

# Full wwPDB X-ray Structure Validation Report (i)

Sep 19, 2023 – 03:30 pm BST

PDB ID : 8BO9

Title: NanoLuc-D9R/H57A/K89R mutant complexed with azacoelenterazine bound

in intra-barrel catalytic site

Authors: Marek, M.; Janin, L.Y.

Deposited on : 2022-11-15

Resolution : 3.10 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.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 : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.35.1

 $buster-report \quad : \quad 1.1.7 \ (2018)$ 

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)

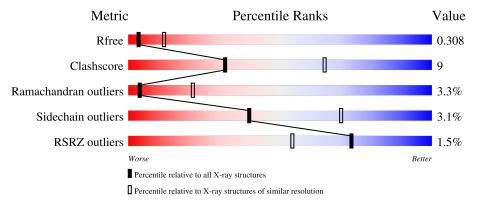
Validation Pipeline (wwPDB-VP) : 2.35.1

## 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 3.10 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
$R_{free}$	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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	181	77%	18%					
1	В	181	73%	21%	• 5%				
1	С	181	60%	33%					



# 2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4217 atoms, of which 0 are hydrogens and 0 are deuteriums.

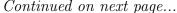
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called Non structural polyprotein.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	174	Total	С	N	О	S	0	0	0
1	A	174	1370	881	232	253	4	0	U	0
1	D	172	Total	С	N	О	S	0	1	0
1	Б	172	1367	880	234	249	4	0	1	0
1	С	173	Total	С	N	О	S	0	0	0
		119	1364	878	231	251	4		U	0

There are 42 discrepancies between the modelled and reference sequences:

A	Chain	Residue	Modelled	Actual	Comment	Reference
A         -9         HIS         -         expression tag         UNP A0A482LN           A         -8         HIS         -         expression tag         UNP A0A482LN           A         -7         HIS         -         expression tag         UNP A0A482LN           A         -6         HIS         -         expression tag         UNP A0A482LN           A         -5         HIS         -         expression tag         UNP A0A482LN           A         -4         SER         -         expression tag         UNP A0A482LN           A         -3         ASP         -         expression tag         UNP A0A482LN           A         -1         MET         -         expression tag         UNP A0A482LN           A         9         ARG         ASP         engineered mutation         UNP A0A482LN           A         57         ALA         HIS         engineered mutation         UNP A0A482LN           B         -11         MET         -         initiating methionine         UNP A0A482LN           B         -10         HIS         -         expression tag         UNP A0A482LN           B         -9         HIS         -         ex	A	-11	MET	-	initiating methionine	UNP A0A482LYE4
A         -8         HIS         -         expression tag         UNP A0A482LN           A         -7         HIS         -         expression tag         UNP A0A482LN           A         -6         HIS         -         expression tag         UNP A0A482LN           A         -5         HIS         -         expression tag         UNP A0A482LN           A         -4         SER         -         expression tag         UNP A0A482LN           A         -3         ASP         -         expression tag         UNP A0A482LN           A         -2         ASN         -         expression tag         UNP A0A482LN           A         -1         MET         -         expression tag         UNP A0A482LN           A         9         ARG         ASP         engineered mutation         UNP A0A482LN           A         89         ARG         LYS         engineered mutation         UNP A0A482LN           B         -11         MET         -         initiating methionine         UNP A0A482LN           B         -10         HIS         -         expression tag         UNP A0A482LN           B         -9         HIS         -         ex	A	-10	HIS	-	expression tag	UNP A0A482LYE4
A         -7         HIS         -         expression tag         UNP A0A482LN           A         -6         HIS         -         expression tag         UNP A0A482LN           A         -5         HIS         -         expression tag         UNP A0A482LN           A         -4         SER         -         expression tag         UNP A0A482LN           A         -3         ASP         -         expression tag         UNP A0A482LN           A         -1         MET         -         expression tag         UNP A0A482LN           A         9         ARG         ASP         engineered mutation         UNP A0A482LN           A         57         ALA         HIS         engineered mutation         UNP A0A482LN           B         -11         MET         -         initiating methionine         UNP A0A482LN           B         -10         HIS         -         expression tag         UNP A0A482LN           B         -9         HIS         -         expression tag         UNP A0A482LN           B         -9         HIS         -         expression tag         UNP A0A482LN           B         -7         HIS         -         ex	A	-9	HIS	-	expression tag	UNP A0A482LYE4
A         -6         HIS         -         expression tag         UNP A0A482LN           A         -5         HIS         -         expression tag         UNP A0A482LN           A         -4         SER         -         expression tag         UNP A0A482LN           A         -3         ASP         -         expression tag         UNP A0A482LN           A         -2         ASN         -         expression tag         UNP A0A482LN           A         -1         MET         -         expression tag         UNP A0A482LN           A         57         ALA         HIS         engineered mutation         UNP A0A482LN           A         89         ARG         LYS         engineered mutation         UNP A0A482LN           B         -11         MET         -         initiating methionine         UNP A0A482LN           B         -10         HIS         -         expression tag         UNP A0A482LN           B         -9         HIS         -         expression tag         UNP A0A482LN           B         -8         HIS         -         expression tag         UNP A0A482LN           B         -6         HIS         -         e	A	-8	HIS	-	expression tag	UNP A0A482LYE4
A         -5         HIS         -         expression tag         UNP A0A482LM           A         -4         SER         -         expression tag         UNP A0A482LM           A         -3         ASP         -         expression tag         UNP A0A482LM           A         -2         ASN         -         expression tag         UNP A0A482LM           A         -1         MET         -         expression tag         UNP A0A482LM           A         9         ARG         ASP         engineered mutation         UNP A0A482LM           A         57         ALA         HIS         engineered mutation         UNP A0A482LM           B         -11         MET         -         initiating methionine         UNP A0A482LM           B         -10         HIS         -         expression tag         UNP A0A482LM           B         -9         HIS         -         expression tag         UNP A0A482LM           B         -8         HIS         -         expression tag         UNP A0A482LM           B         -6         HIS         -         expression tag         UNP A0A482LM	A	-7	HIS	-	expression tag	UNP A0A482LYE4
A         -4         SER         -         expression tag         UNP A0A482LY           A         -3         ASP         -         expression tag         UNP A0A482LY           A         -2         ASN         -         expression tag         UNP A0A482LY           A         -1         MET         -         expression tag         UNP A0A482LY           A         9         ARG         ASP         engineered mutation         UNP A0A482LY           A         57         ALA         HIS         engineered mutation         UNP A0A482LY           B         -11         MET         -         initiating methionine         UNP A0A482LY           B         -10         HIS         -         expression tag         UNP A0A482LY           B         -9         HIS         -         expression tag         UNP A0A482LY           B         -8         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	A	-6	HIS	-	expression tag	UNP A0A482LYE4
A         -3         ASP         -         expression tag         UNP A0A482LY           A         -2         ASN         -         expression tag         UNP A0A482LY           A         -1         MET         -         expression tag         UNP A0A482LY           A         9         ARG         ASP         engineered mutation         UNP A0A482LY           A         57         ALA         HIS         engineered mutation         UNP A0A482LY           A         89         ARG         LYS         engineered mutation         UNP A0A482LY           B         -11         MET         -         initiating methionine         UNP A0A482LY           B         -10         HIS         -         expression tag         UNP A0A482LY           B         -9         HIS         -         expression tag         UNP A0A482LY           B         -8         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	A	-5	HIS	-	expression tag	UNP A0A482LYE4
A         -2         ASN         -         expression tag         UNP A0A482LY           A         -1         MET         -         expression tag         UNP A0A482LY           A         9         ARG         ASP         engineered mutation         UNP A0A482LY           A         57         ALA         HIS         engineered mutation         UNP A0A482LY           A         89         ARG         LYS         engineered mutation         UNP A0A482LY           B         -11         MET         -         initiating methionine         UNP A0A482LY           B         -10         HIS         -         expression tag         UNP A0A482LY           B         -9         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	A	-4	SER	-	expression tag	UNP A0A482LYE4
A         -1         MET         -         expression tag         UNP A0A482LY           A         9         ARG         ASP         engineered mutation         UNP A0A482LY           A         57         ALA         HIS         engineered mutation         UNP A0A482LY           A         89         ARG         LYS         engineered mutation         UNP A0A482LY           B         -11         MET         -         initiating methionine         UNP A0A482LY           B         -10         HIS         -         expression tag         UNP A0A482LY           B         -9         HIS         -         expression tag         UNP A0A482LY           B         -8         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	A	-3	ASP	-	expression tag	UNP A0A482LYE4
A 9 ARG ASP engineered mutation UNP A0A482LY A 57 ALA HIS engineered mutation UNP A0A482LY A 89 ARG LYS engineered mutation UNP A0A482LY B -11 MET - initiating methionine UNP A0A482LY B -10 HIS - expression tag UNP A0A482LY B -9 HIS - expression tag UNP A0A482LY B -8 HIS - expression tag UNP A0A482LY B -7 HIS - expression tag UNP A0A482LY B -7 HIS - expression tag UNP A0A482LY B -6 HIS - expression tag UNP A0A482LY	A	-2	ASN	-	expression tag	UNP A0A482LYE4
A         57         ALA         HIS         engineered mutation         UNP A0A482LY           A         89         ARG         LYS         engineered mutation         UNP A0A482LY           B         -11         MET         -         initiating methionine         UNP A0A482LY           B         -10         HIS         -         expression tag         UNP A0A482LY           B         -9         HIS         -         expression tag         UNP A0A482LY           B         -8         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	A	-1	MET	-	expression tag	UNP A0A482LYE4
A         89         ARG         LYS         engineered mutation         UNP A0A482LY           B         -11         MET         -         initiating methionine         UNP A0A482LY           B         -10         HIS         -         expression tag         UNP A0A482LY           B         -9         HIS         -         expression tag         UNP A0A482LY           B         -8         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	A	9	ARG	ASP	engineered mutation	UNP A0A482LYE4
B         -11         MET         -         initiating methionine         UNP A0A482LY           B         -10         HIS         -         expression tag         UNP A0A482LY           B         -9         HIS         -         expression tag         UNP A0A482LY           B         -8         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	A	57	ALA	HIS	engineered mutation	UNP A0A482LYE4
B         -10         HIS         -         expression tag         UNP A0A482LY           B         -9         HIS         -         expression tag         UNP A0A482LY           B         -8         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	A	89	ARG	LYS	engineered mutation	UNP A0A482LYE4
B         -9         HIS         -         expression tag         UNP A0A482LY           B         -8         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	В	-11	MET	-	initiating methionine	UNP A0A482LYE4
B         -8         HIS         -         expression tag         UNP A0A482LY           B         -7         HIS         -         expression tag         UNP A0A482LY           B         -6         HIS         -         expression tag         UNP A0A482LY	В	-10	HIS	-	expression tag	UNP A0A482LYE4
B -7 HIS - expression tag UNP A0A482LY B -6 HIS - expression tag UNP A0A482LY	В	-9	HIS	-	expression tag	UNP A0A482LYE4
B -6 HIS - expression tag UNP A0A482LY	В	-8	HIS	-	expression tag	UNP A0A482LYE4
	В	-7	HIS	-	expression tag	UNP A0A482LYE4
B -5 HIS - expression tag UNP A0A482LY	В	-6	HIS	-	expression tag	UNP A0A482LYE4
	В	-5	HIS	-	expression tag	UNP A0A482LYE4
B -4 SER - expression tag UNP A0A482LY	В	-4	SER	-	expression tag	UNP A0A482LYE4
B -3 ASP - expression tag UNP A0A482LY	В	-3	ASP	-	expression tag	UNP A0A482LYE4

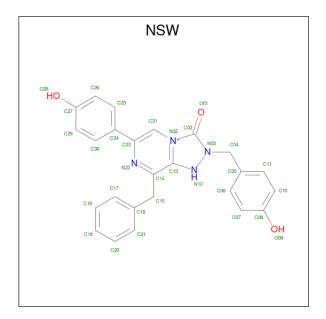




Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
В	-2	ASN	=	expression tag	UNP A0A482LYE4
В	-1	MET	-	expression tag	UNP A0A482LYE4
В	9	ARG	ASP	engineered mutation	UNP A0A482LYE4
В	57	ALA	HIS	engineered mutation	UNP A0A482LYE4
В	89	ARG	LYS	engineered mutation	UNP A0A482LYE4
С	-11	MET	-	initiating methionine	UNP A0A482LYE4
С	-10	HIS	-	expression tag	UNP A0A482LYE4
С	-9	HIS	-	expression tag	UNP A0A482LYE4
С	-8	HIS	-	expression tag	UNP A0A482LYE4
С	-7	HIS	-	expression tag	UNP A0A482LYE4
С	-6	HIS	-	expression tag	UNP A0A482LYE4
С	-5	HIS	-	expression tag	UNP A0A482LYE4
С	-4	SER	-	expression tag	UNP A0A482LYE4
С	-3	ASP	-	expression tag	UNP A0A482LYE4
С	-2	ASN	-	expression tag	UNP A0A482LYE4
С	-1	MET	-	expression tag	UNP A0A482LYE4
С	9	ARG	ASP	engineered mutation	UNP A0A482LYE4
С	57	ALA	HIS	engineered mutation	UNP A0A482LYE4
С	89	ARG	LYS	engineered mutation	UNP A0A482LYE4

• Molecule 2 is 3-(4-hydroxyphenyl)-8-[(4-hydroxyphenyl)methyl]-5-(phenylmethyl)-1\$l^{ 4},4,7,8-tetrazabicyclo[4.3.0]nona-1(6),2,4-trien-9-one (three-letter code: NSW) (formula:  $C_{25}H_{21}N_4O_3$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	A	Aton	ns		ZeroOcc	AltConf
2	A	1	Total			O	0	0
_		_	32	25	4	3		



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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	В	1	Total 32			0	0
2	C	1	Total 32			0	0

#### • Molecule 3 is water.

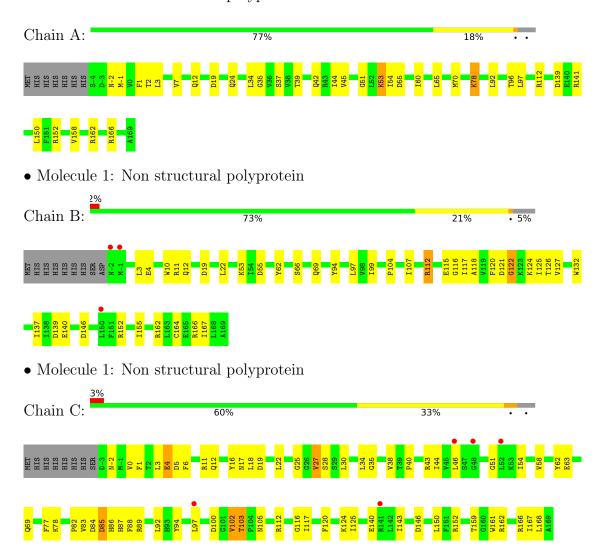
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	13	Total O 13 13	0	0
3	В	5	Total O 5 5	0	0
3	С	2	Total O 2 2	0	0



# 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: Non structural polyprotein





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	147.91Å 112.60Å 59.70Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.80^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	46.77 - 3.10	Depositor
rtesolution (A)	46.77 - 3.10	EDS
% Data completeness	96.9 (46.77-3.10)	Depositor
(in resolution range)	96.9 (46.77-3.10)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.10 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.14-3260-0000	Depositor
D D.	0.272 , $0.307$	Depositor
$R, R_{free}$	0.273 , $0.308$	DCC
$R_{free}$ test set	894 reflections $(5.18\%)$	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	111.3	Xtriage
Anisotropy	0.335	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.23 , 32.0	EDS
L-test for twinning <sup>2</sup>	$< L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	0.046 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4217	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	109.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.13% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: NSW

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	Chain	RMSZ $ \# Z  > 5$		RMSZ	# Z  > 5	
1	A	0.25	0/1398	0.47	0/1898	
1	В	0.24	0/1395	0.45	0/1894	
1	С	0.26	0/1392	0.51	1/1890 (0.1%)	
All	All	0.25	0/4185	0.48	1/5682 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mo	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	С	34	LEU	CA-CB-CG	6.49	130.23	115.30

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	1370	0	1375	17	0
1	В	1367	0	1379	23	0
1	С	1364	0	1370	35	0
2	A	32	0	0	2	0
2	В	32	0	0	0	0
2	С	32	0	0	0	0
3	A	13	0	0	0	0



Continued from previous page...

Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
3	В	5	0	0	1	0
3	С	2	0	0	0	0
All	All	4217	0	4124	74	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 9.

All (74) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1         Atom-2         distance (Å)           1:C:105:ASN:HB2         1:C:116:GLY:O         1.88           1:A:51:GLY:HA2         1:A:97:LEU:O         1.89           1:C:4:GLU:O         1:C:6:PHE:N         2.24           1:C:12:GLN:OE1         1:C:162:ARG:NH1         2.32           1:A:42:GLN:OE1         1:A:141:ARG:NH2         2.32           1:A:53:LYS:HD2         1:A:96:THR:HG22         1.82           1:C:44:ILE:HG12         1:C:54:ILE:HG12         1.83           1:C:30:LEU:HD22         1:C:69:GLN:HG2         1.84           1:C:77:PHE:HE1         1:C:92:LEU:HG         1.66           1:A:7:VAL:O         1:A:166:ARG:NH1         2.34           1:C:85:ASP:OD1         1:C:86:HIS:ND1         2.36           1:A:44:ILE:HG12         1:A:54:ILE:HG12         1.87           1:B:66:SER:N         1:B:69:GLN:OE1         2.34           1:C:152:ARG:HG3         1:C:161:TRP:HB3         1.88           1:B:97:LEU:HD21         1:B:107:ILE:HD11         1.89           1:C:17:ASN:ND2         1:C:159:THR:O         2.35           1:B:140:GLU:OE1         1:B:152:ARG:NH2         2.38           1:C:102:VAL:HG12         1:C:103:THR:H         1.73           1:B:104:PRO:HB2         1	Clash
1:A:51:GLY:HA2       1:A:97:LEU:O       1.89         1:C:4:GLU:O       1:C:6:PHE:N       2.24         1:C:12:GLN:OE1       1:C:162:ARG:NH1       2.32         1:A:42:GLN:OE1       1:A:141:ARG:NH2       2.32         1:A:53:LYS:HD2       1:A:96:THR:HG22       1.82         1:C:44:ILE:HG12       1:C:54:ILE:HG12       1.83         1:C:30:LEU:HD22       1:C:69:GLN:HG2       1.84         1:C:77:PHE:HE1       1:C:92:LEU:HG       1.66         1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2 <t< th=""><th>overlap (Å)</th></t<>	overlap (Å)
1:C:4:GLU:O       1:C:6:PHE:N       2.24         1:C:12:GLN:OE1       1:C:162:ARG:NH1       2.32         1:A:42:GLN:OE1       1:A:141:ARG:NH2       2.32         1:A:53:LYS:HD2       1:A:96:THR:HG22       1.82         1:C:44:ILE:HG12       1:C:54:ILE:HG12       1.83         1:C:30:LEU:HD22       1:C:69:GLN:HG2       1.84         1:C:77:PHE:HE1       1:C:92:LEU:HG       1.66         1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:104:PRO:HB2	0.73
1:C:12:GLN:OE1       1:C:162:ARG:NH1       2.32         1:A:42:GLN:OE1       1:A:141:ARG:NH2       2.32         1:A:53:LYS:HD2       1:A:96:THR:HG22       1.82         1:C:44:ILE:HG12       1:C:54:ILE:HG12       1.83         1:C:30:LEU:HD22       1:C:69:GLN:HG2       1.84         1:C:77:PHE:HE1       1:C:92:LEU:HG       1.66         1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:15:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:22:LEU:HD22	0.72
1:A:42:GLN:OE1       1:A:141:ARG:NH2       2.32         1:A:53:LYS:HD2       1:A:96:THR:HG22       1.82         1:C:44:ILE:HG12       1:C:54:ILE:HG12       1.83         1:C:30:LEU:HD22       1:C:69:GLN:HG2       1.84         1:C:77:PHE:HE1       1:C:92:LEU:HG       1.66         1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:17:ILE:O       1:B:127:VAL:HA       2.11         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.69
1:A:53:LYS:HD2       1:A:96:THR:HG22       1.82         1:C:44:ILE:HG12       1:C:54:ILE:HG12       1.83         1:C:30:LEU:HD22       1:C:69:GLN:HG2       1.84         1:C:77:PHE:HE1       1:C:92:LEU:HG       1.66         1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:17:ILE:O       1:B:127:VAL:HA       2.11         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.62
1:C:44:ILE:HG12       1:C:54:ILE:HG12       1.83         1:C:30:LEU:HD22       1:C:69:GLN:HG2       1.84         1:C:77:PHE:HE1       1:C:92:LEU:HG       1.66         1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:27:VAL:HG11       1.94	0.62
1:C:30:LEU:HD22       1:C:69:GLN:HG2       1.84         1:C:77:PHE:HE1       1:C:92:LEU:HG       1.66         1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.60
1:C:77:PHE:HE1       1:C:92:LEU:HG       1.66         1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:17:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.60
1:A:7:VAL:O       1:A:166:ARG:NH1       2.34         1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.60
1:A:12:GLN:OE1       1:A:162:ARG:NH1       2.29         1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.59
1:C:85:ASP:OD1       1:C:86:HIS:ND1       2.36         1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.58
1:A:44:ILE:HG12       1:A:54:ILE:HG12       1.87         1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.58
1:B:66:SER:N       1:B:69:GLN:OE1       2.34         1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.57
1:C:152:ARG:HG3       1:C:161:TRP:HB3       1.88         1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.56
1:B:97:LEU:HD21       1:B:107:ILE:HD11       1.89         1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.55
1:C:17:ASN:ND2       1:C:159:THR:O       2.35         1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.55
1:B:140:GLU:OE1       1:B:152:ARG:NH2       2.38         1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.55
1:C:102:VAL:HG12       1:C:103:THR:H       1.73         1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.54
1:A:34:LEU:HD21       1:A:60:ILE:HG23       1.89         1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.53
1:C:22:LEU:HB3       1:C:27:VAL:HG21       1.91         1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.53
1:B:104:PRO:HB2       1:B:115:GLU:HB3       1.91         1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.53
1:B:117:ILE:O       1:B:127:VAL:HA       2.11         1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.53
1:C:120:PHE:CD1       1:C:125:ILE:HG12       2.48         1:C:22:LEU:HD22       1:C:27:VAL:HG11       1.94	0.51
1:C:22:LEU:HD22 1:C:27:VAL:HG11 1.94	0.51
	0.49
1 A CF I DIL IID01	0.49
1:A:65:LEU:HD21   1:A:70:MET:HE2   1.94	0.49
1:A:92:LEU:HD21 2:A:201:NSW:O01 2.13	0.48
1:B:146:ASP:OD1 1:B:146:ASP:N 2.44	0.48
1:B:53:LYS:NZ 1:B:55:ASP:OD2 2.46	0.48
1:B:124:LYS:NZ 1:B:126:THR:OG1 2.42	0.48
1:B:4:GLU:OE2 1:C:89:ARG:NH1 2.47	0.48



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

Continuea from previo		Interatomic	Clash	
Atom-1	Atom-2	${\rm distance}\ (\mathring{\rm A})$	$overlap(\AA)$	
1:B:12:GLN:OE1	1:B:162:ARG:NH1	2.40	0.47	
1:A:12:GLN:HB3	1:A:39:THR:HG23	1.94	0.47	
1:C:11:ARG:HD2	1:C:167:ILE:HG13	1.97	0.47	
1:A:35:GLY:HA3	2:A:201:NSW:C10	2.45	0.47	
1:B:107:ILE:HD12	1:B:116:GLY:HA3	1.97	0.47	
1:B:10:TRP:HB3	1:B:164:CYS:HB3	1.96	0.47	
1:B:166:ARG:NH2	3:B:302:HOH:O	2.48	0.47	
1:C:19:ASP:OD1	1:C:19:ASP:N	2.43	0.47	
1:C:105:ASN:ND2	1:C:117:ILE:HA	2.31	0.46	
1:B:137:ILE:HG13	1:B:155:ILE:HG12	1.97	0.46	
1:A:53:LYS:NZ	1:A:55:ASP:OD1	2.40	0.46	
1:B:3:LEU:H	1:B:3:LEU:HD12	1.80	0.46	
1:C:6:PHE:HE1	1:C:143:ILE:HD13	1.79	0.46	
1:A:34:LEU:HD11	1:A:60:ILE:HG12	1.98	0.46	
1:C:84:ASP:OD1	1:C:87:HIS:N	2.49	0.45	
1:C:27:VAL:HG23	1:C:28:SER:H	1.82	0.45	
1:B:19:ASP:HA	1:B:22:LEU:HD12	1.99	0.45	
1:B:94:TYR:HE1	1:B:97:LEU:HD11	1.82	0.45	
1:C:100:ASP:OD1	1:C:103:THR:OG1	2.34	0.45	
1:C:3:LEU:HD23	1:C:4:GLU:HB3	1.99	0.45	
1:C:40:PRO:HB3	1:C:58:VAL:HG22	1.98	0.44	
1:C:125:ILE:O	1:C:140:GLU:HA	2.18	0.44	
1:B:121:ASP:OD1	1:B:122:GLY:N	2.44	0.44	
1:A:24:GLN:HG3	1:A:158:VAL:HG21	1.98	0.44	
1:A:45:VAL:HG13	1:A:53:LYS:HB3	1.99	0.44	
1:B:112[A]:ARG:HG2	1:B:132:TRP:CD1	2.52	0.44	
1:C:54:ILE:O	1:C:94:TYR:HB3	2.17	0.44	
1:C:43:ARG:HH22	1:C:89:ARG:NH1	2.16	0.43	
1:C:16:TYR:CZ	1:C:17:ASN:HB3	2.54	0.43	
1:C:124:LYS:HD2	1:C:140:GLU:OE1	2.19	0.43	
1:C:166:ARG:HH11	1:C:168:LEU:HD11	1.84	0.43	
1:B:120:PHE:HD1	1:B:125:ILE:HG12	1.84	0.42	
1:C:97:LEU:HD23	1:C:105:ASN:HB3	2.00	0.42	
1:B:11:ARG:HD2	1:B:167:ILE:HD11	2.00	0.42	
1:C:150:LEU:HD11	1:C:161:TRP:HB2	2.01	0.42	
1:A:2:THR:HG22	1:A:3:LEU:H	1.85	0.42	
1:C:77:PHE:CE1	1:C:92:LEU:HG	2.51	0.42	
1:B:127:VAL:HB	1:B:139:ASP:OD2	2.20	0.42	
1:C:35:GLY:O	1:C:38:VAL:HG22	2.19	0.41	
1:B:99:ILE:HD13	1:B:118:ALA:HB1	2.03	0.41	
1:C:16:TYR:C	1:C:18:LEU:H	2.24	0.41	



Continued from previous page...

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:A:150:LEU:HD21	1:A:152:ARG:HB2	2.03	0.41
1:C:82:PRO:HA	1:C:88:PHE:HA	2.02	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	172/181 (95%)	159 (92%)	10 (6%)	3 (2%)	9 36
1	В	171/181 (94%)	159 (93%)	11 (6%)	1 (1%)	25 59
1	С	171/181 (94%)	142 (83%)	16 (9%)	13 (8%)	1 5
All	All	514/543 (95%)	460 (90%)	37 (7%)	17 (3%)	4 21

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	С	5	ASP
1	A	37	SER
1	С	-2	ASN
1	С	62	TYR
1	С	63	GLU
1	A	-2	ASN
1	A	78	LYS
1	С	0	VAL
1	С	27	VAL
1	С	78	LYS
1	С	103	THR
1	С	146	ASP
1	В	122	GLY
1	С	83	VAL
1	С	102	VAL



Continued from previous page...

Mol	Chain	Res	Type
1	С	25	GLY
1	С	51	GLY

#### 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	150/157 (96%)	143 (95%)	7 (5%)	26 59		
1	В	149/157 (95%)	146 (98%)	3 (2%)	55 80		
1	С	149/157 (95%)	144 (97%)	5 (3%)	37 69		
All	All	448/471 (95%)	433 (97%)	15 (3%)	40 69		

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-1	MET
1	A	1	PHE
1	A	19	ASP
1	A	53	LYS
1	A	78	LYS
1	A	112	ARG
1	A	139	ASP
1	В	62	TYR
1	В	112[A]	ARG
1	В	112[B]	ARG
1	С	1	PHE
1	С	4	GLU
1	С	46	LEU
1	С	85	ASP
1	С	112	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.



#### 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		Chain	Res	Link	Во	Bond lengths			Bond angles		
MIOI	Mol Type Chai		nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
2	NSW	В	201	-	31,36,36	1.52	4 (12%)	40,51,51	1.13	4 (10%)	
2	NSW	С	201	-	31,36,36	1.56	4 (12%)	40,51,51	1.08	5 (12%)	
2	NSW	A	201	-	31,36,36	1.57	3 (9%)	40,51,51	1.11	5 (12%)	

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	NSW	В	201	-	-	2/12/12/12	0/5/5/5
2	NSW	С	201	-	-	2/12/12/12	0/5/5/5
2	NSW	A	201	-	-	0/12/12/12	0/5/5/5

All (11) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
2	A	201	NSW	C24-C23	-6.48	1.38	1.48
2	С	201	NSW	C24-C23	-6.37	1.38	1.48
2	В	201	NSW	C24-C23	-6.31	1.39	1.48
2	A	201	NSW	C02-N03	-3.55	1.33	1.37
2	С	201	NSW	C02-N03	-3.42	1.33	1.37
2	В	201	NSW	C02-N03	-3.33	1.33	1.37
2	A	201	NSW	O01-C02	-3.33	1.18	1.22
2	С	201	NSW	O01-C02	-3.09	1.18	1.22
2	В	201	NSW	O01-C02	-2.76	1.18	1.22
2	С	201	NSW	C15-C14	2.45	1.53	1.51
2	В	201	NSW	C15-C14	2.31	1.53	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	201	NSW	C31-C23-C24	-3.25	118.58	121.90
2	В	201	NSW	C24-C23-N22	3.18	120.54	116.02
2	С	201	NSW	C05-C04-N03	-3.18	108.89	113.57
2	В	201	NSW	C15-C14-N22	3.03	122.23	116.25
2	A	201	NSW	C05-C04-N03	-2.90	109.30	113.57
2	С	201	NSW	C15-C14-N22	2.47	121.12	116.25
2	A	201	NSW	C24-C23-N22	2.42	119.47	116.02
2	С	201	NSW	C24-C23-N22	2.34	119.35	116.02
2	A	201	NSW	C16-C15-C14	-2.20	106.75	112.40
2	С	201	NSW	C13-N12-N03	2.17	107.65	104.89
2	В	201	NSW	C13-N12-N03	2.15	107.62	104.89
2	A	201	NSW	C13-N12-N03	2.08	107.53	104.89
2	С	201	NSW	C23-N22-C14	2.05	120.13	118.35
2	A	201	NSW	C31-C23-C24	-2.01	119.84	121.90

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	201	NSW	C13-C14-C15-C16
2	В	201	NSW	N22-C14-C15-C16
2	С	201	NSW	C14-C15-C16-C21
2	С	201	NSW	C14-C15-C16-C17

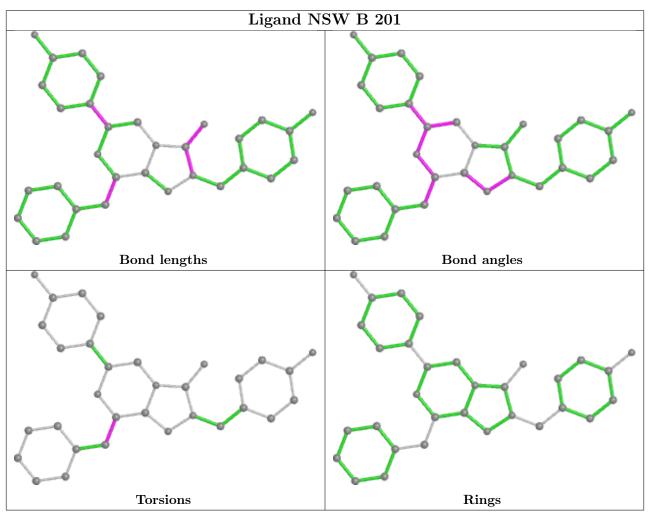
There are no ring outliers.

1 monomer is involved in 2 short contacts:

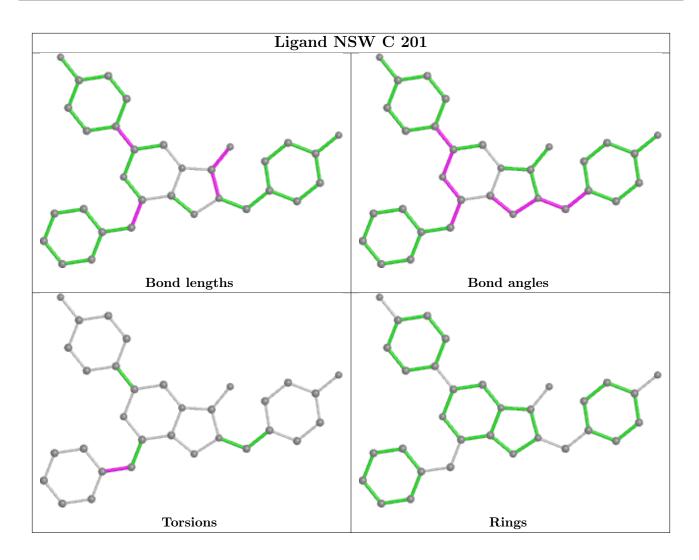


Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	201	NSW	2	0

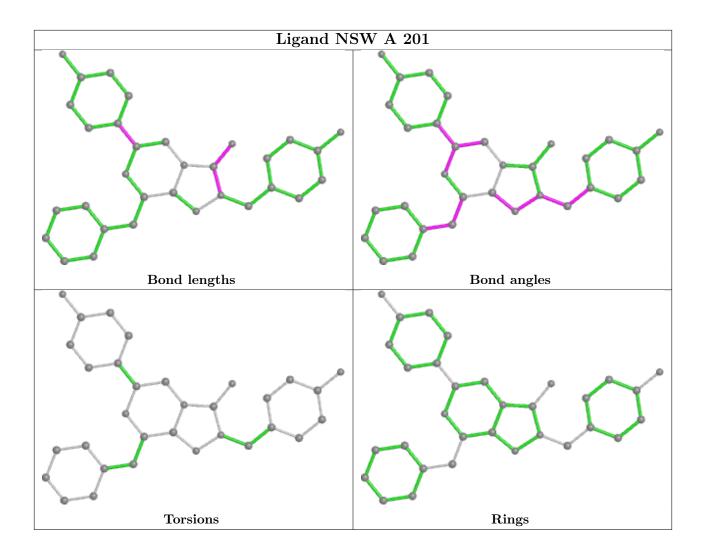
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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>	# RSRZ > 2		$\mathrm{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	$174/181 \; (96\%)$	-0.42	0 100 1	.00	86, 105, 128, 159	0
1	В	172/181 (95%)	-0.23	3 (1%) 70	49	71, 105, 126, 138	0
1	С	173/181 (95%)	-0.14	5 (2%) 51	28	79, 116, 163, 193	0
All	All	519/543 (95%)	-0.27	8 (1%) 73	54	71, 107, 144, 193	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	97	LEU	3.4
1	В	-2	ASN	3.3
1	С	48	GLY	2.7
1	В	-1	MET	2.6
1	С	141	ARG	2.4
1	С	46	LEU	2.3
1	С	52	LEU	2.3
1	В	150	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 monosaccharides in this entry.

### 6.4 Ligands (i)

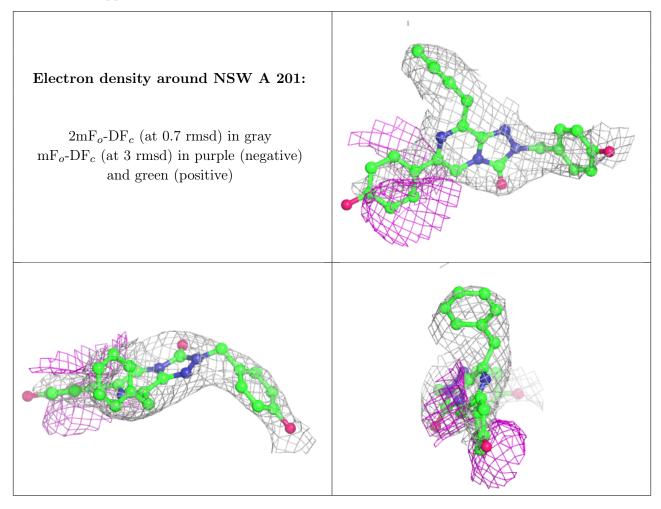
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,



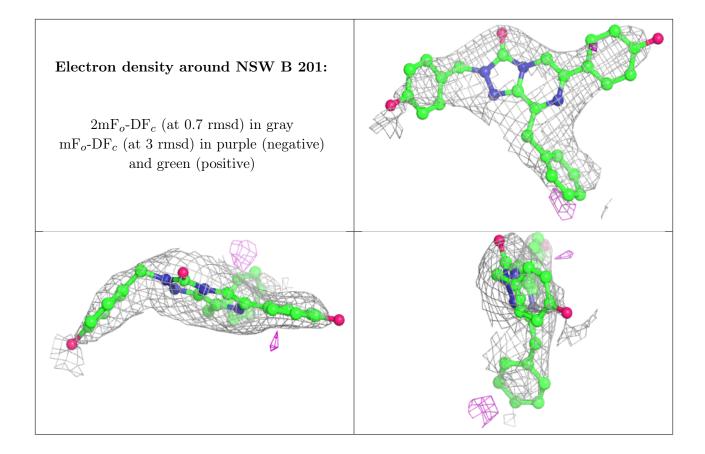
median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	NSW	A	201	32/32	0.89	0.42	97,108,112,114	0
2	NSW	В	201	32/32	0.92	0.42	85,96,110,113	0
2	NSW	С	201	32/32	0.92	0.41	98,106,111,114	0

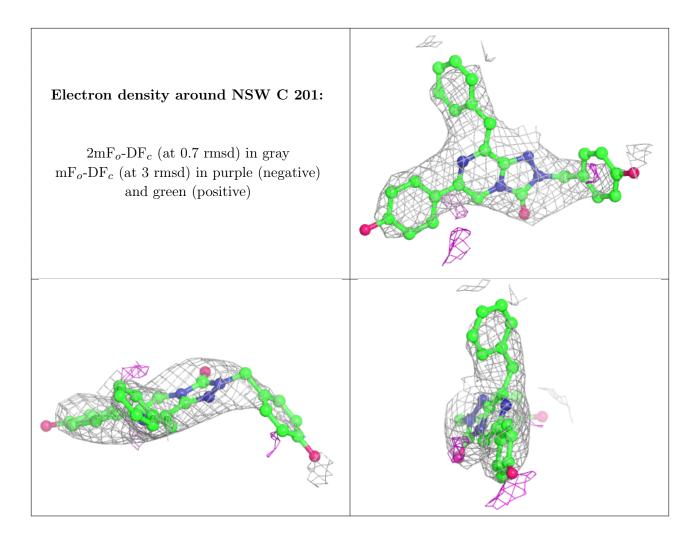
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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











# 6.5 Other polymers (i)

There are no such residues in this entry.

