



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 6, 2024 – 04:09 AM EDT

PDB ID : 1NUN
Title : Crystal Structure Analysis of the FGF10-FGFR2b Complex
Authors : Yeh, B.K.; Igarashi, M.; Eliseenkova, A.V.; Plotnikov, A.N.; Sher, I.; Ron, D.; Aaronson, S.A.; Mohammadi, M.
Deposited on : 2003-01-31
Resolution : 2.90 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

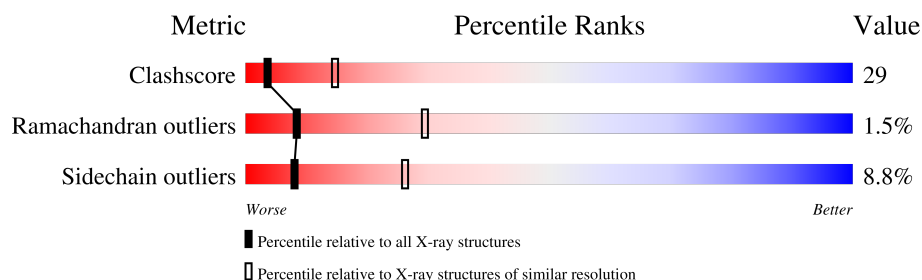
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	180529	2564 (2.90-2.90)
Ramachandran outliers	177936	2514 (2.90-2.90)
Sidechain outliers	177891	2516 (2.90-2.90)

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	145	
2	B	230	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2727 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 Fibroblast growth factor-10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	139	Total	C	N	O	S	0	0	0
			1080	686	193	196	5			

- Molecule 2 is a protein called fibroblast growth factor receptor 2 isoform 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	209	Total	C	N	O	S	Se	0	0	0
			1593	1011	281	293	4	4			

There are 4 discrepancies between the modelled and reference sequences:

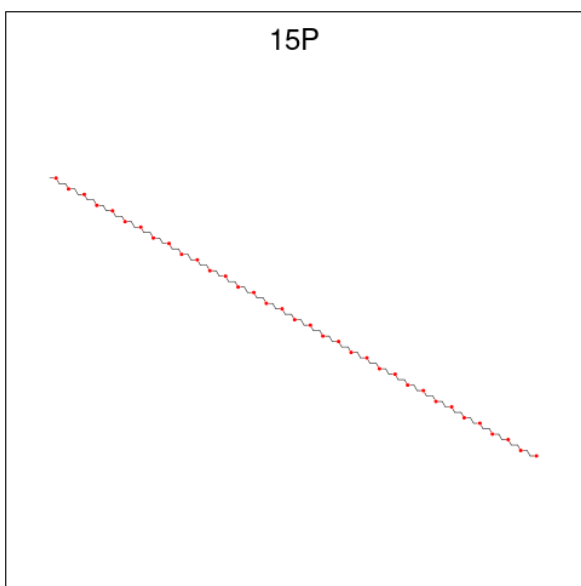
Chain	Residue	Modelled	Actual	Comment	Reference
B	162	MSE	MET	modified residue	UNP P21802
B	186	MSE	MET	modified residue	UNP P21802
B	189	MSE	MET	modified residue	UNP P21802
B	218	MSE	MET	modified residue	UNP P21802

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is POLYETHYLENE GLYCOL (N=34) (three-letter code: 15P) (formula: $C_{69}H_{140}O_{35}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			19	12	7		

- Molecule 5 is water.

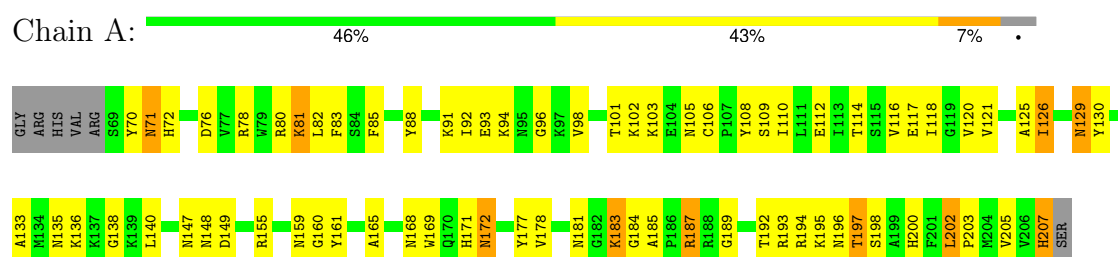
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	13	Total 13	O 13	0	0
5	B	12	Total 12	O 12	0	0

3 Residue-property plots

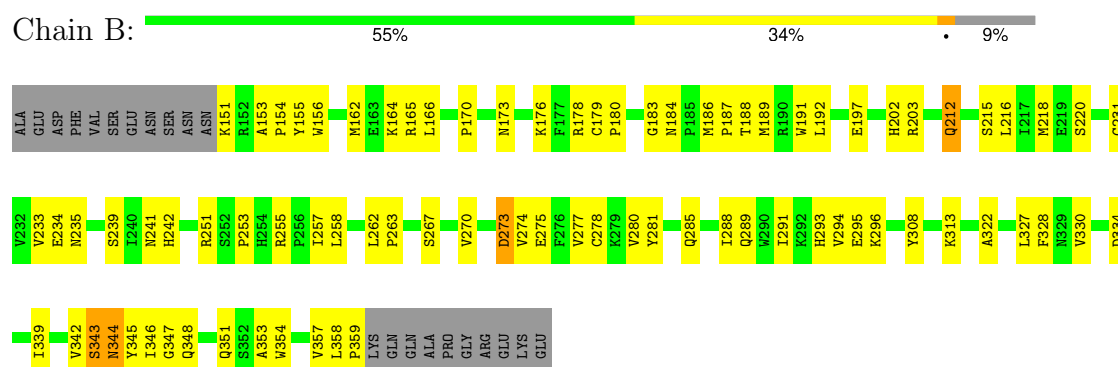
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: Fibroblast growth factor-10



• Molecule 2: fibroblast growth factor receptor 2 isoform 2



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, α , β , γ	113.93Å 113.93Å 164.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.00 – 2.90	Depositor
% Data completeness (in resolution range)	97.7 (25.00-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.239 , 0.288	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2727	wwPDB-VP
Average B, all atoms (Å ²)	41.0	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: 15P, SO4

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	0.42	0/1105	0.67	0/1495
2	B	0.45	0/1633	0.67	1/2222 (0.0%)
All	All	0.44	0/2738	0.67	1/3717 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	359	PRO	N-CA-CB	5.39	109.77	103.30

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	1080	0	1012	71	0
2	B	1593	0	1512	88	0
3	A	10	0	0	1	0
4	B	19	0	24	3	0
5	A	13	0	0	0	0
5	B	12	0	0	0	0
All	All	2727	0	2548	148	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 29.

All (148) 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:101:THR:HG22	1:A:103:LYS:H	1.24	1.02
2:B:294:VAL:HG12	2:B:295:GLU:H	1.29	0.96
2:B:343:SER:HB3	2:B:348:GLN:HB3	1.48	0.93
1:A:202:LEU:HD23	2:B:170:PRO:HD3	1.52	0.91
2:B:289:GLN:HG3	2:B:291:ILE:HD11	1.56	0.88
1:A:93:GLU:HA	1:A:108:TYR:HD2	1.38	0.88
1:A:93:GLU:HA	1:A:108:TYR:CD2	2.13	0.81
2:B:212:GLN:NE2	2:B:212:GLN:H	1.78	0.81
1:A:159:ASN:HD21	1:A:200:HIS:CD2	2.01	0.79
1:A:135:ASN:HA	1:A:149:ASP:OD2	1.83	0.78
2:B:151:LYS:HA	2:B:184:ASN:HD22	1.49	0.78
2:B:294:VAL:HG12	2:B:295:GLU:N	2.00	0.76
2:B:343:SER:HB3	2:B:348:GLN:CB	2.16	0.76
2:B:170:PRO:HG2	2:B:173:ASN:ND2	2.02	0.75
2:B:251:ARG:O	2:B:253:PRO:HD3	1.87	0.74
2:B:258:LEU:HD12	2:B:351:GLN:HG3	1.67	0.74
2:B:178:ARG:HG2	2:B:215:SER:HB3	1.69	0.73
2:B:348:GLN:HG2	4:B:370:15P:H19	1.71	0.73
1:A:102:LYS:HE3	2:B:164:LYS:HD2	1.74	0.70
2:B:339:ILE:HD13	4:B:370:15P:H162	1.73	0.69
1:A:101:THR:HG22	1:A:102:LYS:N	2.11	0.66
1:A:181:ASN:OD1	1:A:185:ALA:HB3	1.96	0.66
2:B:344:ASN:C	2:B:344:ASN:HD22	1.98	0.66
2:B:344:ASN:HD22	2:B:346:ILE:H	1.41	0.66
2:B:344:ASN:ND2	2:B:346:ILE:H	1.93	0.65
1:A:187:ARG:HG3	3:A:300:SO4:O2	1.97	0.65
1:A:91:LYS:HD3	1:A:101:THR:OG1	1.98	0.64
2:B:289:GLN:HG3	2:B:291:ILE:CD1	2.28	0.63
2:B:234:GLU:HB3	2:B:239:SER:OG	1.98	0.63
1:A:148:ASN:HB3	1:A:168:ASN:OD1	1.99	0.62
1:A:147:ASN:OD1	1:A:149:ASP:HB2	2.00	0.62
2:B:178:ARG:NH2	2:B:180:PRO:HG3	2.16	0.61
1:A:96:GLY:HA2	1:A:130:TYR:CE1	2.36	0.60
1:A:121:VAL:HG12	2:B:285:GLN:HG2	1.83	0.60
2:B:344:ASN:ND2	2:B:347:GLY:H	1.99	0.59
2:B:151:LYS:HA	2:B:184:ASN:ND2	2.18	0.59
1:A:168:ASN:HB3	1:A:169:TRP:CE3	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:273:ASP:OD2	2:B:328:PHE:HD1	1.87	0.58
2:B:277:VAL:HG12	2:B:278:CYS:N	2.17	0.58
1:A:88:TYR:OH	1:A:183:LYS:HA	2.04	0.57
2:B:186:MSE:HE2	2:B:186:MSE:HA	1.87	0.57
2:B:234:GLU:HB3	2:B:239:SER:CB	2.34	0.57
1:A:116:VAL:HG23	1:A:117:GLU:HG2	1.87	0.56
1:A:76:ASP:O	1:A:78:ARG:HG3	2.05	0.56
2:B:179:CYS:HB2	2:B:189:MSE:CE	2.36	0.56
2:B:154:PRO:HD3	2:B:235:ASN:CG	2.26	0.56
1:A:102:LYS:CE	2:B:164:LYS:HD2	2.35	0.56
2:B:154:PRO:HD3	2:B:235:ASN:ND2	2.21	0.56
2:B:313:LYS:HE2	2:B:322:ALA:HA	1.88	0.56
1:A:136:LYS:HA	1:A:169:TRP:CG	2.41	0.56
2:B:191:TRP:CH2	2:B:231:CYS:HB3	2.40	0.56
2:B:291:ILE:HD12	2:B:291:ILE:N	2.21	0.56
1:A:112:GLU:HB2	1:A:126:ILE:HG12	1.87	0.55
2:B:345:TYR:CZ	2:B:346:ILE:HD11	2.42	0.55
2:B:178:ARG:HG2	2:B:215:SER:CB	2.37	0.54
2:B:358:LEU:HD22	2:B:358:LEU:H	1.72	0.54
2:B:280:VAL:HG22	2:B:342:VAL:HG21	1.89	0.54
2:B:263:PRO:HG2	2:B:353:ALA:HB2	1.89	0.54
2:B:212:GLN:NE2	2:B:212:GLN:N	2.55	0.54
1:A:171:HIS:CE1	1:A:172:ASN:HB2	2.44	0.53
2:B:294:VAL:CG1	2:B:295:GLU:H	2.10	0.53
2:B:176:LYS:HD3	2:B:178:ARG:HD2	1.91	0.52
1:A:159:ASN:HD21	1:A:200:HIS:HD2	1.51	0.52
2:B:296:LYS:HG3	2:B:308:TYR:CD2	2.45	0.52
1:A:94:LYS:H	1:A:108:TYR:HE2	1.58	0.52
1:A:181:ASN:HD21	1:A:183:LYS:HE3	1.75	0.52
1:A:160:GLY:O	2:B:251:ARG:HG3	2.10	0.51
1:A:207:HIS:CD2	1:A:207:HIS:N	2.77	0.51
2:B:164:LYS:HE3	2:B:166:LEU:O	2.10	0.51
1:A:83:PHE:CZ	2:B:164:LYS:HE2	2.46	0.50
1:A:140:LEU:HD21	1:A:178:VAL:HG13	1.92	0.50
2:B:187:PRO:HB2	2:B:233:VAL:HG12	1.91	0.50
1:A:117:GLU:CG	1:A:120:VAL:HB	2.42	0.50
1:A:183:LYS:O	1:A:185:ALA:N	2.45	0.50
2:B:274:VAL:HG22	2:B:275:GLU:N	2.26	0.50
2:B:153:ALA:HA	2:B:235:ASN:HD21	1.76	0.50
1:A:161:TYR:HB3	1:A:200:HIS:HB3	1.94	0.50
2:B:178:ARG:HH22	2:B:180:PRO:HG3	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:THR:CG2	1:A:102:LYS:N	2.75	0.49
1:A:181:ASN:HD21	1:A:183:LYS:CD	2.24	0.49
2:B:156:TRP:CZ3	2:B:179:CYS:HB3	2.47	0.49
1:A:70:TYR:O	1:A:72:HIS:N	2.45	0.49
2:B:186:MSE:HE2	2:B:187:PRO:HD2	1.95	0.49
2:B:212:GLN:H	2:B:212:GLN:HE21	1.58	0.49
1:A:82:LEU:HD23	1:A:203:PRO:HA	1.95	0.48
2:B:251:ARG:C	2:B:253:PRO:HD3	2.33	0.48
1:A:101:THR:HG22	1:A:103:LYS:N	2.09	0.47
1:A:181:ASN:HD21	1:A:183:LYS:CE	2.27	0.47
2:B:188:THR:O	2:B:233:VAL:HA	2.14	0.47
2:B:203:ARG:HD3	2:B:218:MSE:HG2	1.95	0.47
2:B:212:GLN:N	2:B:212:GLN:HE21	2.13	0.47
1:A:101:THR:HG22	1:A:102:LYS:H	1.80	0.47
1:A:165:ALA:HB2	1:A:177:TYR:CE2	2.50	0.47
1:A:177:TYR:CZ	1:A:194:ARG:HB2	2.50	0.47
2:B:162:MSE:HE2	2:B:242:HIS:CD2	2.50	0.47
1:A:102:LYS:HZ2	2:B:164:LYS:CE	2.28	0.46
1:A:171:HIS:ND1	1:A:172:ASN:HB2	2.29	0.46
2:B:358:LEU:HD22	2:B:358:LEU:N	2.30	0.46
1:A:117:GLU:HG2	1:A:120:VAL:HB	1.97	0.46
1:A:81:LYS:HE2	1:A:109:SER:OG	2.16	0.46
1:A:196:ASN:O	1:A:198:SER:N	2.49	0.45
1:A:98:VAL:HG11	1:A:140:LEU:HD13	1.99	0.45
2:B:277:VAL:HG12	2:B:278:CYS:H	1.81	0.45
2:B:288:ILE:HD12	2:B:322:ALA:HB3	1.99	0.45
2:B:166:LEU:CD1	2:B:166:LEU:N	2.80	0.45
1:A:83:PHE:HZ	2:B:164:LYS:HE2	1.82	0.45
1:A:92:ILE:HB	1:A:125:ALA:HB2	1.98	0.45
2:B:165:ARG:C	2:B:166:LEU:HD12	2.38	0.45
1:A:81:LYS:HG3	1:A:109:SER:O	2.17	0.44
2:B:166:LEU:N	2:B:166:LEU:HD12	2.31	0.44
1:A:168:ASN:HB3	1:A:169:TRP:CZ3	2.53	0.44
1:A:171:HIS:CE1	1:A:172:ASN:HD22	2.34	0.44
2:B:187:PRO:HB2	2:B:233:VAL:CG1	2.46	0.44
2:B:291:ILE:CD1	2:B:291:ILE:N	2.80	0.44
1:A:91:LYS:HA	1:A:108:TYR:O	2.16	0.44
2:B:330:VAL:HG13	2:B:334:ASP:HB2	2.00	0.44
1:A:102:LYS:NZ	2:B:164:LYS:HD2	2.31	0.44
1:A:138:GLY:O	1:A:189:GLY:N	2.39	0.44
2:B:162:MSE:HE3	2:B:179:CYS:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:LYS:HZ2	2:B:164:LYS:HE2	1.82	0.44
1:A:80:ARG:HD3	1:A:205:VAL:HA	2.00	0.43
1:A:149:ASP:CG	1:A:169:TRP:HE1	2.21	0.43
1:A:161:TYR:CB	1:A:200:HIS:HB3	2.48	0.43
1:A:110:ILE:O	1:A:126:ILE:HB	2.18	0.43
2:B:191:TRP:CD2	2:B:216:LEU:HD22	2.53	0.43
2:B:191:TRP:NE1	2:B:216:LEU:HB2	2.34	0.43
2:B:270:VAL:HG22	2:B:357:VAL:HG12	2.00	0.43
1:A:169:TRP:N	1:A:169:TRP:CD2	2.83	0.43
1:A:181:ASN:HD21	1:A:183:LYS:HD2	1.84	0.43
2:B:262:LEU:HA	2:B:263:PRO:C	2.39	0.43
1:A:192:THR:O	1:A:193:ARG:HD3	2.18	0.42
1:A:160:GLY:HA3	2:B:170:PRO:HB2	2.01	0.42
1:A:91:LYS:CD	1:A:101:THR:OG1	2.66	0.42
2:B:155:TYR:HE1	2:B:183:GLY:HA2	1.85	0.42
1:A:105:ASN:O	1:A:106:CYS:C	2.56	0.42
2:B:212:GLN:H	2:B:212:GLN:CD	2.19	0.42
1:A:85:PHE:HB2	1:A:200:HIS:HB2	2.01	0.41
1:A:196:ASN:ND2	1:A:198:SER:OG	2.53	0.41
2:B:267:SER:HB3	2:B:358:LEU:HD21	2.02	0.41
1:A:133:ALA:HB1	1:A:149:ASP:O	2.21	0.41
2:B:257:ILE:HG12	2:B:281:TYR:HB2	2.02	0.41
2:B:191:TRP:CE2	2:B:216:LEU:HB2	2.56	0.41
2:B:344:ASN:C	2:B:344:ASN:ND2	2.70	0.41
1:A:78:ARG:HD3	1:A:80:ARG:NH1	2.35	0.41
2:B:191:TRP:CZ3	2:B:231:CYS:HB3	2.56	0.41
2:B:339:ILE:HD13	4:B:370:15P:C16	2.45	0.40
2:B:192:LEU:HD23	2:B:197:GLU:HA	2.02	0.40
2:B:277:VAL:CG1	2:B:278:CYS:N	2.84	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	137/145 (94%)	115 (84%)	17 (12%)	5 (4%)	3	12
2	B	207/230 (90%)	187 (90%)	20 (10%)	0	100	100
All	All	344/375 (92%)	302 (88%)	37 (11%)	5 (2%)	8	29

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	GLY
1	A	71	ASN
1	A	197	THR
1	A	118	ILE
1	A	129	ASN

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	107/126 (85%)	94 (88%)	13 (12%)	4	13
2	B	165/192 (86%)	154 (93%)	11 (7%)	13	39
All	All	272/318 (86%)	248 (91%)	24 (9%)	8	26

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	81	LYS
1	A	114	THR
1	A	126	ILE
1	A	129	ASN
1	A	155	ARG
1	A	172	ASN
1	A	183	LYS
1	A	187	ARG
1	A	195	LYS
1	A	197	THR

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Mol	Chain	Res	Type
1	A	202	LEU
1	A	207	HIS
2	B	202	HIS
2	B	212	GLN
2	B	220	SER
2	B	241	ASN
2	B	255	ARG
2	B	273	ASP
2	B	293	HIS
2	B	327	LEU
2	B	343	SER
2	B	344	ASN
2	B	354	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	74	GLN
1	A	105	ASN
1	A	172	ASN
1	A	175	GLN
1	A	196	ASN
1	A	200	HIS
1	A	207	HIS
2	B	158	ASN
2	B	184	ASN
2	B	202	HIS
2	B	212	GLN
2	B	241	ASN
2	B	242	HIS
2	B	289	GLN
2	B	318	ASN
2	B	344	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
3	SO4	A	300	-	4,4,4	0.38	0	6,6,6	0.09	0
3	SO4	A	301	-	4,4,4	0.42	0	6,6,6	0.09	0
4	15P	B	370	-	18,18,103	0.90	0	17,17,102	0.78	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
4	15P	B	370	-	-	2/16/16/101	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

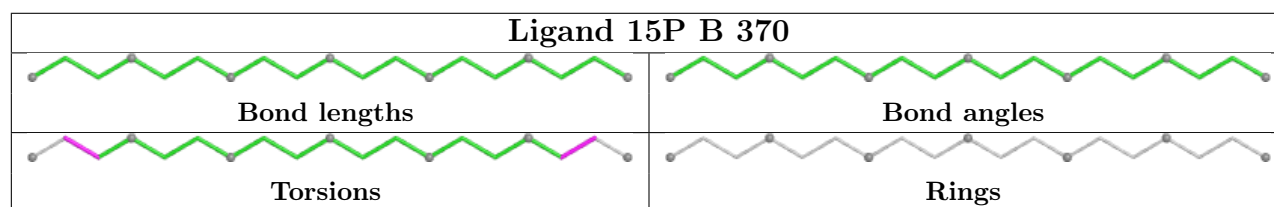
Mol	Chain	Res	Type	Atoms
4	B	370	15P	O3-C7-C8-O4
4	B	370	15P	O8-C17-C18-O9

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	300	SO4	1	0
4	B	370	15P	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

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.