

Full wwPDB X-ray Structure Validation Report (i)

Oct 19, 2022 – 12:01 PM EDT

PDB ID : 3N7S

Title : Crystal structure of the ectodomain complex of the CGRP receptor, a Class-B

GPCR, reveals the site of drug antagonism

Authors : Ter Haar, E. Deposited on : 2010-05-27

Resolution : 2.10 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.orgA user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.31.2 buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

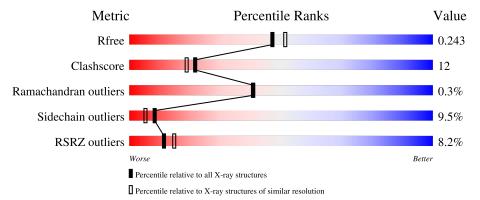
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 2.10 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	115	71%	9% •	18%					
1	В	115	7% 62%	17% •	17%					
2	С	96	70%	17%	8% 5%					
2	D	96	72%	11% •	12%					

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard



residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	3N7	В	1	-	-	X	-



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 3116 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 Calcitonin gene-related peptide type 1 receptor.

\mathbf{Mol}	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	94	Total 740	C 460		O 143	S 9	0	0	0
1	В	95	Total 760			O 147	S 9	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	GLY	-	expression tag	UNP Q16602
A	20	SER	-	expression tag	UNP Q16602
A	21	HIS	-	expression tag	UNP Q16602
A	22	MET	-	expression tag	UNP Q16602
В	19	GLY	-	expression tag	UNP Q16602
В	20	SER	-	expression tag	UNP Q16602
В	21	HIS	-	expression tag	UNP Q16602
В	22	MET	-	expression tag	UNP Q16602

• Molecule 2 is a protein called Receptor activity-modifying protein 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
9	C	91	Total	С	N	О	S	0	0	0
2	2 C	91	725	458	129	130	8	0	U	
9	D	84	Total	С	N	О	S	0	0	0
2	D	04	675	430	119	118	8	0	0	

There are 8 discrepancies between the modelled and reference sequences:

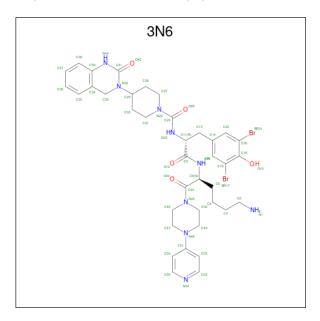
Chain	Residue	Modelled	Actual	Comment	Reference
С	22	GLY	-	expression tag	UNP O60894
С	23	SER	-	expression tag	UNP O60894
С	24	HIS	-	expression tag	UNP O60894
С	25	MET	=	expression tag	UNP O60894



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Chain	Residue	Modelled	Actual	Comment	Reference
D	22	GLY	-	expression tag	UNP O60894
D	23	SER	-	expression tag	UNP O60894
D	24	HIS	-	expression tag	UNP O60894
D	25	MET	-	expression tag	UNP O60894

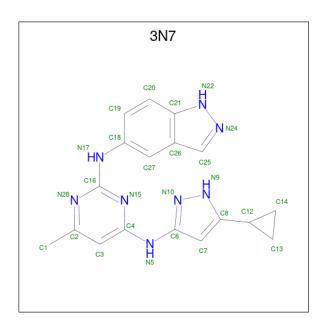
• Molecule 3 is N-{(1S)-5-amino-1-[(4-pyridin-4-ylpiperazin-1-yl)carbonyl]pentyl}-3,5-dibrom o-Nalpha-{[4-(2-oxo-1,4-dihydroquinazolin-3 (2H)-yl)piperidin-1-yl]carbonyl}-D-tyrosinami de (three-letter code: 3N6) (formula: $C_{38}H_{47}Br_2N_9O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
9	Λ	1	Total	Br	С	N	О	0	0
3	A	1	54	2	38	9	5	U	

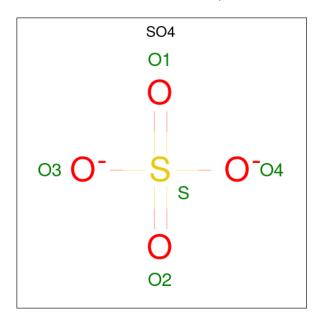
• Molecule 4 is N 4 -(5-cyclopropyl-1H-pyrazol-3-yl)-N 2 -1H-indazol-5-yl-6-methylpyrimidine -2,4-diamine (three-letter code: 3N7) (formula: $C_{18}H_{18}N_8$).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	В	1	Total 26	C 18	N 8	0	0

 \bullet Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: $\mathrm{O_4S}).$



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

• Molecule 6 is water.



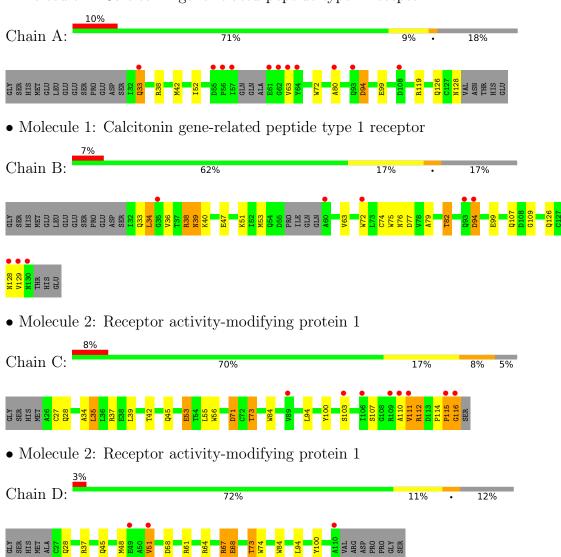
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	27	Total O 27 27	0	0
6	В	41	Total O 41 41	0	0
6	С	35	Total O 35 35	0	0
6	D	28	Total O 28 28	0	0



3 Residue-property plots (i)

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

• Molecule 1: Calcitonin gene-related peptide type 1 receptor





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants	73.31Å 119.13Å 137.16Å	Donogitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.17 - 2.10	Depositor
Resolution (A)	46.17 - 2.10	EDS
% Data completeness	(Not available) (46.17-2.10)	Depositor
(in resolution range)	86.7 (46.17-2.10)	EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.36 (at 2.10Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.9.2, BUSTER 2.9.2	Depositor
D D.	0.208 , 0.226	Depositor
R, R_{free}	0.218 , 0.243	DCC
R_{free} test set	1509 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.648	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 51.2	EDS
L-test for twinning ²	$< L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3116	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.32% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

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: 3N7, 3N6, 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		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.45	0/761	0.68	0/1036	
1	В	0.45	0/780	0.65	0/1058	
2	С	0.48	0/746	0.87	3/1012 (0.3%)	
2	D	0.45	0/694	0.63	0/941	
All	All	0.46	0/2981	0.71	3/4047 (0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	В	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

	Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
	2	С	116	GLY	N-CA-C	-7.07	95.43	113.10
ſ	2	С	110	ALA	N-CA-C	6.01	127.22	111.00
	2	С	115	PRO	CB-CA-C	5.89	126.73	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	128	ASN	Peptide



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	740	0	629	14	0
1	В	760	0	667	23	0
2	С	725	0	663	17	0
2	D	675	0	621	18	0
3	A	54	0	46	3	0
4	В	26	0	18	16	0
5	С	5	0	0	0	0
6	A	27	0	0	0	0
6	В	41	0	0	4	0
6	С	35	0	0	3	0
6	D	28	0	0	2	0
All	All	3116	0	2644	67	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 12.

All (67) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
7100111-1	1100111-2	${f distance}({f A})$	overlap(A)
2:D:37:ARG:NH2	6:D:205:HOH:O	1.90	1.03
4:B:1:3N7:H25	6:B:216:HOH:O	1.63	0.98
1:B:76:ASN:H	4:B:1:3N7:H27	1.37	0.89
1:B:79:ALA:O	1:B:82:THR:HG23	1.76	0.85
2:C:111:VAL:HG12	2:C:112:ARG:N	1.92	0.84
2:C:73:THR:CG2	2:C:84:TRP:HE1	1.90	0.83
2:C:94:LEU:HB3	6:C:230:HOH:O	1.80	0.82
2:D:73:THR:CG2	2:D:84:TRP:HE1	1.93	0.82
1:B:38:ARG:NH2	2:C:71:ASP:OD2	2.16	0.78
2:C:111:VAL:HG12	2:C:112:ARG:H	1.47	0.78
1:B:75:TRP:HA	4:B:1:3N7:H27	1.66	0.77
1:A:99:GLU:HG2	1:A:126:GLN:O	1.85	0.75
1:A:52:ILE:HG22	2:D:94:LEU:HD21	1.67	0.75
2:C:73:THR:HG23	2:C:84:TRP:HE1	1.53	0.72
2:C:111:VAL:CG1	2:C:112:ARG:N	2.54	0.70
1:B:76:ASN:N	4:B:1:3N7:H27	2.05	0.70



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Continuea from prev		Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	$\text{overlap } (\mathring{\mathbf{A}})$
4:B:1:3N7:H14	6:B:208:HOH:O	1.95	0.67
2:C:37:ARG:NH2	6:C:209:HOH:O	2.29	0.65
2:D:73:THR:HG23	2:D:84:TRP:HE1	1.62	0.63
1:A:119:ARG:HH12	2:C:35:LEU:HD13	1.66	0.61
2:D:64:ARG:O	2:D:68:GLU:HG2	2.00	0.61
1:B:76:ASN:H	4:B:1:3N7:C27	2.11	0.60
2:D:58:ASP:OD2	2:D:61:ARG:HG2	2.04	0.58
2:D:73:THR:HG22	2:D:84:TRP:HE1	1.69	0.57
4:B:1:3N7:N15	4:B:1:3N7:H19	2.20	0.57
2:D:45:GLN:HG2	2:D:100:TYR:OH	2.05	0.57
2:C:111:VAL:HG12	2:C:112:ARG:HG2	1.87	0.56
1:B:39:ASN:ND2	6:B:218:HOH:O	2.40	0.55
1:B:51:LYS:HE3	4:B:1:3N7:H1A	1.89	0.55
1:A:63:VAL:O	1:A:80:ALA:HB2	2.08	0.54
1:A:42:MET:HG3	2:D:67:ARG:HB2	1.90	0.54
1:A:38:ARG:CZ	2:D:67:ARG:HG3	2.38	0.54
1:B:72:TRP:NE1	6:B:238:HOH:O	2.16	0.52
1:B:36:VAL:O	1:B:40:LYS:HG3	2.09	0.51
1:A:119:ARG:HD2	2:C:34:ALA:HB1	1.91	0.51
2:D:48:MET:HA	2:D:51:VAL:HG13	1.94	0.49
2:C:53:GLU:HA	2:C:56:TRP:CD2	2.47	0.49
1:B:33:GLN:O	1:B:38:ARG:HB2	2.14	0.48
2:D:64:ARG:O	2:D:68:GLU:CG	2.61	0.47
1:B:47:GLU:OE2	4:B:1:3N7:H3	2.15	0.47
1:A:72:TRP:CZ3	3:A:1:3N6:H33A	2.50	0.47
2:C:114:PRO:HA	2:C:115:PRO:HD2	1.64	0.47
1:B:36:VAL:CG1	1:B:40:LYS:HE3	2.45	0.46
2:C:111:VAL:CG1	2:C:112:ARG:HG2	2.46	0.46
1:B:51:LYS:HD2	4:B:1:3N7:C1	2.46	0.46
1:B:74:CYS:HB3	4:B:1:3N7:N28	2.32	0.45
3:A:1:3N6:H2A	2:D:74:TRP:CE2	2.52	0.45
1:B:99:GLU:HG3	1:B:126:GLN:O	2.16	0.45
1:B:34:LEU:CD1	1:B:38:ARG:NH1	2.79	0.45
2:D:67:ARG:NH2	6:D:209:HOH:O	2.48	0.44
1:A:33:GLN:HG2	1:A:33:GLN:O	2.17	0.44
1:A:38:ARG:NH2	2:D:67:ARG:HG2	2.33	0.44
1:A:52:ILE:CG2	2:D:94:LEU:HD21	2.42	0.43
2:C:45:GLN:HG2	2:C:100:TYR:OH	2.18	0.43
1:A:94:ASP:OD1	1:A:94:ASP:N	2.50	0.43
1:A:38:ARG:NE	2:D:67:ARG:HG3	2.34	0.43
2:C:103:SER:HB2	6:C:226:HOH:O	2.18	0.42



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Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:B:94:ASP:OD1	1:B:94:ASP:N	2.46	0.42
3:A:1:3N6:H2A	2:D:74:TRP:CD1	2.54	0.42
1:B:51:LYS:CE	4:B:1:3N7:H1A	2.49	0.42
1:B:63:VAL:HG12	1:B:109:GLY:HA3	2.01	0.42
1:A:52:ILE:HD13	1:A:52:ILE:HG21	1.63	0.41
1:B:75:TRP:HA	4:B:1:3N7:C27	2.45	0.41
4:B:1:3N7:C3	4:B:1:3N7:C7	2.95	0.41
2:C:115:PRO:HA	2:C:116:GLY:HA2	1.83	0.41
1:B:75:TRP:CA	4:B:1:3N7:H27	2.42	0.40
1:B:51:LYS:HD2	4:B:1:3N7:H1A	2.03	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	Perce	ntiles
1	A	90/115 (78%)	86 (96%)	4 (4%)	0	100	100
1	В	91/115 (79%)	86 (94%)	4 (4%)	1 (1%)	14	9
2	С	89/96 (93%)	85 (96%)	4 (4%)	0	100	100
2	D	82/96 (85%)	80 (98%)	2 (2%)	0	100	100
All	All	352/422 (83%)	337 (96%)	14 (4%)	1 (0%)	41	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	129	VAL



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	ain Analysed Rotameric Outliers		Percentiles		
1	A	75/104~(72%)	72~(96%)	3 (4%)	31 3	32
1	В	80/104 (77%)	72 (90%)	8 (10%)	7 5	5
2	С	73/79 (92%)	61 (84%)	12 (16%)	2 1	
2	D	67/79 (85%)	62 (92%)	5 (8%)	13 1	.0
All	All	295/366 (81%)	267 (90%)	28 (10%)	8 5	5

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A A	33	GLN
1	A	94	ASP
1	A B	128	ASN
1	В	34	LEU
1	В	38	ARG
1	В	39	ASN
1	В	53	MET
1	В	77	ASP THR
1	В	82	THR
1	В	94	ASP GLN
1	В	107	GLN
2	С	27	CYS
2 2 2	С	28	GLN
2	С	35	LEU
	С	39	LEU
2 2	С	42	THR
	С	53	GLU
2 2	С	55	LEU
2	С	71	ASP
2 2 2	B C C C C C C C C C C C C C C C D	73	LEU ASP THR
2	С	107	SER
2	С	111	VAL
2	С	112	ARG
2	D	28	GLN



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Mol	Chain	Res	Type
2	D	51	VAL
2	D	67	ARG
2	D	68	GLU
2	D	73	THR

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	33	GLN
1	A	86	GLN
1	В	66	ASN
1	В	86	GLN
2	С	45	GLN
2	D	45	GLN

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 monosaccharides 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 Cha		Chain	Chain Res	Res Link	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	С	1	-	4,4,4	0.46	0	6,6,6	0.25	0
4	3N7	В	1	-	27,30,30	2.84	13 (48%)	33,43,43	5.74	17 (51%)
3	3N6	A	1	-	59,59,59	0.77	1 (1%)	78,82,82	1.33	13 (16%)

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	3N7	В	1	-	-	5/10/14/14	0/5/5/5
3	3N6	A	1	-	-	4/41/73/73	0/6/6/6

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
4	В	1	3N7	C4-N5	6.02	1.49	1.38
4	В	1	3N7	C7-C8	-5.59	1.29	1.39
4	В	1	3N7	C25-C26	-5.18	1.29	1.40
4	В	1	3N7	C3-C4	4.97	1.52	1.39
4	В	1	3N7	C27-C26	-4.32	1.32	1.42
4	В	1	3N7	N10-N9	3.35	1.44	1.37
4	В	1	3N7	C8-N9	3.25	1.38	1.34
4	В	1	3N7	C20-C21	-3.22	1.36	1.41
4	В	1	3N7	C19-C18	2.77	1.43	1.39
3	A	1	3N6	C39-C34	2.29	1.43	1.40
4	В	1	3N7	C6-N5	2.27	1.42	1.38
4	В	1	3N7	C18-N17	2.18	1.45	1.40
4	В	1	3N7	C8-C12	2.14	1.55	1.50
4	В	1	3N7	C25-N24	-2.01	1.27	1.33

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
4	В	1	3N7	C14-C12-C8	-15.76	101.81	120.33
4	В	1	3N7	C12-C8-N9	14.81	142.11	120.23
4	В	1	3N7	C13-C12-C8	13.42	136.10	120.33
4	В	1	3N7	C8-C7-C6	10.09	114.98	106.07
4	В	1	3N7	C7-C8-C12	-9.11	115.24	129.25
4	В	1	3N7	C6-N5-C4	-7.72	103.61	128.62
4	В	1	3N7	C7-C8-N9	-5.70	102.65	110.28



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}({}^o)$	$\operatorname{Ideal}({}^{o})$
4	В	1	3N7	C1-C2-N28	5.03	124.58	116.56
4	В	1	3N7	C3-C4-N15	-4.97	112.88	123.41
4	В	1	3N7	C3-C2-N28	-4.73	114.61	121.49
4	В	1	3N7	C19-C20-C21	-3.60	116.31	120.84
4	В	1	3N7	C16-N15-C4	3.49	123.22	116.28
4	В	1	3N7	C16-N28-C2	3.39	123.34	115.99
4	В	1	3N7	N28-C16-N15	-3.20	121.17	126.23
4	В	1	3N7	C19-C18-C27	-3.17	114.56	119.33
3	A	1	3N6	O42-C41-N32	-3.00	119.34	123.11
3	A	1	3N6	C34-C33-N32	2.95	116.65	111.88
4	В	1	3N7	C7-C6-N10	-2.93	106.28	110.47
4	В	1	3N7	C3-C4-N5	2.85	129.27	120.24
3	A	1	3N6	C50-N45-C46	2.78	117.97	112.62
3	A	1	3N6	C31-N26-C27	2.70	117.83	112.62
3	A	1	3N6	C47-N48-C51	-2.70	110.81	118.09
3	A	1	3N6	C35-C34-C39	2.67	120.95	118.32
3	A	1	3N6	C55-N54-C53	2.64	123.07	116.85
3	A	1	3N6	BR17-C16-C18	2.55	121.67	118.80
3	A	1	3N6	O42-C41-N40	-2.52	117.42	121.54
3	A	1	3N6	C49-N48-C51	-2.49	111.38	118.09
3	A	1	3N6	C20-C18-C16	2.47	119.64	116.56
3	A	1	3N6	C15-C16-C18	-2.22	119.48	121.90
3	A	1	3N6	C52-C53-N54	-2.20	119.80	123.62

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	В	1	3N7	C13-C12-C8-C7
4	В	1	3N7	C13-C12-C8-N9
3	A	1	3N6	C2-C3-C4-C5
4	В	1	3N7	C14-C12-C8-C7
4	В	1	3N7	C14-C12-C8-N9
3	A	1	3N6	C52-C51-N48-C47
4	В	1	3N7	N15-C4-N5-C6
3	A	1	3N6	C56-C51-N48-C47
3	A	1	3N6	N1-C2-C3-C4

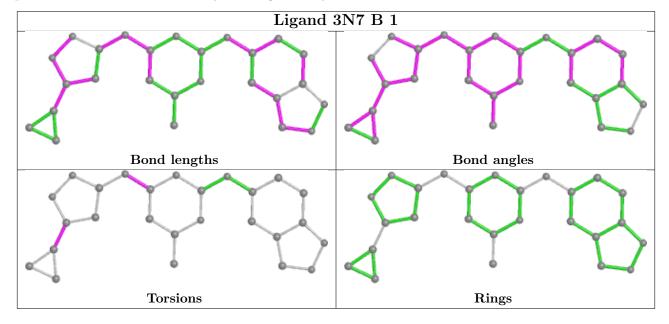
There are no ring outliers.

2 monomers are involved in 19 short contacts:

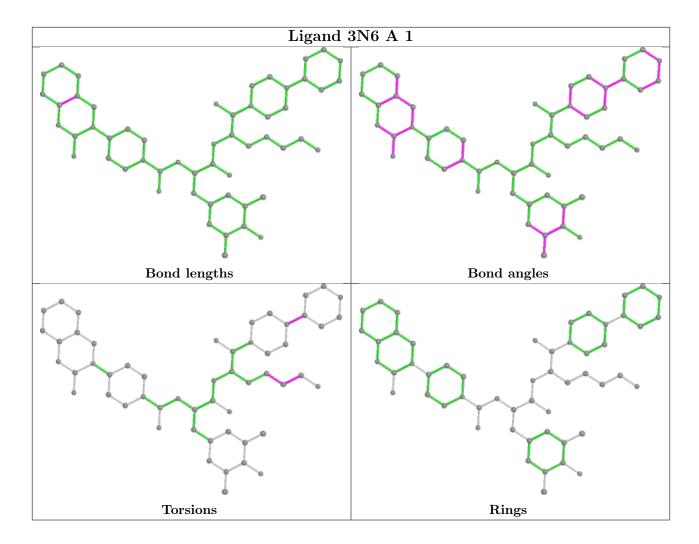


Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	В	1	3N7	16	0
3	A	1	3N6	3	0

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 then 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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95^{th} 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>	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	94/115 (81%)	0.41	11 (11%) 4 6	28, 51, 78, 95	0
1	В	95/115 (82%)	0.32	8 (8%) 11 14	19, 39, 74, 87	0
2	С	91/96 (94%)	0.70	8 (8%) 10 12	20, 33, 68, 78	0
2	D	84/96 (87%)	0.05	3 (3%) 42 49	27, 37, 61, 72	0
All	All	$364/422 \ (86\%)$	0.38	30 (8%) 11 15	19, 39, 72, 95	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	С	110	ALA	9.1
1	A	64	TYR	6.1
2	С	115	PRO	5.5
1	В	129	VAL	5.3
2	С	109	ARG	5.2
2	D	110	ALA	5.0
1	A	62	GLY	4.6
1	В	130	ASN	4.5
2	С	116	GLY	4.4
2	С	106	ILE	3.8
1	A	57	ILE	3.7
1	В	94	ASP	3.4
1	A	33	GLN	3.2
1	В	93	GLN	3.1
1	A	63	VAL	2.9
1	В	35	GLY	2.9
1	A	80	ALA	2.7
2	D	51	VAL	2.6
1	В	60	ALA	2.6
2	С	111	VAL	2.5
1	В	128	ASN	2.4



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Mol	Chain	Res	Type	RSRZ	
2	С	103	SER	2.4	
1	A	56	PRO	2.4	
1	A	108	ASP	2.3	
2	D	49	GLU	2.2	
1	A	93	GLN	2.1	
1	В	72	TRP	2.1	
1	A	55	ASP	2.0	
2	С	89	VAL	2.0	
1	A	61	GLU	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 monosaccharides in this entry.

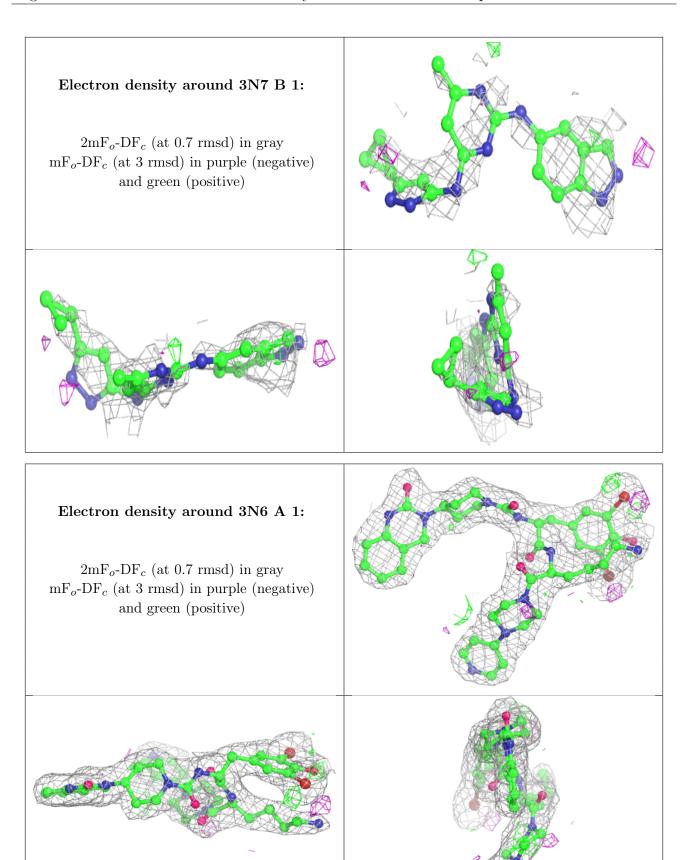
6.4 Ligands (i)

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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{A}^2)$	Q<0.9
4	3N7	В	1	26/26	0.68	0.40	108,110,111,111	0
5	SO4	С	1	5/5	0.91	0.27	78,82,83,84	0
3	3N6	A	1	54/54	0.96	0.13	26,34,47,48	2

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.







6.5 Other polymers (i)

There are no such residues in this entry.

