

Full wwPDB X-ray Structure Validation Report (i)

Oct 12, 2023 – 05:47 AM EDT

PDB ID : 8DQ8

Title: The structure of NicA2 variant F104L/A107T/S146I/G317D/H368R/L449V/

N462S in complex with N-methylmyosmine

Authors: Wu, K.; Dulchavsky, M.; Li, J.; Bardwell, J.C.A.

Deposited on : 2022-07-18

Resolution : 1.90 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 (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 : 2.35.1

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)

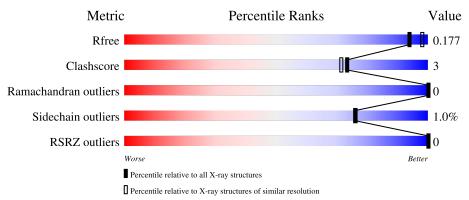
Validation Pipeline (wwPDB-VP) : 2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.90 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 <=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	432	94%	6%					
1	В	432	91%	9%					



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7523 atoms, of which 102 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 Amine oxidase.

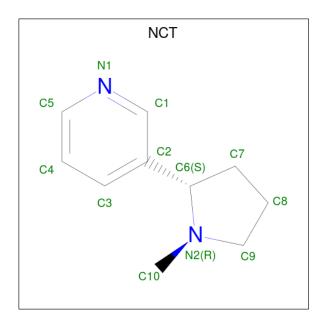
\mathbf{Mol}	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	432	Total 3318	C 2105	N 571	O 629	S 13	0	3	0
1	В	432	Total 3362	C 2133	N 581	O 635	S 13	0	5	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	104	LEU	PHE	engineered mutation	UNP F8G0P2
A	107	THR	ALA	engineered mutation	UNP F8G0P2
A	146	ILE	SER	engineered mutation	UNP F8G0P2
A	317	ASP	GLY	engineered mutation	UNP F8G0P2
A	368	ARG	HIS	engineered mutation	UNP F8G0P2
A	449	VAL	LEU	engineered mutation	UNP F8G0P2
A	462	SER	ASN	engineered mutation	UNP F8G0P2
В	104	LEU	PHE	engineered mutation	UNP F8G0P2
В	107	THR	ALA	engineered mutation	UNP F8G0P2
В	146	ILE	SER	engineered mutation	UNP F8G0P2
В	317	ASP	GLY	engineered mutation	UNP F8G0P2
В	368	ARG	HIS	engineered mutation	UNP F8G0P2
В	449	VAL	LEU	engineered mutation	UNP F8G0P2
В	462	SER	ASN	engineered mutation	UNP F8G0P2

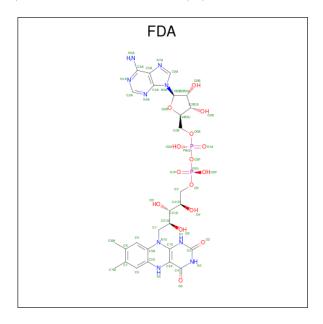
• Molecule 2 is (S)-3-(1-METHYLPYRROLIDIN-2-YL)PYRIDINE (three-letter code: NCT) (formula: $C_{10}H_{14}N_2$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	A	A ton	\mathbf{as}		ZeroOcc	AltConf	
2	Λ	1	Total	С	Н	N	0	0	
2 A	A	1	24	10	12	2	0	U	
9	D	1	Total	С	Н	N	0	0	
2	2 B	1	24	10	12	2	0		

• Molecule 3 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (three-letter code: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



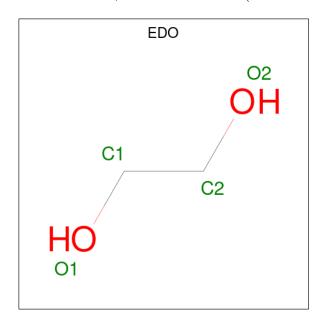
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total 86	C 27	H 33	N 9	O 15	P 2	0	0



 $Continued\ from\ previous\ page...$

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	В	1	Total	С	Н	N	О	Р	0	0
)	В	1	86	27	33	9	15	2	0	0

 \bullet Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\mathrm{C_2H_6O_2}).$



Mol	Chain	Residues	A	ton	ns	ZeroOcc	AltConf
4	A	1	Total 10			0	0
4	В	1	Total 10			0	0

• Molecule 5 is water.

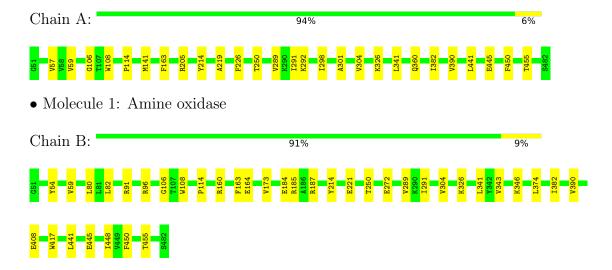
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	288	Total O 288 288	0	0
5	В	315	Total O 315 315	0	0



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: Amine oxidase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants	86.27Å 86.27Å 122.47Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.64 - 1.90	Depositor
resolution (A)	32.64 - 1.90	EDS
% Data completeness	100.0 (32.64 - 1.90)	Depositor
(in resolution range)	100.0 (32.64-1.90)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.87 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.140 , 0.177	Depositor
it, it free	0.140 , 0.177	DCC
R_{free} test set	3521 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	20.1	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 40.6	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	0.487 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7523	wwPDB-VP
Average B, all atoms (\mathring{A}^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.27% 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: FDA, EDO, NCT

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		nd lengths	Bond angles		
Moi Chain		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.80	1/3396 (0.0%)	0.72	0/4610	
1	В	0.80	1/3440 (0.0%)	0.74	0/4665	
All	All	0.80	$2/6836 \ (0.0\%)$	0.73	0/9275	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
1	A	59	VAL	CB-CG1	5.20	1.63	1.52
1	В	59	VAL	CB-CG1	5.13	1.63	1.52

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	3318	0	3230	18	0
1	В	3362	0	3305	29	0
2	A	12	12	13	0	0
2	В	12	12	13	0	0
3	A	53	33	33	1	0
3	В	53	33	33	1	0
4	A	4	6	6	0	0



Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	В	4	6	6	0	0
5	A	288	0	0	0	3
5	В	315	0	0	1	4
All	All	7421	102	6639	45	4

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 3.

All (45) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Content	Atom-1	Atom-2	Interatomic	Clash
1:A:289:VAL:HG21 1:A:304:VAL:HG23 1.31 1.11 1:B:289[A]:VAL:HG21 1:B:304[A]:VAL:CG2 2.03 0.88 1:A:289:VAL:HG21 1:A:304:VAL:CG2 2.09 0.81 1:A:341:LEU:HD22 1:A:382:ILE:HD11 1.73 0.70 1:A:341:LEU:CD2 1:A:382:ILE:HD11 2.24 0.67 1:B:184:GLU:OE1 1:B:187:ARG:NH1 2.33 0.62 1:B:341:LEU:HG 1:B:455:THR:HG22 1.81 0.60 1:B:341:LEU:C 1:B:341:LEU:HD12 2.22 0.58 1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:304[B]:VAL:GG2 1:B:448:ILE:HG12 2.36 0.55 1:B:306:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.38 0.53 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:304[B]:VAL:HG23 1:B:448:ILE:			${ m distance}({ m \AA})$	overlap (Å)
1:B:289[A]:VAL:HG21 1:B:304[A]:VAL:CG2 2.09 0.81 1:A:289:VAL:HG21 1:A:304:VAL:CG2 2.09 0.81 1:A:341:LEU:HD22 1:A:382:ILE:HD11 1.73 0.70 1:A:341:LEU:CD2 1:A:382:ILE:HD11 2.24 0.67 1:B:184:GLU:OE1 1:B:187:ARG:NH1 2.33 0.62 1:B:341:LEU:HG 1:B:455:THR:HG22 1.81 0.60 1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.38 0.53 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:341:LEU:HD12 1:B:382:ILE:CD1	1:B:289[A]:VAL:HG21	1:B:304[A]:VAL:HG23	1.30	1.14
1:A:289:VAL:HG21 1:A:304:VAL:CG2 2.09 0.81 1:A:341:LEU:HD22 1:A:382:ILE:HD11 1.73 0.70 1:A:341:LEU:CD2 1:A:382:ILE:HD11 2.24 0.67 1:B:184:GLU:OE1 1:B:187:ARG:NH1 2.33 0.62 1:B:341:LEU:HG 1:B:455:THR:HG22 1.81 0.60 1:B:341:LEU:C 1:B:341:LEU:HD12 2.22 0.58 1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 <t< td=""><td>1:A:289:VAL:HG21</td><td>1:A:304:VAL:HG23</td><td>1.31</td><td>1.11</td></t<>	1:A:289:VAL:HG21	1:A:304:VAL:HG23	1.31	1.11
1:A:341:LEU:HD22 1:A:382:ILE:HD11 1.73 0.70 1:A:341:LEU:CD2 1:A:382:ILE:HD11 2.24 0.67 1:B:184:GLU:OE1 1:B:187:ARG:NH1 2.33 0.62 1:B:441:LEU:HG 1:B:455:THR:HG22 1.81 0.60 1:B:341:LEU:C 1:B:341:LEU:HD12 2.22 0.58 1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:304[B]:VAL:HG23 1:B:348:ILE:HD10 2.40 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23	1:B:289[A]:VAL:HG21	1:B:304[A]:VAL:CG2	2.03	0.88
1:A:341:LEU:CD2 1:A:382:ILE:HD11 2.24 0.67 1:B:184:GLU:OE1 1:B:187:ARG:NH1 2.33 0.62 1:B:441:LEU:HG 1:B:455:THR:HG22 1.81 0.60 1:B:341:LEU:C 1:B:341:LEU:HD12 2.22 0.58 1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:CG1	1:A:289:VAL:HG21	1:A:304:VAL:CG2	2.09	0.81
1:B:184:GLU:OE1 1:B:187:ARG:NH1 2.33 0.62 1:B:441:LEU:HG 1:B:455:THR:HG22 1.81 0.60 1:B:341:LEU:C 1:B:341:LEU:HD12 2.22 0.58 1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.50 1:B:116:OHB2 1:B:1848:ILE:HG23 1.93	1:A:341:LEU:HD22	1:A:382:ILE:HD11	1.73	0.70
1:B:441:LEU:HG 1:B:455:THR:HG22 1.81 0.60 1:B:341:LEU:C 1:B:341:LEU:HD12 2.22 0.58 1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:A:441:LEU:HG 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:18543:VAL:HG23 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:B:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1	1:A:341:LEU:CD2	1:A:382:ILE:HD11	2.24	0.67
1:B:341:LEU:C 1:B:341:LEU:HD12 2.22 0.58 1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:B:304[B]:VAL:HG2 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:343:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1	1:B:184:GLU:OE1	1:B:187:ARG:NH1	2.33	0.62
1:B:341:LEU:CD1 1:B:343:VAL:HG23 2.35 0.56 1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:448:ILE:HG12 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:A:441:LEU:HG 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.44 0.46 1:B:382:ILE:HD13 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1	1:B:441:LEU:HG	1:B:455:THR:HG22	1.81	0.60
1:A:292:LYS:HE2 1:A:298:ILE:HD11 1.88 0.55 1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:A:441:LEU:HG 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:B:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:B:80:LEU:HD21 1:B:80:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53		1:B:341:LEU:HD12	2.22	0.58
1:B:304[B]:VAL:CG2 1:B:448:ILE:HG12 2.36 0.55 1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:A:441:LEU:HG 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96<	1:B:341:LEU:CD1	1:B:343:VAL:HG23	2.35	0.56
1:B:326:LYS:HE2 1:B:450:PHE:CD1 2.43 0.54 1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:A:441:LEU:HG 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96	1:A:292:LYS:HE2	1:A:298:ILE:HD11	1.88	0.55
1:A:106:GLY:HA2 3:A:502:FDA:C4X 2.38 0.53 1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:A:441:LEU:HG 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:B:304[B]:VAL:CG2	1:B:448:ILE:HG12	2.36	0.55
1:B:106:GLY:HA2 3:B:502:FDA:C4X 2.39 0.53 1:A:441:LEU:HG 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:B:326:LYS:HE2	1:B:450:PHE:CD1	2.43	0.54
1:A:441:LEU:HG 1:A:455:THR:HG22 1.90 0.52 1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:A:106:GLY:HA2	3:A:502:FDA:C4X	2.38	0.53
1:B:304[B]:VAL:HG23 1:B:448:ILE:HG23 1.93 0.51 1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:B:106:GLY:HA2	3:B:502:FDA:C4X	2.39	0.53
1:B:160:ARG:HD2 5:B:731:HOH:O 2.10 0.50 1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:A:441:LEU:HG	1:A:455:THR:HG22	1.90	0.52
1:A:341:LEU:HD22 1:A:382:ILE:CD1 2.40 0.50 1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43		1:B:448:ILE:HG23	1.93	0.51
1:B:173:VAL:HG22 1:B:185:ARG:HG2 1.93 0.49 1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:B:160:ARG:HD2	5:B:731:HOH:O	2.10	0.50
1:B:341:LEU:HD11 1:B:343:VAL:HG23 1.95 0.48 1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:A:341:LEU:HD22	1:A:382:ILE:CD1	2.40	0.50
1:A:141:MET:HE1 1:A:360:GLN:OE1 2.14 0.48 1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:B:173:VAL:HG22	1:B:185:ARG:HG2	1.93	0.49
1:A:382:ILE:HD13 1:A:390:VAL:CG1 2.46 0.46 1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:B:341:LEU:HD11	1:B:343:VAL:HG23	1.95	0.48
1:B:382:ILE:HD13 1:B:390:VAL:CG1 2.44 0.46 1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:A:141:MET:HE1	1:A:360:GLN:OE1	2.14	0.48
1:A:445:GLU:HG3 1:A:450:PHE:CE1 2.50 0.46 1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:A:382:ILE:HD13	1:A:390:VAL:CG1	2.46	0.46
1:B:80:LEU:HD21 1:B:82:LEU:HD21 1.99 0.45 1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43			2.44	0.46
1:A:114:PRO:HB3 1:B:114:PRO:HA 1.99 0.44 1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43			2.50	0.46
1:A:326:LYS:HE2 1:A:450:PHE:CD1 2.53 0.43 1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43	1:B:80:LEU:HD21		1.99	0.45
1:B:341:LEU:CD1 1:B:343:VAL:CG2 2.96 0.43				
			2.53	0.43
1:B:346:LYS:HE3 1:B:408:GLU:OE1 2.18 0.43				
	1:B:346:LYS:HE3	1:B:408:GLU:OE1	2.18	0.43



n previous	paae
	n previous

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:326:LYS:HE2	1:B:450:PHE:CE1	2.54	0.43
1:B:160:ARG:O	1:B:164:GLU:HG3	2.18	0.43
1:A:219:ALA:HB2	1:A:226:PHE:CG	2.54	0.43
1:B:54:TYR:OH	1:B:272:GLU:OE1	2.23	0.42
1:A:114:PRO:HA	1:B:114:PRO:HB3	2.02	0.42
1:A:291:ILE:HD11	1:A:304:VAL:CG2	2.49	0.42
1:B:341:LEU:HD11	1:B:343:VAL:CG2	2.49	0.42
1:B:346:LYS:HB3	1:B:408:GLU:HG3	2.01	0.42
1:B:291:ILE:HD11	1:B:304[B]:VAL:CG1	2.50	0.41
1:B:91:ARG:HA	1:B:417:TRP:CZ3	2.56	0.41
1:B:374:LEU:O	1:B:374:LEU:HG	2.21	0.41
1:A:57:VAL:HG23	1:A:301:ALA:HB2	2.03	0.41
1:A:108:TRP:CD2	1:A:250:THR:HA	2.56	0.41
1:B:445:GLU:HG3	1:B:450:PHE:CE1	2.56	0.41
1:B:108:TRP:CD2	1:B:250:THR:HA	2.56	0.40

All (4) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
5:A:822:HOH:O	5:B:904:HOH:O[2_654]	2.11	0.09
5:B:850:HOH:O	5:B:868:HOH:O[3_554]	2.14	0.06
5:A:880:HOH:O	5:B:860:HOH:O[2_654]	2.17	0.03
5:A:884:HOH:O	5:B:880:HOH:O[2_654]	2.19	0.01

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	entiles
1	A	433/432 (100%)	427 (99%)	6 (1%)	0	100	100
1	В	435/432 (101%)	428 (98%)	7 (2%)	0	100	100



Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
All	All	868/864 (100%)	855 (98%)	13 (2%)	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	340/349~(97%)	337 (99%)	3 (1%)	78 79		
1	В	349/349 (100%)	345 (99%)	4 (1%)	73 73		
All	All	689/698 (99%)	682 (99%)	7 (1%)	76 76		

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	163	PHE
1	A	205	ARG
1	A	214	TYR
1	В	96	ARG
1	В	163	PHE
1	В	214	TYR
1	В	221	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	208	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)

6 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 Ch		Chain	Chain Res L		Bond lengths		Bond angles			
MIOI	Mol Type Chain	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NCT	A	501	_	13,13,13	0.92	0	17,17,17	2.75	9 (52%)
3	FDA	В	502	-	52,58,58	0.84	2 (3%)	60,89,89	1.02	2 (3%)
4	EDO	В	503	-	3,3,3	0.42	0	2,2,2	0.20	0
3	FDA	A	502	_	52,58,58	0.89	1 (1%)	60,89,89	1.05	3 (5%)
4	EDO	A	503	-	3,3,3	0.36	0	2,2,2	0.22	0
2	NCT	В	501	-	13,13,13	0.90	0	17,17,17	2.72	9 (52%)

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	NCT	A	501	-	-	0/4/14/14	0/2/2/2
3	FDA	В	502	-	-	1/30/50/50	0/6/6/6
4	EDO	В	503	-	-	0/1/1/1	-
3	FDA	A	502	-	-	1/30/50/50	0/6/6/6
4	EDO	A	503	-	-	0/1/1/1	_
2	NCT	В	501	-	-	0/4/14/14	0/2/2/2

All (3) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
3	В	502	FDA	C4A-N3A	-2.13	1.32	1.35
3	В	502	FDA	O4'-C4'	-2.04	1.39	1.43
3	A	502	FDA	C2A-N3A	2.02	1.35	1.32

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	501	NCT	C10-N2-C6	4.77	127.33	112.83
2	A	501	NCT	C7-C6-C2	4.76	122.82	113.61
2	В	501	NCT	C10-N2-C6	4.67	127.03	112.83
2	A	501	NCT	C3-C2-C1	4.45	121.61	116.88
2	В	501	NCT	C3-C2-C1	4.37	121.52	116.88
2	В	501	NCT	C7-C6-C2	4.37	122.06	113.61
2	A	501	NCT	C2-C6-N2	4.19	123.12	112.37
2	В	501	NCT	C10-N2-C9	4.18	125.80	112.70
2	В	501	NCT	C2-C6-N2	4.10	122.89	112.37
2	A	501	NCT	C10-N2-C9	4.05	125.39	112.70
2	В	501	NCT	C2-C1-N1	-3.14	119.22	124.14
3	В	502	FDA	O4B-C1B-C2B	-3.08	102.43	106.93
2	A	501	NCT	C4-C3-C2	-3.06	116.86	120.65
2	A	501	NCT	C2-C1-N1	-2.79	119.75	124.14
3	В	502	FDA	O2P-P-O1P	2.66	125.40	112.24
3	A	502	FDA	O4B-C1B-C2B	-2.63	103.09	106.93
2	В	501	NCT	C5-N1-C1	2.58	121.32	116.85
3	A	502	FDA	O2P-P-O1P	2.50	124.59	112.24
2	В	501	NCT	C4-C3-C2	-2.36	117.72	120.65
3	A	502	FDA	C5X-N5-C4X	-2.23	115.75	121.02
2	A	501	NCT	C5-N1-C1	2.09	120.46	116.85
2	A	501	NCT	C7-C6-N2	2.04	108.32	102.56
2	В	501	NCT	C7-C6-N2	2.01	108.24	102.56

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	502	FDA	O4B-C4B-C5B-O5B
3	A	502	FDA	O4B-C4B-C5B-O5B

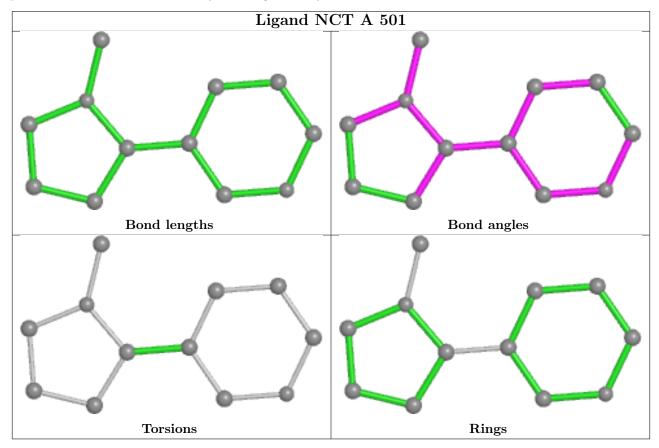
There are no ring outliers.

2 monomers are involved in 2 short contacts:

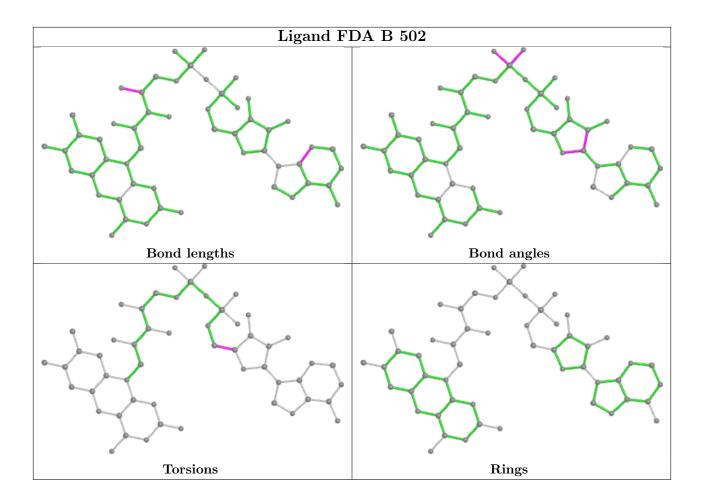


Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	502	FDA	1	0
3	A	502	FDA	1	0

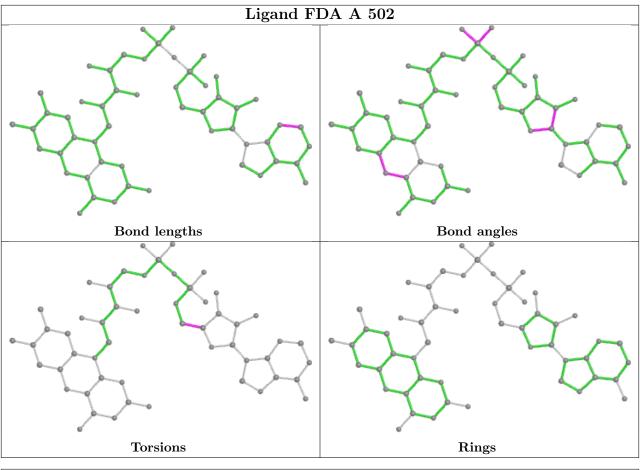
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

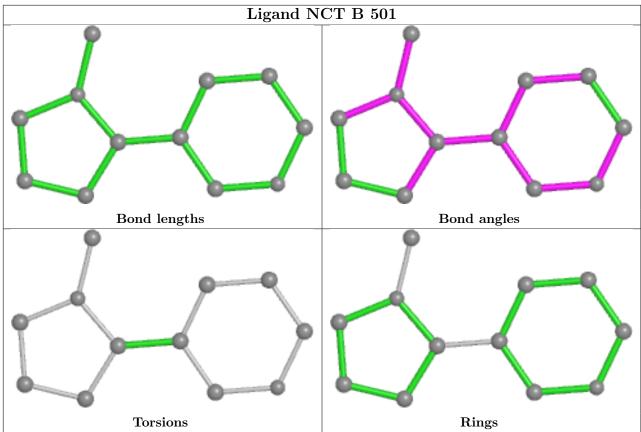














5.7 Other polymers (i)

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	$\langle { m RSRZ} \rangle$	$\#\text{RSRZ}{>}2$		$\mathbf{ZZ} > 2$	$OWAB(A^2)$	Q<0.9
1	A	432/432 (100%)	-0.82	0	100	100	12, 19, 33, 45	0
1	В	432/432 (100%)	-0.82	0	100	100	12, 19, 33, 45	0
All	All	864/864 (100%)	-0.82	0	100	100	12, 19, 33, 45	0

There are no RSRZ outliers to report.

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.

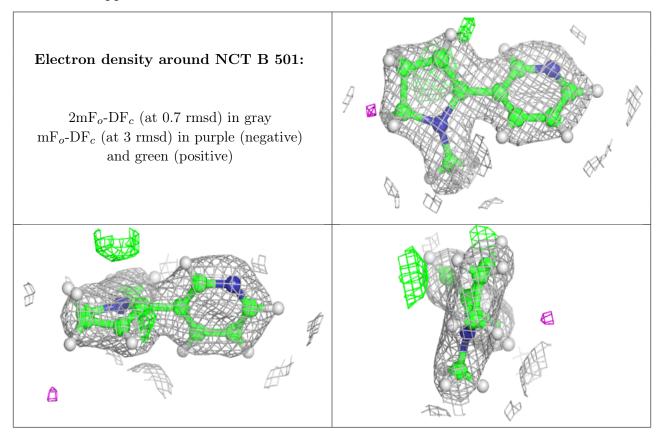
6.4 Ligands (i)

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	EDO	В	503	4/4	0.94	0.14	30,39,51,51	0
4	EDO	A	503	4/4	0.96	0.13	27,37,46,55	0
2	NCT	В	501	12/12	0.96	0.12	20,24,28,33	0
2	NCT	A	501	12/12	0.97	0.12	20,26,31,35	0
3	FDA	A	502	53/53	0.99	0.07	12,15,21,23	0
3	FDA	В	502	53/53	0.99	0.07	11,15,20,24	0



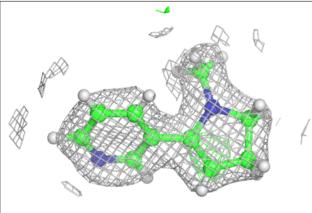
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

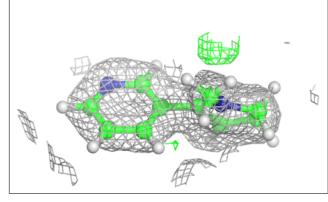


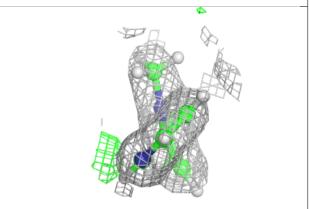


Electron density around NCT A 501:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

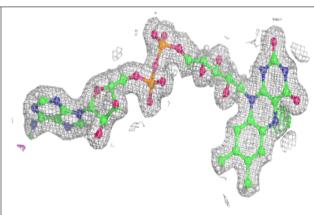


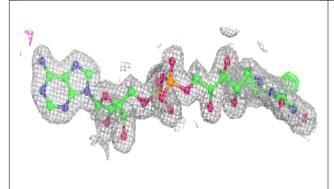


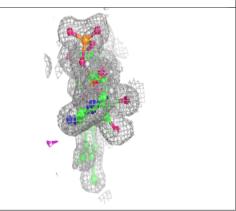


Electron density around FDA A 502:

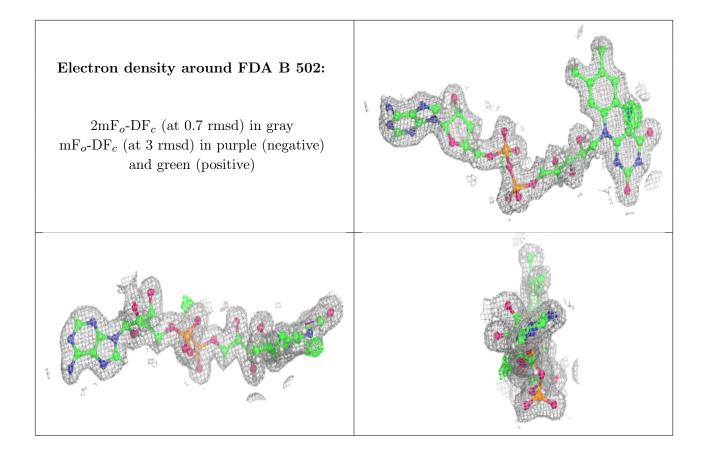
 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)











6.5 Other polymers (i)

There are no such residues in this entry.

