



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 11:09 AM UTC

PDB ID : 7DDZ / pdb_00007ddz
Title : The Crystal Structure of Human Neuropeptide Y Y2 Receptor with JNJ-31020028
Authors : Tang, T.; Han, S.; Zhao, Q.; Wu, B.
Deposited on : 2020-10-30
Resolution : 2.80 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

<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

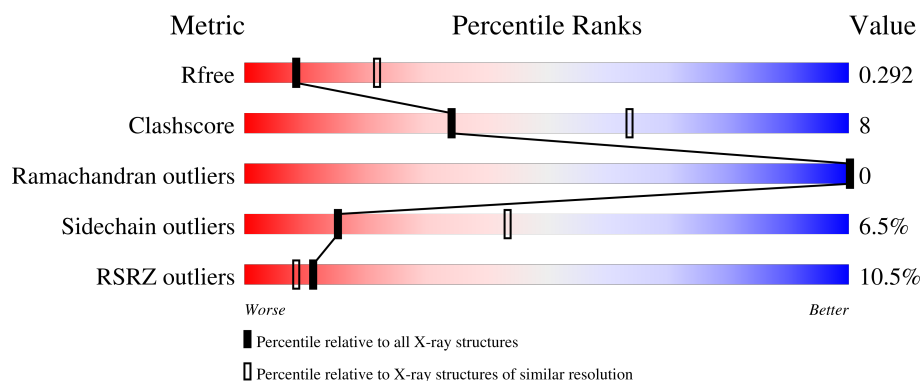
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 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	665	7% 51% 15% • 34%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3487 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.

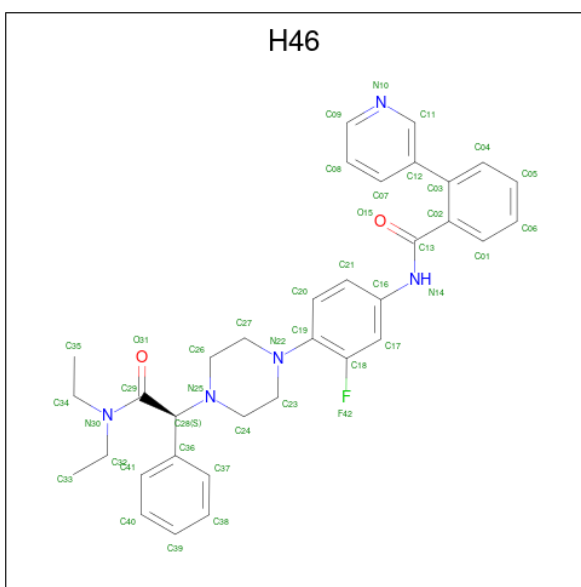
- Molecule 1 is a protein called Human Neuropeptide Y Y2 Receptor fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	437	3414	2222	551	622	19	0	0	0

There are 17 discrepancies between the modelled and reference sequences:

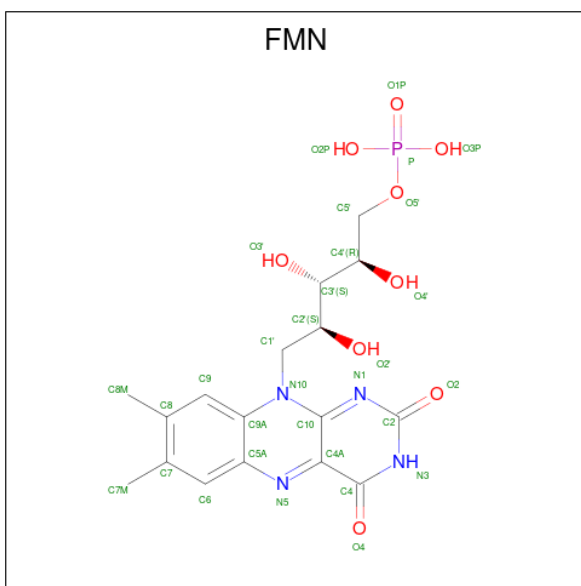
Chain	Residue	Modelled	Actual	Comment	Reference
A	-162	GLY	-	expression tag	UNP A0A097J809
A	-161	ALA	-	expression tag	UNP A0A097J809
A	-160	PRO	-	expression tag	UNP A0A097J809
A	-107	THR	CYS	engineered mutation	UNP A0A097J809
A	-64	ALA	CYS	engineered mutation	UNP A0A097J809
A	149	TYR	HIS	engineered mutation	UNP P49146
A	1000	ALA	-	linker	UNP P49146
A	1096	TRP	TYR	engineered mutation	UNP P00323
A	280	CYS	SER	engineered mutation	UNP P49146
A	354	GLU	-	expression tag	UNP P49146
A	355	PHE	-	expression tag	UNP P49146
A	356	LEU	-	expression tag	UNP P49146
A	357	GLU	-	expression tag	UNP P49146
A	358	VAL	-	expression tag	UNP P49146
A	359	LEU	-	expression tag	UNP P49146
A	360	PHE	-	expression tag	UNP P49146
A	361	GLN	-	expression tag	UNP P49146

- Molecule 2 is {N}-[4-[4-[(1 {S})-2-(diethylamino)-2-oxidanylidene-1-phenyl-ethyl]piperazin-1-yl]-3-fluoranyl-phenyl]-2-pyridin-3-yl-benzamide (CCD ID: H46) (formula: C₃₄H₃₆FN₅O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			42	34	1	5	2		

- Molecule 3 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	96.42Å 50.86Å 184.63Å 90.00° 90.67° 90.00°	Depositor
Resolution (Å)	37.74 – 2.80 37.74 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.7 (37.74-2.80) 96.8 (37.74-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.255 , 0.289 0.256 , 0.292	Depositor DCC
R_{free} test set	2021 reflections (8.95%)	wwPDB-VP
Wilson B-factor (Å ²)	63.1	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3487	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.33% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: H46, FMN

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	0.43	0/3490	0.64	0/4751

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3414	0	3428	53	0
2	A	42	0	0	1	0
3	A	31	0	19	0	0
All	All	3487	0	3447	53	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 8.

All (53) 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:300:LEU:HA	1:A:303:TYR:HB3	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:LEU:HD21	1:A:315:MET:HG3	1.72	0.71
1:A:135:GLN:HB2	1:A:176:SER:HB2	1.82	0.62
1:A:1076:LEU:HD23	1:A:1109:LYS:HG2	1.84	0.59
1:A:1086:VAL:HG21	1:A:1110:LEU:HD13	1.88	0.56
1:A:79:LYS:HA	1:A:82:ARG:HG3	1.88	0.54
1:A:96:ASP:HB3	1:A:318:THR:HB	1.89	0.54
1:A:55:LEU:HA	1:A:58:CYS:SG	2.47	0.54
1:A:1093:ASP:HB3	1:A:1096:TRP:HD1	1.73	0.54
1:A:50:GLN:NE2	1:A:112:LEU:O	2.41	0.53
1:A:101:THR:O	1:A:105:PRO:HG2	2.08	0.52
1:A:146:LEU:O	1:A:150:ARG:HG2	2.10	0.52
1:A:1050:LEU:HD13	1:A:1146:ILE:HD11	1.91	0.51
1:A:308:THR:HG22	2:A:1201:H46:C33	2.42	0.50
1:A:305:LEU:O	1:A:309:VAL:HG12	2.13	0.49
1:A:48:GLU:HB3	1:A:51:VAL:HG12	1.94	0.49
1:A:308:THR:O	1:A:312:ILE:HG13	2.14	0.47
1:A:128:TYR:HB2	1:A:184:ALA:HB2	1.96	0.47
1:A:61:ILE:O	1:A:65:VAL:HG13	2.15	0.47
1:A:118:MET:HB3	1:A:122:LEU:HD12	1.96	0.46
1:A:302:GLU:O	1:A:306:ILE:HG13	2.16	0.46
1:A:70:LEU:HD21	1:A:340:PHE:CE1	2.50	0.45
1:A:328:MET:HE3	1:A:328:MET:HB2	1.54	0.45
1:A:319:PHE:O	1:A:322:PRO:HD2	2.16	0.45
1:A:120:PRO:HB3	1:A:189:TYR:CG	2.51	0.45
1:A:1016:THR:HG21	1:A:1124:ILE:HD11	1.97	0.45
1:A:1063:ILE:HD13	1:A:1101:GLY:HA3	1.98	0.45
1:A:1093:ASP:HB3	1:A:1096:TRP:CD1	2.51	0.45
1:A:318:THR:OG1	1:A:319:PHE:N	2.49	0.45
1:A:209:GLY:HA3	1:A:212:LYS:HG2	1.98	0.45
1:A:86:ASN:HA	1:A:89:ILE:HB	1.98	0.44
1:A:120:PRO:HB3	1:A:189:TYR:CD2	2.52	0.44
1:A:327:TRP:CE3	1:A:328:MET:HE2	2.52	0.44
1:A:1006:TYR:HA	1:A:1054:GLY:O	2.18	0.43
1:A:131:GLY:O	1:A:135:GLN:HG2	2.18	0.43
1:A:261:GLN:HE21	1:A:265:LYS:HE2	1.84	0.43
1:A:214:ILE:O	1:A:218:VAL:HG13	2.19	0.42
1:A:90:ALA:O	1:A:94:VAL:HG23	2.20	0.42
1:A:144:ILE:CG2	1:A:270:LEU:HD13	2.50	0.42
1:A:324:LEU:HD22	1:A:328:MET:HE1	2.00	0.42
1:A:230:LEU:HB3	1:A:231:PRO:HD3	2.01	0.42
1:A:1054:GLY:HA2	1:A:1089:PHE:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1103:VAL:O	1:A:1107:GLU:HG3	2.20	0.41
1:A:54:ILE:HG12	1:A:112:LEU:HD11	2.02	0.41
1:A:194:ILE:H	1:A:194:ILE:HG13	1.62	0.41
1:A:221:LEU:HD23	1:A:221:LEU:HA	1.87	0.41
1:A:192:ILE:O	1:A:200:ILE:HG23	2.20	0.41
1:A:79:LYS:HA	1:A:79:LYS:HD2	1.92	0.41
1:A:212:LYS:HA	1:A:212:LYS:HD3	1.87	0.41
1:A:315:MET:O	1:A:318:THR:HG23	2.21	0.40
1:A:56:ALA:O	1:A:60:ILE:HG13	2.21	0.40
1:A:242:ILE:HD13	1:A:242:ILE:HG21	1.81	0.40
1:A:300:LEU:HD23	1:A:303:TYR:CD1	2.57	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	435/665 (65%)	419 (96%)	16 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	368/563 (65%)	344 (94%)	24 (6%)	15	43

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

Mol	Chain	Res	Type
1	A	158	SER
1	A	188	GLU
1	A	192	ILE
1	A	193	GLU
1	A	197	ASP
1	A	198	PHE
1	A	201	VAL
1	A	204	THR
1	A	213	SER
1	A	214	ILE
1	A	218	VAL
1	A	224	LEU
1	A	249	HIS
1	A	1034	ARG
1	A	1061	ASP
1	A	1085	LYS
1	A	1118	VAL
1	A	1143	ARG
1	A	263	ARG
1	A	294	ASP
1	A	295	SER
1	A	297	VAL
1	A	318	THR
1	A	343	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	248	ASN
1	A	249	HIS
1	A	1112	ASN
1	A	260	HIS
1	A	261	GLN
1	A	285	HIS

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	H46	A	1201	-	46,46,46	3.08	24 (52%)	62,63,63	2.96	21 (33%)
3	FMN	A	1202	-	33,33,33	1.17	2 (6%)	48,50,50	1.59	10 (20%)

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	H46	A	1201	-	-	11/36/46/46	0/5/5/5
3	FMN	A	1202	-	-	0/18/18/18	0/3/3/3

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	H46	C29-N30	7.22	1.45	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1201	H46	C24-N25	-6.53	1.35	1.47
2	A	1201	H46	C26-N25	-6.48	1.35	1.47
2	A	1201	H46	C16-N14	6.11	1.54	1.41
2	A	1201	H46	C13-N14	5.46	1.51	1.35
2	A	1201	H46	F42-C18	5.27	1.49	1.35
2	A	1201	H46	C38-C37	4.48	1.46	1.38
2	A	1201	H46	C36-C28	3.88	1.57	1.52
2	A	1201	H46	C21-C20	3.72	1.44	1.38
2	A	1201	H46	C40-C41	3.59	1.45	1.38
2	A	1201	H46	C11-N10	3.46	1.41	1.34
2	A	1201	H46	C17-C18	3.29	1.43	1.37
2	A	1201	H46	C04-C03	3.26	1.44	1.40
3	A	1202	FMN	C4A-N5	3.19	1.37	1.30
2	A	1201	H46	C02-C13	3.09	1.56	1.50
2	A	1201	H46	C28-N25	-2.96	1.42	1.47
2	A	1201	H46	C21-C16	2.78	1.43	1.39
2	A	1201	H46	C03-C12	2.72	1.54	1.49
2	A	1201	H46	C37-C36	2.70	1.43	1.39
3	A	1202	FMN	C10-N1	2.60	1.38	1.33
2	A	1201	H46	C40-C39	2.56	1.43	1.38
2	A	1201	H46	O31-C29	2.53	1.26	1.22
2	A	1201	H46	C11-C12	2.49	1.43	1.39
2	A	1201	H46	C39-C38	2.41	1.43	1.38
2	A	1201	H46	C09-N10	2.21	1.40	1.33
2	A	1201	H46	C08-C09	2.18	1.44	1.37

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	H46	C18-C19-N22	-9.64	109.14	120.42
2	A	1201	H46	C36-C28-C29	-8.43	95.06	111.87
2	A	1201	H46	C29-C28-N25	-7.90	99.70	110.24
2	A	1201	H46	C16-N14-C13	-6.14	110.43	126.61
2	A	1201	H46	C27-N22-C23	5.85	124.73	111.57
2	A	1201	H46	C24-N25-C28	-5.42	100.01	112.19
2	A	1201	H46	F42-C18-C19	-4.94	113.67	118.37
2	A	1201	H46	C17-C18-C19	-4.89	119.03	123.35
2	A	1201	H46	F42-C18-C17	4.30	127.24	118.64
2	A	1201	H46	C20-C19-C18	3.95	125.10	117.31
2	A	1201	H46	C24-C23-N22	-3.55	103.30	110.78
3	A	1202	FMN	C5A-C9A-N10	3.51	121.14	117.97
3	A	1202	FMN	C4-N3-C2	-3.39	119.63	125.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1202	FMN	C9A-C5A-N5	-3.35	118.90	122.45
2	A	1201	H46	C36-C28-N25	3.09	116.09	111.53
3	A	1202	FMN	O4'-C4'-C5'	-3.00	103.37	109.99
2	A	1201	H46	C26-N25-C24	2.81	114.49	109.13
3	A	1202	FMN	C5'-C4'-C3'	2.77	117.45	112.22
2	A	1201	H46	C07-C08-C09	2.75	122.90	118.92
3	A	1202	FMN	C4A-C4-N3	2.74	120.24	113.25
3	A	1202	FMN	O4-C4-C4A	-2.71	119.38	126.53
2	A	1201	H46	C35-C34-N30	-2.41	102.48	111.86
3	A	1202	FMN	C4A-C10-N1	-2.35	118.82	124.59
2	A	1201	H46	C41-C36-C28	-2.30	117.33	120.69
2	A	1201	H46	C40-C39-C38	-2.26	116.78	119.87
2	A	1201	H46	C09-N10-C11	2.22	120.74	116.85
2	A	1201	H46	C08-C07-C12	-2.20	118.04	120.54
3	A	1202	FMN	O5'-P-O1P	2.12	112.17	106.44
2	A	1201	H46	C20-C19-N22	2.11	125.72	122.42
3	A	1202	FMN	C4-C4A-C10	2.08	120.50	116.93
2	A	1201	H46	C39-C38-C37	2.00	122.71	120.24

There are no chirality outliers.

All (11) torsion outliers are listed below:

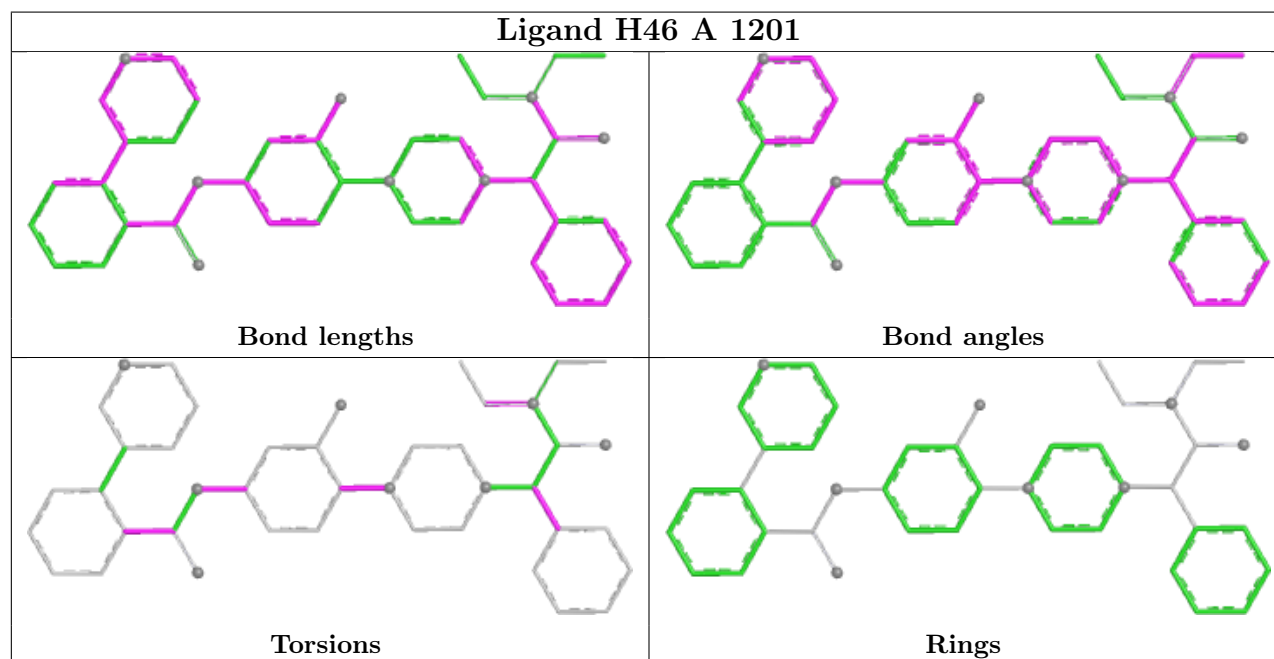
Mol	Chain	Res	Type	Atoms
2	A	1201	H46	C18-C19-N22-C27
2	A	1201	H46	C33-C32-N30-C34
2	A	1201	H46	C21-C16-N14-C13
2	A	1201	H46	C17-C16-N14-C13
2	A	1201	H46	C20-C19-N22-C27
2	A	1201	H46	C01-C02-C13-O15
2	A	1201	H46	C33-C32-N30-C29
2	A	1201	H46	C29-C28-C36-C41
2	A	1201	H46	C01-C02-C13-N14
2	A	1201	H46	C29-C28-C36-C37
2	A	1201	H46	C18-C19-N22-C23

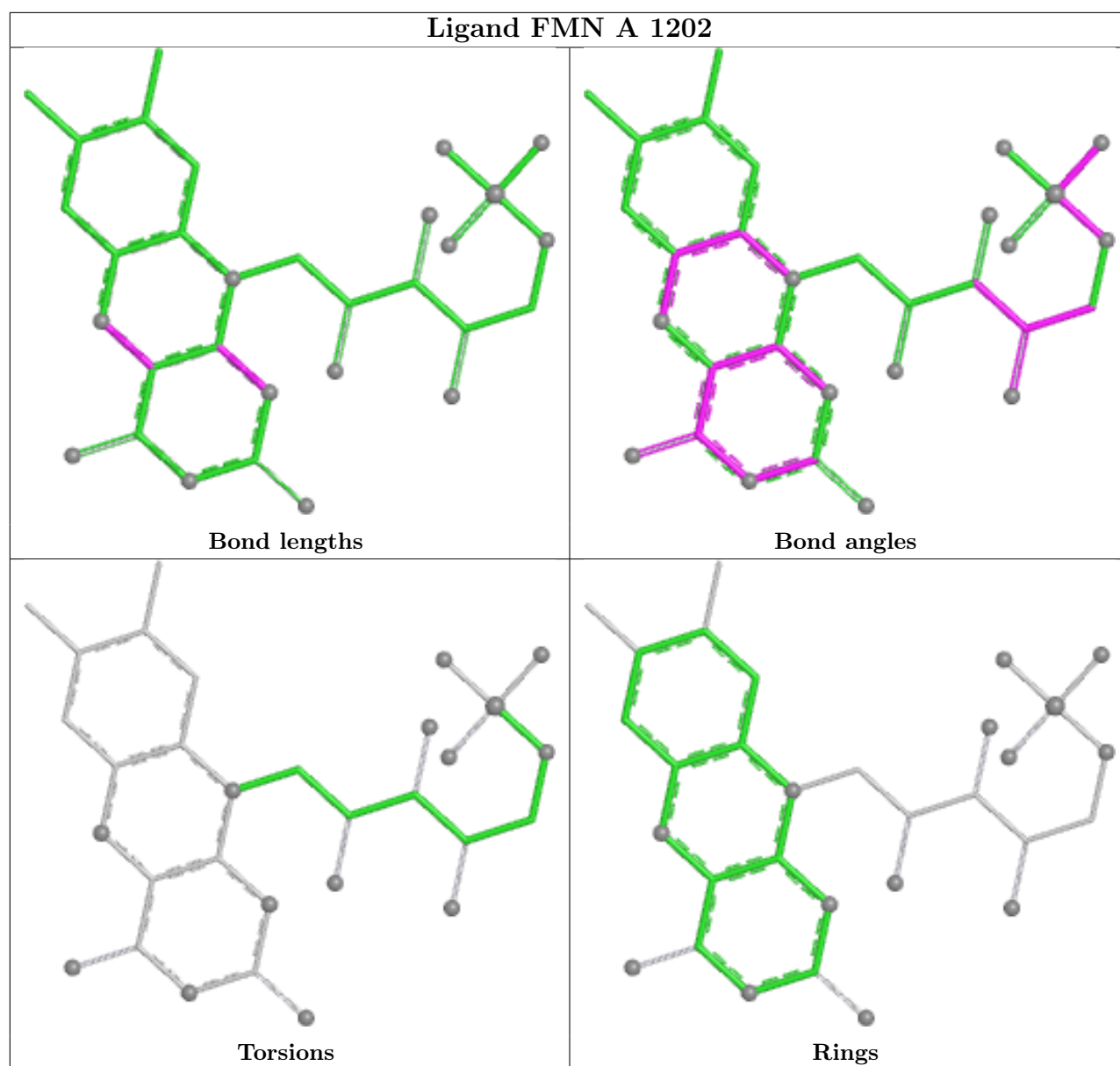
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	H46	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [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	437/665 (65%)	0.70	46 (10%) 11 8	31, 67, 115, 140	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	203	CYS	6.7
1	A	298	LEU	5.8
1	A	291	VAL	4.9
1	A	198	PHE	4.4
1	A	297	VAL	4.1
1	A	292	ASP	4.0
1	A	1116	GLU	3.8
1	A	212	LYS	3.8
1	A	293	ILE	3.5
1	A	202	ALA	3.5
1	A	196	PRO	3.3
1	A	190	SER	3.1
1	A	123	CYS	3.1
1	A	194	ILE	3.1
1	A	301	LYS	3.0
1	A	189	TYR	2.9
1	A	300	LEU	2.9
1	A	49	VAL	2.8
1	A	337	LEU	2.7
1	A	243	TRP	2.7
1	A	126	VAL	2.7
1	A	192	ILE	2.6
1	A	53	LEU	2.4
1	A	120	PRO	2.4
1	A	318	THR	2.4
1	A	268	LYS	2.4
1	A	51	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	119	GLY	2.4
1	A	1119	GLN	2.4
1	A	327	TRP	2.3
1	A	116	TRP	2.3
1	A	208	PRO	2.3
1	A	341	ARG	2.3
1	A	249	HIS	2.2
1	A	215	TYR	2.2
1	A	163	ARG	2.1
1	A	1134	ASP	2.1
1	A	340	PHE	2.1
1	A	214	ILE	2.1
1	A	200	ILE	2.1
1	A	257	ASP	2.1
1	A	161	SER	2.1
1	A	50	GLN	2.0
1	A	52	VAL	2.0
1	A	223	SER	2.0
1	A	132	LEU	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.

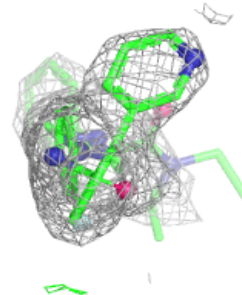
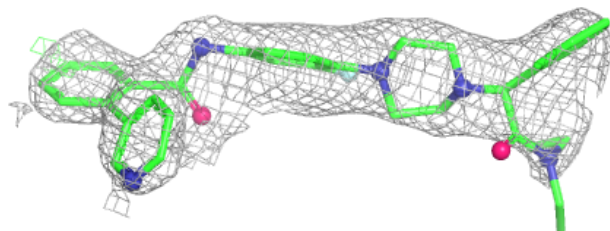
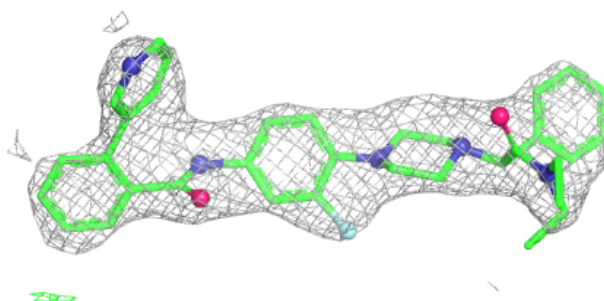
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	H46	A	1201	42/42	0.91	0.15	72,83,96,99	0
3	FMN	A	1202	31/31	0.95	0.10	42,49,54,63	0

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.

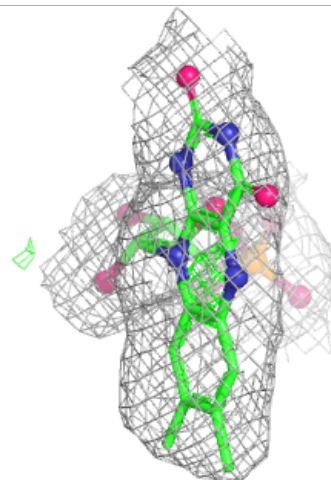
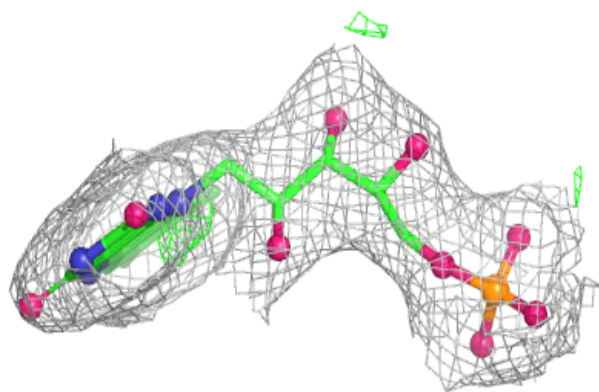
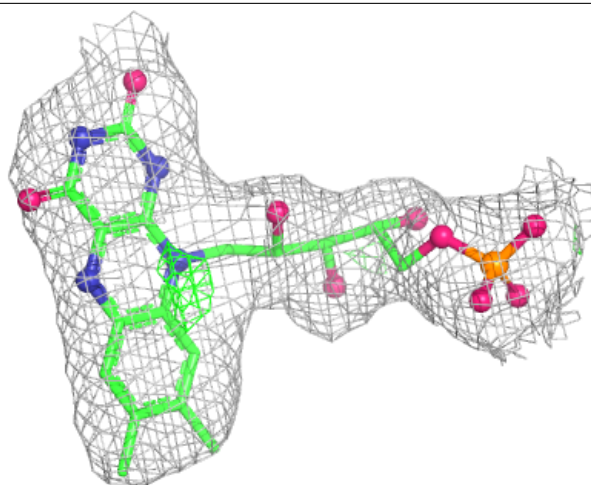
Electron density around H46 A 1201:

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



Electron density around FMN A 1202:

$2mF_o-DF_c$ (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.