:HG2	1.82	0.62
1:A:216:SER:OG	1:A:219:GLN:HG3	1.99	0.61
1:A:199:LYS:HB3	1:A:203:TYR:CE2	2.35	0.61
1:A:210:GLN:HE21	1:A:214:ILE:CD1	2.15	0.59
1:A:264:ALA:HA	1:A:267:ARG:HH11	1.65	0.59
1:A:32:GLN:O	1:A:36:ILE:HG13	2.03	0.59
2:B:62:CYS:HB3	2:B:65:ILE:HG12	1.86	0.58
2:B:4:LEU:HD11	2:B:30:GLU:OE1	2.03	0.58
2:B:258:GLY:HA3	5:B:2265:HOH:O	2.03	0.58
1:A:25:LEU:HD21	1:A:50:LEU:HD13	1.84	0.58
1:A:19:PHE:HE2	1:A:259:VAL:HG13	1.70	0.56
1:A:25:LEU:HD11	1:A:85:LEU:HD11	1.88	0.56
2:B:185:HIS:HA	5:B:2162:HOH:O	2.04	0.56
1:A:2:GLU:N	5:A:2002:HOH:O	2.38	0.56
1:A:43:ALA:CB	1:A:259:VAL:HB	2.36	0.55
1:A:217:PRO:HB3	1:A:265:ALA:HB2	1.89	0.54
2:B:219:LYS:HE3	5:B:2109:HOH:O	2.06	0.54
2:B:270:PRO:HB3	2:B:287:MET:HG3	1.89	0.54
1:A:252:LEU:O	1:A:256:ARG:HG3	2.08	0.54
2:B:150:ARG:HE	2:B:156:VAL:HB	1.73	0.53
1:A:150:PRO:HD2	1:A:171:ARG:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:VAL:HA	1:A:80:GLN:HE21	1.73	0.53
2:B:103:LYS:HD3	5:B:2213:HOH:O	2.09	0.52
1:A:240:ILE:O	1:A:243:LYS:HG2	2.09	0.52
1:A:21:PRO:HD2	1:A:47:ALA:O	2.09	0.52
1:A:60:ASP:HB3	1:A:64:ILE:HB	1.91	0.52
1:A:154:CYS:SG	1:A:196:LEU:HD21	2.50	0.51
1:A:170:GLY:O	1:A:171:ARG:HD2	2.11	0.50
1:A:43:ALA:HB1	1:A:259:VAL:HB	1.92	0.50
2:B:143:SER:O	2:B:147:PHE:HD1	1.94	0.50
1:A:173:TYR:HB2	1:A:209:LEU:HD13	1.94	0.50
1:A:178:SER:H	1:A:212:PHE:HB2	1.76	0.49
1:A:263:LYS:HD2	1:A:267:ARG:NH2	2.28	0.49
2:B:167:LYS:HG3	2:B:279:TYR:OH	2.13	0.49
1:A:56:ASP:OD2	2:B:294:ILE:HB	2.13	0.49
1:A:217:PRO:HG3	1:A:261:ALA:O	2.13	0.48
2:B:143:SER:OG	2:B:144:PRO:HD3	2.13	0.48
1:A:221:SER:HB3	1:A:225:ARG:HH12	1.78	0.48
2:B:341:ARG:HD2	5:B:2330:HOH:O	2.13	0.48
1:A:76:VAL:HA	1:A:80:GLN:NE2	2.29	0.48
1:A:132:PRO:HD3	2:B:17:VAL:O	2.14	0.47
1:A:20:VAL:HB	1:A:232:ILE:HG12	1.95	0.47
1:A:39:THR:CG2	1:A:256:ARG:HG2	2.44	0.47
1:A:58:LEU:HD22	2:B:174:LEU:HD12	1.97	0.47
1:A:54:PHE:O	1:A:57:PRO:HD3	2.15	0.46
1:A:216:SER:N	1:A:219:GLN:OE1	2.48	0.46
1:A:199:LYS:N	1:A:199:LYS:HD2	2.29	0.46
2:B:111:GLY:H	3:B:1396:FOO:C	2.28	0.46
2:B:367:GLU:HG2	5:B:2347:HOH:O	2.14	0.46
1:A:99:LEU:HD11	1:A:123:VAL:HG21	1.98	0.46
2:B:109:GLU:CD	5:B:2165:HOH:O	2.54	0.46
1:A:155:PRO:CA	1:A:177:LEU:HD12	2.41	0.46
1:A:117:ARG:NH1	1:A:120:GLN:OE1	2.47	0.46
1:A:7:LEU:HD22	1:A:96:PRO:HG2	1.98	0.45
1:A:100:LEU:C	1:A:100:LEU:HD13	2.37	0.45
1:A:255:LEU:O	1:A:259:VAL:HG23	2.16	0.45
1:A:19:PHE:CE2	1:A:259:VAL:HG13	2.50	0.45
2:B:112:ALA:HB3	3:B:1396:FOO:HB	1.98	0.44
2:B:177:TRP:O	2:B:181:TYR:HB3	2.16	0.44
2:B:117:VAL:HG13	2:B:152:MET:HE1	2.00	0.44
2:B:306:PHE:CD1	2:B:307:PRO:HD2	2.52	0.44
1:A:247:SER:HB2	1:A:250:GLN:CG	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:11:GLU:HG2	2:B:11:GLU:O	2.18	0.44
1:A:256:ARG:CZ	1:A:256:ARG:HB3	2.48	0.43
2:B:88:THR:O	2:B:91:VAL:HG22	2.17	0.43
1:A:247:SER:HB2	1:A:250:GLN:HG3	1.99	0.43
1:A:206:ALA:O	1:A:207:PRO:C	2.56	0.43
1:A:215:SER:N	1:A:219:GLN:OE1	2.50	0.43
1:A:27:ASP:OD1	1:A:70:ARG:NE	2.49	0.43
2:B:117:VAL:HG13	2:B:152:MET:CE	2.49	0.43
1:A:58:LEU:HD12	1:A:58:LEU:C	2.39	0.43
2:B:116:GLY:CA	2:B:132:ILE:HD13	2.49	0.43
1:A:58:LEU:HD22	2:B:174:LEU:CD1	2.49	0.42
2:B:327:ILE:HG23	2:B:331:GLU:HB2	2.00	0.42
2:B:166:LEU:HD23	2:B:306:PHE:HB2	2.01	0.42
1:A:104:ASN:HB2	2:B:278:ILE:O	2.20	0.42
2:B:219:LYS:HE3	5:B:2110:HOH:O	2.19	0.42
1:A:158:ALA:HB1	1:A:162:LEU:HD23	2.02	0.42
1:A:26:GLY:HA3	1:A:76:VAL:HG21	2.02	0.42
2:B:109:GLU:OE1	2:B:109:GLU:N	2.45	0.42
1:A:200:LEU:HB3	1:A:205:ALA:HB3	2.01	0.42
1:A:178:SER:HB2	1:A:212:PHE:O	2.19	0.42
1:A:158:ALA:CB	1:A:162:LEU:HD23	2.49	0.42
2:B:29:GLU:O	2:B:33:VAL:HG23	2.19	0.42
2:B:105:GLU:HG2	2:B:129:LYS:HB3	2.02	0.41
2:B:16:TYR:O	2:B:281:GLY:HA2	2.21	0.41
1:A:210:GLN:HG2	1:A:214:ILE:HD11	2.02	0.41

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:2151:HOH:O	5:B:2151:HOH:O[2_656]	2.00	0.20
5:B:2104:HOH:O	5:B:2104:HOH:O[2_655]	2.08	0.12

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	248/268 (92%)	235 (95%)	10 (4%)	3 (1%)	16	4
2	B	392/397 (99%)	384 (98%)	8 (2%)	0	100	100
All	All	640/665 (96%)	619 (97%)	18 (3%)	3 (0%)	34	17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	212	PHE
1	A	234	GLY
1	A	44	GLY

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	197/208 (95%)	193 (98%)	4 (2%)	63	49
2	B	307/311 (99%)	302 (98%)	5 (2%)	70	59
All	All	504/519 (97%)	495 (98%)	9 (2%)	66	54

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LEU
1	A	105	LEU
1	A	163	LEU
1	A	199	LYS
2	B	188	LEU
2	B	206	ARG
2	B	347	PRO
2	B	367	GLU
2	B	384	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	GLN
1	A	66	ASN
1	A	68	ASN
1	A	80	GLN
1	A	141	GLN
1	A	210	GLN
2	B	44	GLN
2	B	246	ASN
2	B	317	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
3	FOO	B	1396	-	18,21,21	4.92	11 (61%)	21,30,30	2.65	8 (38%)

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	FOO	B	1396	-	-	0/10/15/15	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1396	FOO	P-O4P	-4.90	1.43	1.60
3	B	1396	FOO	C-CA	-4.65	1.44	1.52
3	B	1396	FOO	C4-C7	-3.82	1.40	1.47
3	B	1396	FOO	P-O1P	-3.57	1.41	1.54
3	B	1396	FOO	P-O3P	-3.44	1.42	1.54
3	B	1396	FOO	P-O2P	-2.76	1.42	1.51
3	B	1396	FOO	O3-C3	-2.17	1.31	1.37
3	B	1396	FOO	CB-C7	2.74	1.40	1.32
3	B	1396	FOO	C6-C5	4.22	1.47	1.37
3	B	1396	FOO	C4-C3	5.44	1.47	1.40
3	B	1396	FOO	C3-C2	16.71	1.52	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1396	FOO	C3-C4-C5	-4.08	115.05	118.11
3	B	1396	FOO	C5A-C5-C6	-3.27	113.09	119.28
3	B	1396	FOO	O1P-P-O2P	-2.42	102.79	110.58
3	B	1396	FOO	O1P-P-O4P	2.08	112.56	106.56
3	B	1396	FOO	C7-CB-CA	2.16	128.60	125.72
3	B	1396	FOO	C4-C7-CB	2.58	134.29	128.92
3	B	1396	FOO	O4P-P-O2P	5.42	120.94	107.14
3	B	1396	FOO	O4P-C5A-C5	7.08	120.69	108.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1396	FOO	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	252/268 (94%)	1.34	76 (30%) 1 0	18, 40, 50, 52	0
2	B	394/397 (99%)	0.19	19 (4%) 34 28	13, 20, 39, 49	0
All	All	646/665 (97%)	0.64	95 (14%) 3 2	13, 26, 48, 52	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	212	PHE	7.4
1	A	194	HIS	6.9
1	A	195	HIS	6.1
1	A	214	ILE	6.1
1	A	247	SER	6.1
1	A	246	ALA	5.9
1	A	243	LYS	5.4
2	B	179	GLY	5.1
1	A	178	SER	5.1
1	A	62	PRO	5.1
1	A	213	GLY	5.0
1	A	245	LEU	4.8
1	A	250	GLN	4.6
1	A	224	VAL	4.4
1	A	249	LYS	4.2
2	B	164	ALA	4.2
1	A	242	GLU	4.2
2	B	395	GLY	4.1
1	A	15	ARG	4.0
2	B	393	ALA	4.0
1	A	239	LYS	3.9
1	A	264	ALA	3.8
1	A	9	ALA	3.8
1	A	218	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	204	HIS	3.7
1	A	234	GLY	3.7
1	A	258	PHE	3.5
1	A	13	ASP	3.5
1	A	251	MET	3.4
1	A	259	VAL	3.4
2	B	63	GLN	3.3
1	A	260	SER	3.3
1	A	176	LEU	3.2
1	A	255	LEU	3.2
1	A	222	ALA	3.2
2	B	2	THR	3.2
1	A	229	ALA	3.2
1	A	253	ALA	3.2
1	A	30	ILE	3.1
2	B	156	VAL	3.1
1	A	196	LEU	3.1
1	A	261	ALA	3.1
1	A	198	GLU	3.0
1	A	73	ALA	3.0
1	A	203	TYR	3.0
1	A	244	ASN	3.0
1	A	43	ALA	3.0
1	A	237	ILE	3.0
2	B	129	LYS	2.9
2	B	140	GLU	2.9
1	A	161	ASP	2.9
2	B	158	PRO	2.9
1	A	227	GLY	2.9
1	A	240	ILE	2.9
1	A	25	LEU	2.8
1	A	232	ILE	2.8
1	A	17	GLY	2.8
1	A	265	ALA	2.8
2	B	178	SER	2.8
1	A	12	ASN	2.7
2	B	147	PHE	2.7
1	A	220	VAL	2.6
1	A	215	SER	2.6
1	A	256	ARG	2.6
1	A	10	GLN	2.6
2	B	183	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	69	LEU	2.6
1	A	44	GLY	2.5
1	A	236	ALA	2.5
1	A	18	ALA	2.5
1	A	257	SER	2.5
2	B	144	PRO	2.5
1	A	210	GLN	2.5
1	A	2	GLU	2.4
2	B	389	ASP	2.4
1	A	109	ASN	2.4
1	A	16	GLU	2.3
1	A	217	PRO	2.3
1	A	225	ARG	2.3
1	A	72	PHE	2.3
1	A	241	ILE	2.2
1	A	252	LEU	2.2
1	A	219	GLN	2.2
1	A	209	LEU	2.2
2	B	154	ALA	2.1
1	A	238	VAL	2.1
2	B	157	ILE	2.1
1	A	254	GLU	2.1
1	A	154	CYS	2.1
1	A	5	GLU	2.1
1	A	262	MET	2.1
2	B	40	GLU	2.0
1	A	235	SER	2.0
1	A	63	THR	2.0
2	B	132	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	FOO	B	1396	21/21	0.96	0.10	0.12	17,20,35,39	0
4	NA	B	1397	1/1	0.99	0.04	-4.28	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.