



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2024 – 07:22 PM EST

PDB ID : 3VT2  
Title : Crystal structure of Ct1,3Gal43A in complex with isopropyl-beta-D-thiogalactoside  
Authors : Jiang, D.; Fan, J.; Wang, X.; Zhao, Y.; Huang, B.; Zhang, X.C.  
Deposited on : 2012-05-18  
Resolution : 3.00 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) 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 : 2.36  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 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) : 2.36

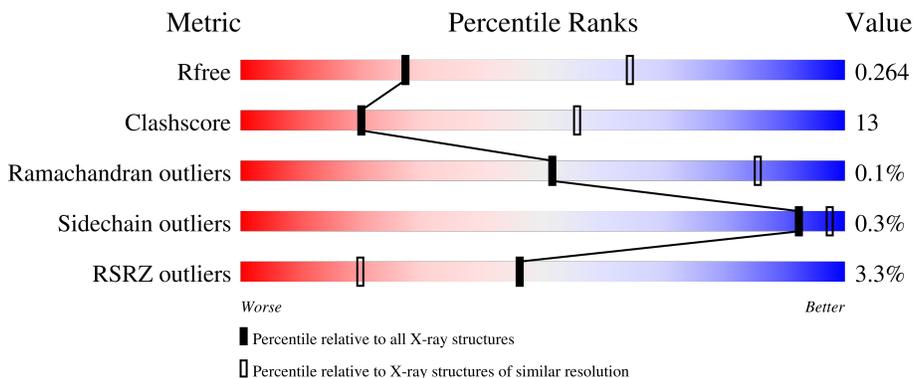
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	526	
1	B	526	
1	C	526	
1	D	526	
1	E	526	

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Mol	Chain	Length	Quality of chain
1	F	526	 70% 18% 12%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IPT	D	601	-	-	-	X
2	IPT	F	602	-	-	-	X

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 22274 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 Ricin B lectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	461	3664	2323	623	703	15	0	0	0
1	B	461	3664	2323	623	703	15	0	0	0
1	C	482	3807	2406	651	732	18	0	0	0
1	D	461	3664	2323	623	703	15	0	0	0
1	E	461	3664	2323	623	703	15	0	0	0
1	F	461	3664	2323	623	703	15	0	0	0

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	expression tag	UNP A3DD67
A	-34	GLY	-	expression tag	UNP A3DD67
A	-33	SER	-	expression tag	UNP A3DD67
A	-32	SER	-	expression tag	UNP A3DD67
A	-31	HIS	-	expression tag	UNP A3DD67
A	-30	HIS	-	expression tag	UNP A3DD67
A	-29	HIS	-	expression tag	UNP A3DD67
A	-28	HIS	-	expression tag	UNP A3DD67
A	-27	HIS	-	expression tag	UNP A3DD67
A	-26	HIS	-	expression tag	UNP A3DD67
A	-25	SER	-	expression tag	UNP A3DD67
A	-24	SER	-	expression tag	UNP A3DD67
A	-23	GLY	-	expression tag	UNP A3DD67
A	-22	LEU	-	expression tag	UNP A3DD67
A	-21	VAL	-	expression tag	UNP A3DD67
A	-20	PRO	-	expression tag	UNP A3DD67
A	-19	ARG	-	expression tag	UNP A3DD67

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	expression tag	UNP A3DD67
A	-17	SER	-	expression tag	UNP A3DD67
A	-16	HIS	-	expression tag	UNP A3DD67
A	-15	MET	-	expression tag	UNP A3DD67
A	-14	ALA	-	expression tag	UNP A3DD67
A	-13	SER	-	expression tag	UNP A3DD67
A	-12	MET	-	expression tag	UNP A3DD67
A	-11	THR	-	expression tag	UNP A3DD67
A	-10	GLY	-	expression tag	UNP A3DD67
A	-9	GLY	-	expression tag	UNP A3DD67
A	-8	GLN	-	expression tag	UNP A3DD67
A	-7	GLN	-	expression tag	UNP A3DD67
A	-6	MET	-	expression tag	UNP A3DD67
A	-5	GLY	-	expression tag	UNP A3DD67
A	-4	ARG	-	expression tag	UNP A3DD67
A	-3	GLY	-	expression tag	UNP A3DD67
A	-2	SER	-	expression tag	UNP A3DD67
A	-1	GLU	-	expression tag	UNP A3DD67
A	0	PHE	-	expression tag	UNP A3DD67
B	-35	MET	-	expression tag	UNP A3DD67
B	-34	GLY	-	expression tag	UNP A3DD67
B	-33	SER	-	expression tag	UNP A3DD67
B	-32	SER	-	expression tag	UNP A3DD67
B	-31	HIS	-	expression tag	UNP A3DD67
B	-30	HIS	-	expression tag	UNP A3DD67
B	-29	HIS	-	expression tag	UNP A3DD67
B	-28	HIS	-	expression tag	UNP A3DD67
B	-27	HIS	-	expression tag	UNP A3DD67
B	-26	HIS	-	expression tag	UNP A3DD67
B	-25	SER	-	expression tag	UNP A3DD67
B	-24	SER	-	expression tag	UNP A3DD67
B	-23	GLY	-	expression tag	UNP A3DD67
B	-22	LEU	-	expression tag	UNP A3DD67
B	-21	VAL	-	expression tag	UNP A3DD67
B	-20	PRO	-	expression tag	UNP A3DD67
B	-19	ARG	-	expression tag	UNP A3DD67
B	-18	GLY	-	expression tag	UNP A3DD67
B	-17	SER	-	expression tag	UNP A3DD67
B	-16	HIS	-	expression tag	UNP A3DD67
B	-15	MET	-	expression tag	UNP A3DD67
B	-14	ALA	-	expression tag	UNP A3DD67
B	-13	SER	-	expression tag	UNP A3DD67

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	MET	-	expression tag	UNP A3DD67
B	-11	THR	-	expression tag	UNP A3DD67
B	-10	GLY	-	expression tag	UNP A3DD67
B	-9	GLY	-	expression tag	UNP A3DD67
B	-8	GLN	-	expression tag	UNP A3DD67
B	-7	GLN	-	expression tag	UNP A3DD67
B	-6	MET	-	expression tag	UNP A3DD67
B	-5	GLY	-	expression tag	UNP A3DD67
B	-4	ARG	-	expression tag	UNP A3DD67
B	-3	GLY	-	expression tag	UNP A3DD67
B	-2	SER	-	expression tag	UNP A3DD67
B	-1	GLU	-	expression tag	UNP A3DD67
B	0	PHE	-	expression tag	UNP A3DD67
C	-35	MET	-	expression tag	UNP A3DD67
C	-34	GLY	-	expression tag	UNP A3DD67
C	-33	SER	-	expression tag	UNP A3DD67
C	-32	SER	-	expression tag	UNP A3DD67
C	-31	HIS	-	expression tag	UNP A3DD67
C	-30	HIS	-	expression tag	UNP A3DD67
C	-29	HIS	-	expression tag	UNP A3DD67
C	-28	HIS	-	expression tag	UNP A3DD67
C	-27	HIS	-	expression tag	UNP A3DD67
C	-26	HIS	-	expression tag	UNP A3DD67
C	-25	SER	-	expression tag	UNP A3DD67
C	-24	SER	-	expression tag	UNP A3DD67
C	-23	GLY	-	expression tag	UNP A3DD67
C	-22	LEU	-	expression tag	UNP A3DD67
C	-21	VAL	-	expression tag	UNP A3DD67
C	-20	PRO	-	expression tag	UNP A3DD67
C	-19	ARG	-	expression tag	UNP A3DD67
C	-18	GLY	-	expression tag	UNP A3DD67
C	-17	SER	-	expression tag	UNP A3DD67
C	-16	HIS	-	expression tag	UNP A3DD67
C	-15	MET	-	expression tag	UNP A3DD67
C	-14	ALA	-	expression tag	UNP A3DD67
C	-13	SER	-	expression tag	UNP A3DD67
C	-12	MET	-	expression tag	UNP A3DD67
C	-11	THR	-	expression tag	UNP A3DD67
C	-10	GLY	-	expression tag	UNP A3DD67
C	-9	GLY	-	expression tag	UNP A3DD67
C	-8	GLN	-	expression tag	UNP A3DD67
C	-7	GLN	-	expression tag	UNP A3DD67

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-6	MET	-	expression tag	UNP A3DD67
C	-5	GLY	-	expression tag	UNP A3DD67
C	-4	ARG	-	expression tag	UNP A3DD67
C	-3	GLY	-	expression tag	UNP A3DD67
C	-2	SER	-	expression tag	UNP A3DD67
C	-1	GLU	-	expression tag	UNP A3DD67
C	0	PHE	-	expression tag	UNP A3DD67
D	-35	MET	-	expression tag	UNP A3DD67
D	-34	GLY	-	expression tag	UNP A3DD67
D	-33	SER	-	expression tag	UNP A3DD67
D	-32	SER	-	expression tag	UNP A3DD67
D	-31	HIS	-	expression tag	UNP A3DD67
D	-30	HIS	-	expression tag	UNP A3DD67
D	-29	HIS	-	expression tag	UNP A3DD67
D	-28	HIS	-	expression tag	UNP A3DD67
D	-27	HIS	-	expression tag	UNP A3DD67
D	-26	HIS	-	expression tag	UNP A3DD67
D	-25	SER	-	expression tag	UNP A3DD67
D	-24	SER	-	expression tag	UNP A3DD67
D	-23	GLY	-	expression tag	UNP A3DD67
D	-22	LEU	-	expression tag	UNP A3DD67
D	-21	VAL	-	expression tag	UNP A3DD67
D	-20	PRO	-	expression tag	UNP A3DD67
D	-19	ARG	-	expression tag	UNP A3DD67
D	-18	GLY	-	expression tag	UNP A3DD67
D	-17	SER	-	expression tag	UNP A3DD67
D	-16	HIS	-	expression tag	UNP A3DD67
D	-15	MET	-	expression tag	UNP A3DD67
D	-14	ALA	-	expression tag	UNP A3DD67
D	-13	SER	-	expression tag	UNP A3DD67
D	-12	MET	-	expression tag	UNP A3DD67
D	-11	THR	-	expression tag	UNP A3DD67
D	-10	GLY	-	expression tag	UNP A3DD67
D	-9	GLY	-	expression tag	UNP A3DD67
D	-8	GLN	-	expression tag	UNP A3DD67
D	-7	GLN	-	expression tag	UNP A3DD67
D	-6	MET	-	expression tag	UNP A3DD67
D	-5	GLY	-	expression tag	UNP A3DD67
D	-4	ARG	-	expression tag	UNP A3DD67
D	-3	GLY	-	expression tag	UNP A3DD67
D	-2	SER	-	expression tag	UNP A3DD67
D	-1	GLU	-	expression tag	UNP A3DD67

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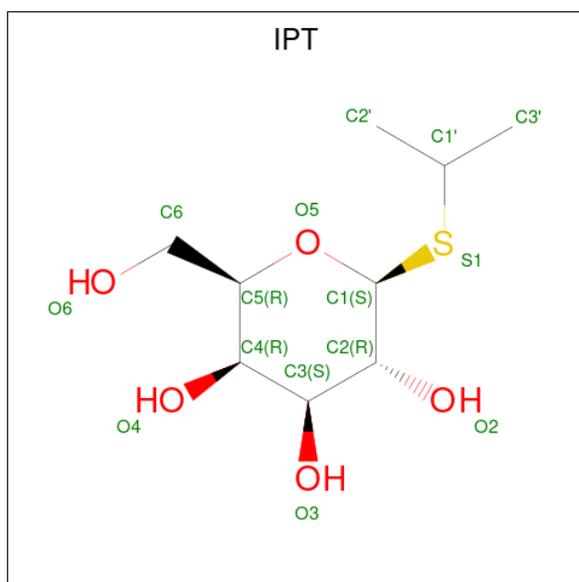
Chain	Residue	Modelled	Actual	Comment	Reference
D	0	PHE	-	expression tag	UNP A3DD67
E	-35	MET	-	expression tag	UNP A3DD67
E	-34	GLY	-	expression tag	UNP A3DD67
E	-33	SER	-	expression tag	UNP A3DD67
E	-32	SER	-	expression tag	UNP A3DD67
E	-31	HIS	-	expression tag	UNP A3DD67
E	-30	HIS	-	expression tag	UNP A3DD67
E	-29	HIS	-	expression tag	UNP A3DD67
E	-28	HIS	-	expression tag	UNP A3DD67
E	-27	HIS	-	expression tag	UNP A3DD67
E	-26	HIS	-	expression tag	UNP A3DD67
E	-25	SER	-	expression tag	UNP A3DD67
E	-24	SER	-	expression tag	UNP A3DD67
E	-23	GLY	-	expression tag	UNP A3DD67
E	-22	LEU	-	expression tag	UNP A3DD67
E	-21	VAL	-	expression tag	UNP A3DD67
E	-20	PRO	-	expression tag	UNP A3DD67
E	-19	ARG	-	expression tag	UNP A3DD67
E	-18	GLY	-	expression tag	UNP A3DD67
E	-17	SER	-	expression tag	UNP A3DD67
E	-16	HIS	-	expression tag	UNP A3DD67
E	-15	MET	-	expression tag	UNP A3DD67
E	-14	ALA	-	expression tag	UNP A3DD67
E	-13	SER	-	expression tag	UNP A3DD67
E	-12	MET	-	expression tag	UNP A3DD67
E	-11	THR	-	expression tag	UNP A3DD67
E	-10	GLY	-	expression tag	UNP A3DD67
E	-9	GLY	-	expression tag	UNP A3DD67
E	-8	GLN	-	expression tag	UNP A3DD67
E	-7	GLN	-	expression tag	UNP A3DD67
E	-6	MET	-	expression tag	UNP A3DD67
E	-5	GLY	-	expression tag	UNP A3DD67
E	-4	ARG	-	expression tag	UNP A3DD67
E	-3	GLY	-	expression tag	UNP A3DD67
E	-2	SER	-	expression tag	UNP A3DD67
E	-1	GLU	-	expression tag	UNP A3DD67
E	0	PHE	-	expression tag	UNP A3DD67
F	-35	MET	-	expression tag	UNP A3DD67
F	-34	GLY	-	expression tag	UNP A3DD67
F	-33	SER	-	expression tag	UNP A3DD67
F	-32	SER	-	expression tag	UNP A3DD67
F	-31	HIS	-	expression tag	UNP A3DD67

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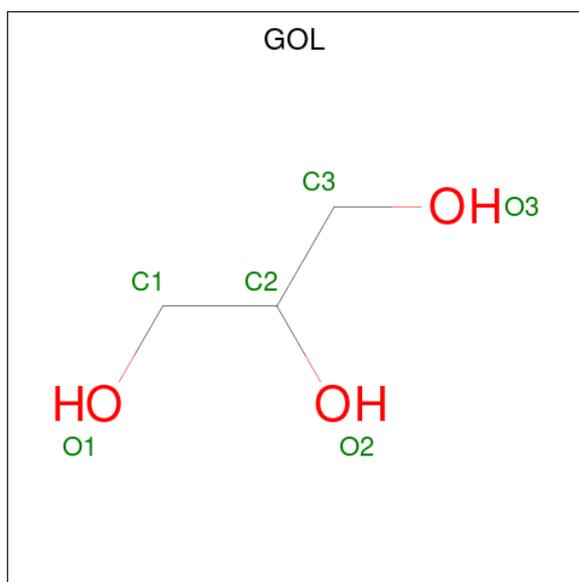
Chain	Residue	Modelled	Actual	Comment	Reference
F	-30	HIS	-	expression tag	UNP A3DD67
F	-29	HIS	-	expression tag	UNP A3DD67
F	-28	HIS	-	expression tag	UNP A3DD67
F	-27	HIS	-	expression tag	UNP A3DD67
F	-26	HIS	-	expression tag	UNP A3DD67
F	-25	SER	-	expression tag	UNP A3DD67
F	-24	SER	-	expression tag	UNP A3DD67
F	-23	GLY	-	expression tag	UNP A3DD67
F	-22	LEU	-	expression tag	UNP A3DD67
F	-21	VAL	-	expression tag	UNP A3DD67
F	-20	PRO	-	expression tag	UNP A3DD67
F	-19	ARG	-	expression tag	UNP A3DD67
F	-18	GLY	-	expression tag	UNP A3DD67
F	-17	SER	-	expression tag	UNP A3DD67
F	-16	HIS	-	expression tag	UNP A3DD67
F	-15	MET	-	expression tag	UNP A3DD67
F	-14	ALA	-	expression tag	UNP A3DD67
F	-13	SER	-	expression tag	UNP A3DD67
F	-12	MET	-	expression tag	UNP A3DD67
F	-11	THR	-	expression tag	UNP A3DD67
F	-10	GLY	-	expression tag	UNP A3DD67
F	-9	GLY	-	expression tag	UNP A3DD67
F	-8	GLN	-	expression tag	UNP A3DD67
F	-7	GLN	-	expression tag	UNP A3DD67
F	-6	MET	-	expression tag	UNP A3DD67
F	-5	GLY	-	expression tag	UNP A3DD67
F	-4	ARG	-	expression tag	UNP A3DD67
F	-3	GLY	-	expression tag	UNP A3DD67
F	-2	SER	-	expression tag	UNP A3DD67
F	-1	GLU	-	expression tag	UNP A3DD67
F	0	PHE	-	expression tag	UNP A3DD67

- Molecule 2 is 1-methylethyl 1-thio-beta-D-galactopyranoside (three-letter code: IPT) (formula: C<sub>9</sub>H<sub>18</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			15	9	5	1		
2	B	1	Total	C	O	S	0	0
			15	9	5	1		
2	C	1	Total	C	O	S	0	0
			15	9	5	1		
2	D	1	Total	C	O	S	0	0
			15	9	5	1		
2	E	1	Total	C	O	S	0	0
			15	9	5	1		
2	F	1	Total	C	O	S	0	0
			15	9	5	1		
2	F	1	Total	C	O	S	0	0
			15	9	5	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



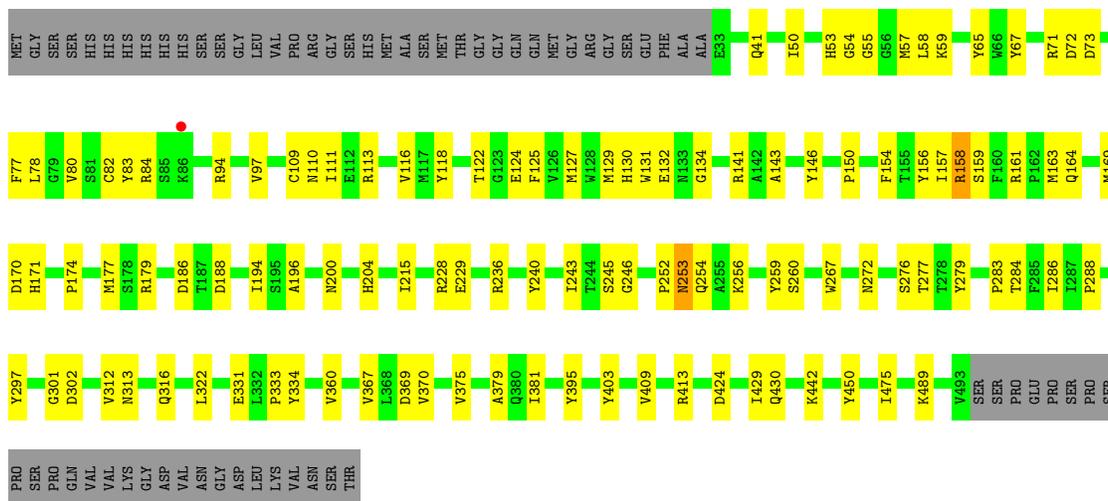
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	C	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0
3	F	1	Total C O 6 3 3	0	0

### 3 Residue-property plots

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

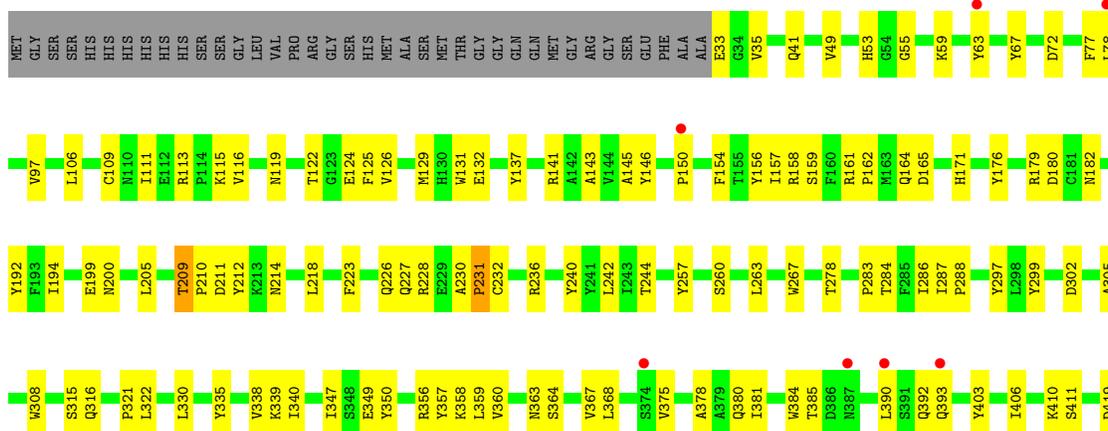
- Molecule 1: Ricin B lectin

Chain A: 



- Molecule 1: Ricin B lectin

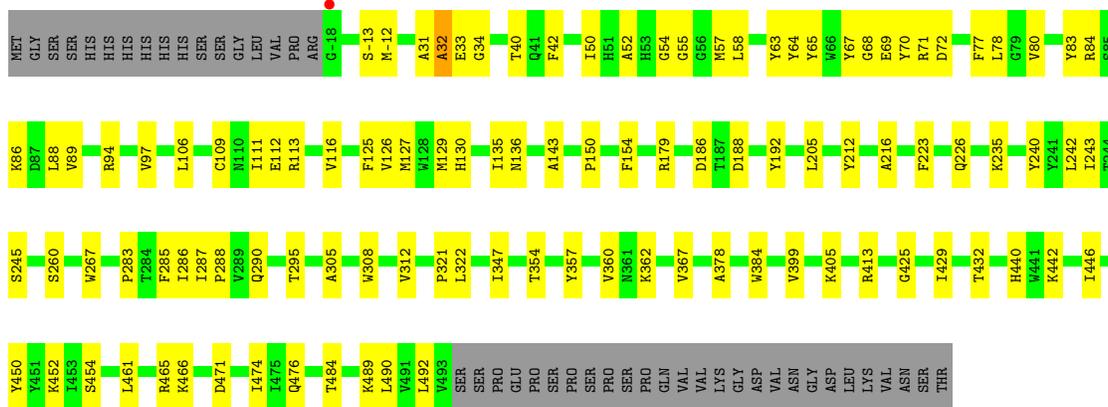
Chain B: 





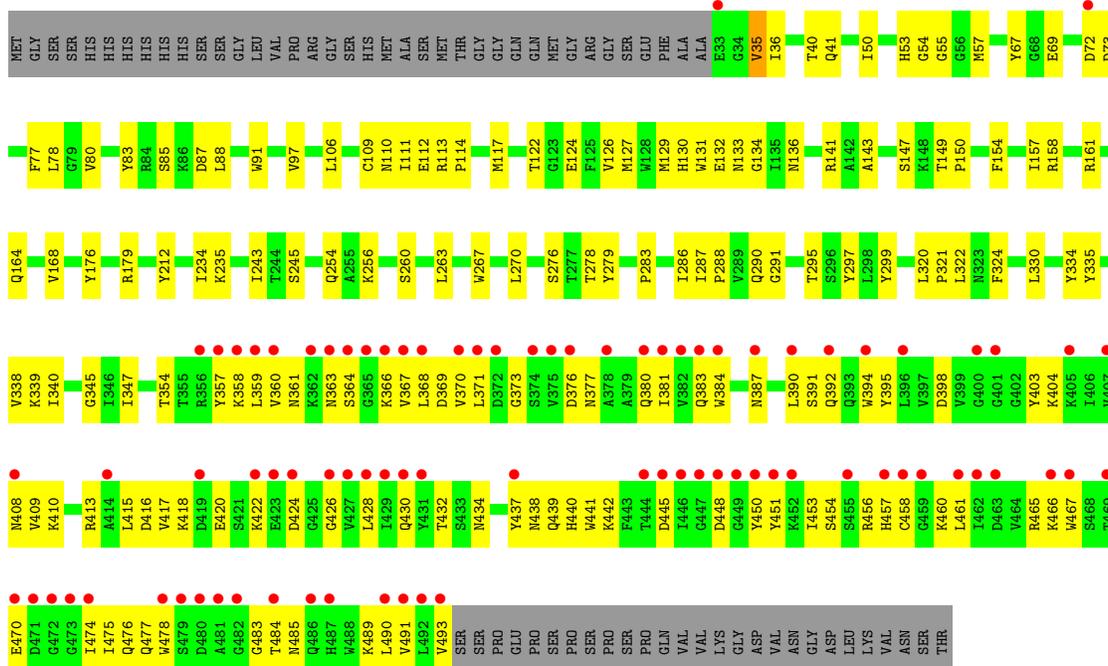
• Molecule 1: Ricin B lectin

Chain C: 71% 20% 8%



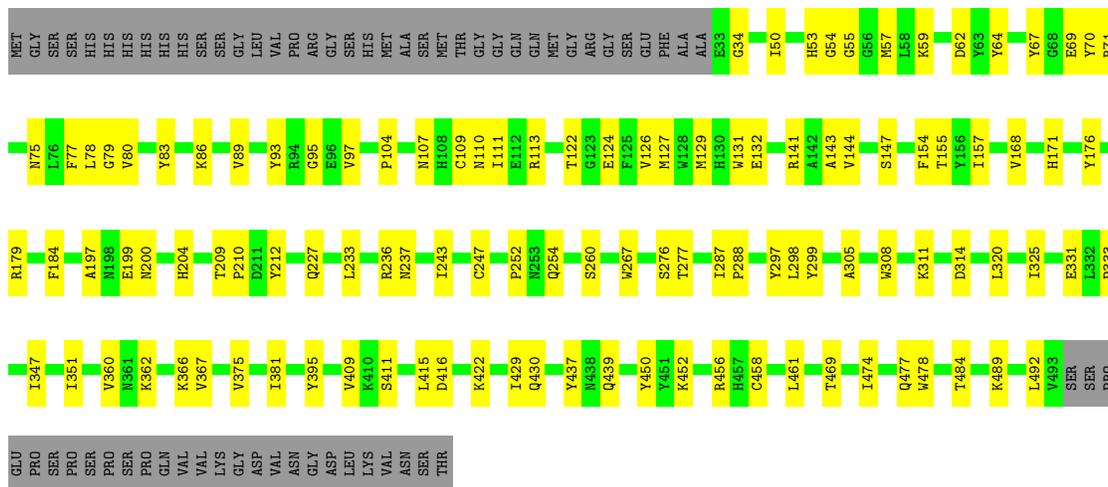
• Molecule 1: Ricin B lectin

Chain D: 16% 56% 32% 12%

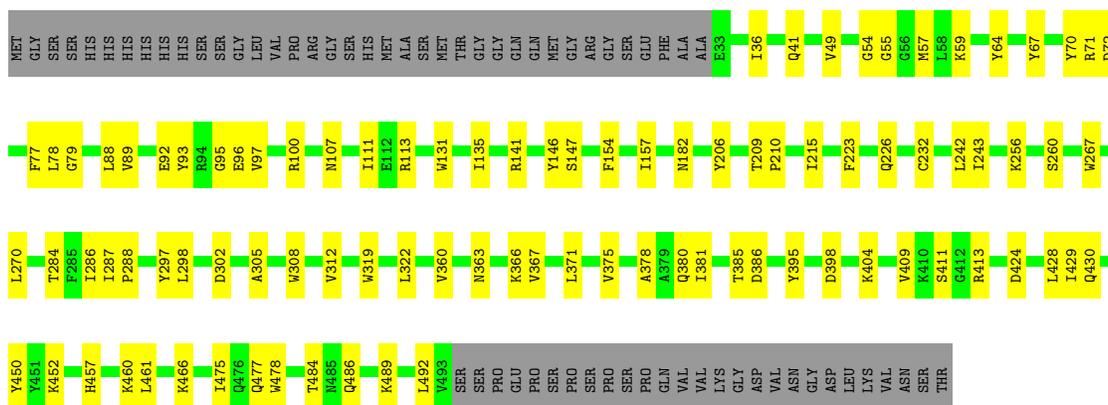


• Molecule 1: Ricin B lectin

Chain E: 67% 21% 12%



● Molecule 1: Ricin B lectin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.23Å 121.97Å 405.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.71 – 3.00 47.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	83.0 (44.71-3.00) 83.0 (47.00-3.00)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 3.01Å)	Xtrriage
Refinement program	PHENIX 1.7_650	Depositor
R, $R_{free}$	0.245 , 0.271 0.236 , 0.264	Depositor DCC
$R_{free}$ test set	1586 reflections (1.78%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.5	Xtrriage
Anisotropy	0.601	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 35.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	22274	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	82.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.20	0/3762	0.34	0/5104
1	B	0.20	0/3762	0.34	0/5104
1	C	0.20	0/3907	0.34	0/5295
1	D	0.20	0/3762	0.34	0/5104
1	E	0.20	0/3762	0.34	0/5104
1	F	0.20	0/3762	0.35	0/5104
All	All	0.20	0/22717	0.34	0/30815

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	3664	0	3480	88	0
1	B	3664	0	3480	104	0
1	C	3807	0	3613	85	0
1	D	3664	0	3480	140	0
1	E	3664	0	3480	72	0
1	F	3664	0	3480	65	0
2	A	15	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	15	0	18	2	0
2	C	15	0	18	0	0
2	D	15	0	18	2	0
2	E	15	0	18	0	0
2	F	30	0	36	0	0
3	A	6	0	8	0	0
3	B	6	0	8	1	0
3	C	12	0	16	1	0
3	E	12	0	16	1	0
3	F	6	0	8	1	0
All	All	22274	0	21195	546	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 13.

All (546) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:416:ASP:HB3	1:E:439:GLN:HG2	1.54	0.89
1:D:35:VAL:HG22	1:D:36:ILE:H	1.38	0.88
1:A:360:VAL:HG12	1:A:367:VAL:HG12	1.55	0.87
1:B:360:VAL:HG12	1:B:367:VAL:HG12	1.56	0.86
1:D:370:VAL:HG12	1:D:430:GLN:HE22	1.43	0.83
1:F:360:VAL:HG22	1:F:367:VAL:HG12	1.60	0.83
1:D:335:TYR:HB2	1:D:338:VAL:HG22	1.61	0.83
1:C:-12:MET:HG3	1:E:155:THR:HG22	1.63	0.81
1:B:360:VAL:HG22	1:B:489:LYS:HB3	1.63	0.81
1:D:387:ASN:H	1:D:392:GLN:HE22	1.29	0.81
1:D:72:ASP:HB3	1:D:78:LEU:HD22	1.63	0.81
1:D:57:MET:HE2	1:D:287:ILE:HG21	1.65	0.79
1:B:72:ASP:HB3	1:B:78:LEU:HG	1.66	0.78
1:B:390:LEU:O	1:B:410:LYS:HB2	1.85	0.77
1:D:35:VAL:HB	1:D:339:LYS:HA	1.65	0.77
1:C:216:ALA:HA	1:D:164:GLN:HE22	1.48	0.75
1:C:360:VAL:HG22	1:C:367:VAL:HG12	1.67	0.75
1:E:422:LYS:HD2	1:E:458:CYS:HB3	1.67	0.75
1:D:451:TYR:HE2	1:D:490:LEU:HB2	1.53	0.74
1:F:461:LEU:HD11	1:F:486:GLN:HB3	1.68	0.73
1:B:146:TYR:CD2	1:B:157:ILE:HD11	2.24	0.72
1:B:53:HIS:HD2	1:B:315:SER:HB2	1.53	0.72
1:A:228:ARG:HH12	1:A:256:LYS:HD2	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:371:LEU:HD12	1:F:380:GLN:HB3	1.72	0.71
1:D:398:ASP:HA	1:D:404:LYS:HA	1.73	0.70
1:A:381:ILE:HG22	1:A:475:ILE:HB	1.74	0.70
1:D:371:LEU:HD22	1:D:380:GLN:HB2	1.74	0.70
1:D:322:LEU:HD21	1:D:330:LEU:HD23	1.74	0.70
1:A:228:ARG:HH21	1:A:246:GLY:H	1.38	0.69
1:C:34:GLY:HA2	1:C:89:VAL:HG21	1.73	0.69
1:D:418:LYS:HA	2:D:601:IPT:H61	1.73	0.69
1:C:72:ASP:HB3	1:C:78:LEU:HD22	1.74	0.69
1:E:360:VAL:HG22	1:E:367:VAL:HG12	1.75	0.68
1:D:451:TYR:CE2	1:D:490:LEU:HB2	2.27	0.68
1:A:260:SER:HB2	1:A:267:TRP:HA	1.76	0.68
1:A:375:VAL:C	1:A:413:ARG:HH22	1.96	0.67
1:A:284:THR:HG21	1:A:302:ASP:OD2	1.94	0.67
1:D:416:ASP:OD1	1:D:439:GLN:HG3	1.94	0.67
1:B:137:TYR:HB3	1:B:179:ARG:HH21	1.59	0.67
1:A:331:GLU:HG2	1:A:333:PRO:HD3	1.75	0.67
1:D:403:TYR:HB3	1:D:440:HIS:HB3	1.75	0.67
1:E:54:GLY:O	1:E:113:ARG:HA	1.95	0.67
1:B:161:ARG:O	1:B:164:GLN:HG3	1.95	0.66
1:C:442:LYS:HG3	1:F:100:ARG:NH2	2.10	0.66
1:A:229:GLU:HG2	1:A:246:GLY:O	1.96	0.66
1:B:364:SER:HA	1:B:469:THR:HG23	1.77	0.66
1:F:182:ASN:HD22	1:F:232:CYS:HA	1.61	0.66
1:C:442:LYS:HG3	1:F:100:ARG:HH22	1.62	0.65
1:D:69:GLU:OE1	1:D:112:GLU:HA	1.96	0.65
1:D:53:HIS:O	1:D:69:GLU:HG2	1.97	0.65
1:A:413:ARG:HH21	1:A:430:GLN:NE2	1.95	0.64
1:B:378:ALA:HA	1:B:429:ILE:HD12	1.78	0.64
1:E:416:ASP:CB	1:E:439:GLN:HG2	2.27	0.64
1:D:453:ILE:O	1:D:461:LEU:HD22	1.97	0.64
1:A:245:SER:HB3	1:A:283:PRO:HD2	1.78	0.64
1:B:137:TYR:HB3	1:B:179:ARG:NH2	2.13	0.64
1:E:53:HIS:O	1:E:69:GLU:HG2	1.98	0.64
1:E:144:VAL:HG13	1:E:157:ILE:HB	1.78	0.64
1:E:57:MET:HE2	1:E:287:ILE:HD13	1.79	0.64
1:C:260:SER:HB2	1:C:267:TRP:HA	1.79	0.64
1:B:461:LEU:HD11	1:B:486:GLN:HB3	1.78	0.63
1:A:72:ASP:HB3	1:A:78:LEU:HD12	1.80	0.63
1:C:65:TYR:CE2	1:C:84:ARG:HD3	2.33	0.63
1:B:340:ILE:HG22	1:B:347:ILE:HG23	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:413:ARG:NH1	1:C:432:THR:HG22	2.13	0.62
1:E:77:PHE:CD2	1:E:111:ILE:HB	2.33	0.62
1:B:122:THR:HG23	1:B:124:GLU:H	1.65	0.62
1:D:358:LYS:HE3	1:D:493:VAL:HG21	1.81	0.62
1:D:370:VAL:HG12	1:D:430:GLN:NE2	2.13	0.62
1:D:359:LEU:HD21	1:D:490:LEU:HD12	1.82	0.61
1:C:413:ARG:HH12	1:C:432:THR:HG22	1.64	0.61
1:F:113:ARG:HH12	1:F:284:THR:HG22	1.65	0.61
1:B:368:LEU:HD12	1:B:475:ILE:HD12	1.82	0.61
1:C:57:MET:HE2	1:C:287:ILE:HD13	1.81	0.61
1:D:465:ARG:HD3	1:D:474:ILE:HB	1.81	0.61
1:B:97:VAL:HB	1:B:154:PHE:CD2	2.35	0.61
1:B:223:PHE:HE2	1:B:242:LEU:HD23	1.63	0.61
1:F:97:VAL:HB	1:F:154:PHE:CD2	2.36	0.61
1:D:424:ASP:OD2	1:D:478:TRP:HA	2.01	0.61
1:B:157:ILE:HG22	1:B:158:ARG:HG2	1.82	0.60
1:C:465:ARG:HH21	1:C:474:ILE:HG21	1.66	0.60
1:D:321:PRO:HD3	1:D:338:VAL:HG11	1.82	0.60
1:D:245:SER:HB3	1:D:283:PRO:HD2	1.82	0.60
1:F:450:TYR:CE1	1:F:489:LYS:HB2	2.37	0.60
1:D:35:VAL:HG21	1:D:338:VAL:O	2.02	0.60
1:D:395:TYR:CE2	1:D:409:VAL:HG22	2.36	0.60
1:D:387:ASN:H	1:D:392:GLN:NE2	1.98	0.60
1:D:72:ASP:CG	1:D:73:ASP:H	2.05	0.60
1:D:370:VAL:HG22	1:D:391:SER:HB3	1.83	0.60
1:A:360:VAL:HG22	1:A:489:LYS:HB3	1.84	0.59
1:B:53:HIS:CD2	1:B:315:SER:HB2	2.36	0.59
1:D:117:MET:HE3	1:D:212:TYR:HB3	1.84	0.59
1:D:35:VAL:HG22	1:D:36:ILE:N	2.14	0.59
1:C:80:VAL:HG11	1:C:127:MET:HE3	1.84	0.59
1:B:406:ILE:HD13	1:B:441:TRP:CD1	2.39	0.58
1:A:84:ARG:HD3	1:A:94:ARG:HH11	1.66	0.58
1:D:426:GLY:O	1:D:476:GLN:HB2	2.03	0.58
1:F:57:MET:HE2	1:F:287:ILE:HD13	1.85	0.58
1:F:286:ILE:HD13	1:F:322:LEU:HD22	1.83	0.58
1:A:130:HIS:CD2	1:A:179:ARG:HA	2.39	0.58
1:C:32:ALA:O	1:C:33:GLU:HG3	2.01	0.58
1:F:260:SER:HB2	1:F:267:TRP:HA	1.86	0.58
1:B:403:TYR:CE1	1:B:442:LYS:HE2	2.38	0.58
1:D:130:HIS:CD2	1:D:179:ARG:HA	2.38	0.58
1:F:375:VAL:HG12	1:F:411:SER:HB3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:HIS:CE1	1:B:199:GLU:HB2	2.39	0.58
1:F:284:THR:HG21	1:F:302:ASP:OD2	2.03	0.58
1:D:366:LYS:HB2	1:D:383:GLN:OE1	2.04	0.57
1:D:408:ASN:HD22	1:D:430:GLN:NE2	2.01	0.57
1:D:467:TRP:HA	1:D:485:ASN:ND2	2.19	0.57
1:B:260:SER:HB2	1:B:267:TRP:HA	1.87	0.57
1:D:420:GLU:HB3	1:D:457:HIS:CE1	2.40	0.57
1:F:366:LYS:HE3	1:F:385:THR:HG22	1.87	0.57
1:D:260:SER:HB2	1:D:267:TRP:HA	1.87	0.57
1:D:450:TYR:HB3	1:D:489:LYS:HG2	1.86	0.57
1:D:460:LYS:C	1:D:461:LEU:HD23	2.24	0.57
1:E:171:HIS:CE1	1:E:199:GLU:HB2	2.40	0.57
1:A:157:ILE:HG22	1:A:158:ARG:HG2	1.87	0.57
1:A:228:ARG:NH1	1:A:256:LYS:HD2	2.20	0.57
1:D:359:LEU:HD22	1:D:490:LEU:HA	1.86	0.57
1:D:420:GLU:HG2	1:D:438:ASN:ND2	2.19	0.56
1:E:474:ILE:HD12	1:E:474:ILE:H	1.69	0.56
1:A:450:TYR:CE1	1:A:489:LYS:HB2	2.39	0.56
1:C:54:GLY:O	1:C:113:ARG:HA	2.05	0.56
1:D:129:MET:HG3	1:D:143:ALA:HB3	1.87	0.56
1:A:67:TYR:HE1	1:A:82:CYS:HG	1.53	0.56
1:C:63:TYR:CE1	1:C:86:LYS:HE3	2.40	0.56
1:E:129:MET:HG2	1:E:143:ALA:HB3	1.88	0.56
1:E:168:VAL:HG11	1:E:176:TYR:CE1	2.40	0.56
1:E:80:VAL:HG11	1:E:127:MET:HE3	1.88	0.56
1:A:161:ARG:O	1:A:164:GLN:HG3	2.06	0.56
1:D:54:GLY:O	1:D:113:ARG:HA	2.05	0.56
1:F:223:PHE:HE2	1:F:242:LEU:HD23	1.69	0.56
1:B:182:ASN:HB2	1:B:231:PRO:HG2	1.87	0.56
1:D:454:SER:HA	1:D:461:LEU:HD22	1.88	0.56
1:A:288:PRO:HG3	1:A:297:TYR:CE1	2.41	0.56
1:A:71:ARG:NH1	1:A:312:VAL:HG11	2.21	0.56
1:D:340:ILE:HG22	1:D:347:ILE:HG23	1.87	0.56
1:C:42:PHE:CD2	1:C:50:ILE:HD12	2.41	0.56
1:E:252:PRO:HB2	1:E:277:THR:HG23	1.87	0.56
1:C:125:PHE:CZ	1:C:150:PRO:HG3	2.42	0.55
1:D:377:ASN:HA	1:D:413:ARG:NH2	2.21	0.55
1:D:381:ILE:HD11	1:D:430:GLN:CD	2.26	0.55
1:D:126:VAL:HG21	1:D:212:TYR:HB2	1.89	0.55
1:D:254:GLN:HG2	1:D:276:SER:HA	1.89	0.55
1:E:179:ARG:HG3	1:E:200:ASN:OD1	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:106:LEU:HD22	1:C:111:ILE:HD11	1.89	0.55
1:F:59:LYS:HD3	1:F:64:TYR:CE1	2.42	0.55
1:E:366:LYS:HE2	1:E:469:THR:O	2.06	0.55
1:F:395:TYR:CE2	1:F:409:VAL:HG22	2.42	0.55
1:B:119:ASN:HB3	1:B:122:THR:HG22	1.89	0.54
1:D:366:LYS:HB3	1:D:384:TRP:O	2.08	0.54
1:C:97:VAL:HB	1:C:154:PHE:CD2	2.42	0.54
1:F:77:PHE:CD1	1:F:111:ILE:HB	2.41	0.54
1:D:417:VAL:HG21	1:D:477:GLN:NE2	2.23	0.54
1:F:100:ARG:HD2	1:F:107:ASN:O	2.07	0.54
1:D:448:ASP:HB2	1:D:450:TYR:CD2	2.43	0.54
1:A:110:ASN:HB2	1:A:132:GLU:HB2	1.89	0.54
1:B:97:VAL:HB	1:B:154:PHE:HD2	1.72	0.54
1:D:50:ILE:HG23	1:D:83:TYR:CZ	2.43	0.54
1:B:360:VAL:CG2	1:B:489:LYS:HB3	2.36	0.54
1:C:84:ARG:HH21	1:C:94:ARG:CZ	2.21	0.54
1:D:420:GLU:O	1:D:457:HIS:HE1	1.90	0.54
1:D:441:TRP:HA	1:D:454:SER:O	2.07	0.54
1:D:453:ILE:HG22	1:D:454:SER:H	1.71	0.54
1:D:357:TYR:CD1	1:D:490:LEU:HD11	2.43	0.53
1:F:305:ALA:HA	1:F:308:TRP:CZ2	2.43	0.53
1:A:116:VAL:HG22	1:A:127:MET:HB2	1.90	0.53
1:F:54:GLY:O	1:F:113:ARG:HA	2.08	0.53
1:A:129:MET:HG2	1:A:143:ALA:HB3	1.90	0.53
1:B:368:LEU:CD1	1:B:475:ILE:HD12	2.38	0.53
1:A:118:TYR:CD1	1:A:125:PHE:HE1	2.26	0.53
1:B:230:ALA:O	1:B:244:THR:HA	2.08	0.53
1:D:110:ASN:HB2	1:D:132:GLU:HB2	1.89	0.53
1:D:437:TYR:O	1:D:456:ARG:HB3	2.09	0.53
1:A:256:LYS:HE2	1:A:272:ASN:ND2	2.23	0.53
1:B:129:MET:HG2	1:B:143:ALA:HB3	1.90	0.53
1:F:223:PHE:HB3	1:F:226:GLN:HG3	1.90	0.53
1:B:41:GLN:HB3	1:B:49:VAL:HG23	1.89	0.53
1:B:106:LEU:HD11	1:B:156:TYR:CD2	2.44	0.53
1:B:284:THR:HG21	1:B:302:ASP:OD2	2.08	0.53
1:A:97:VAL:HB	1:A:154:PHE:CD2	2.44	0.53
1:B:146:TYR:HD2	1:B:157:ILE:HD11	1.74	0.53
1:B:454:SER:HA	1:B:461:LEU:HA	1.90	0.53
1:D:133:ASN:HD21	1:D:136:ASN:ND2	2.06	0.52
1:F:131:TRP:HB3	1:F:141:ARG:HG3	1.91	0.52
1:A:395:TYR:CE2	1:A:409:VAL:HG22	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:GLY:HA3	1:B:67:TYR:O	2.09	0.52
1:B:59:LYS:HZ3	1:B:63:TYR:H	1.57	0.52
1:D:234:ILE:HD11	1:D:286:ILE:O	2.08	0.52
1:A:80:VAL:HG11	1:A:127:MET:HE3	1.91	0.52
1:E:71:ARG:HH11	1:E:75:ASN:ND2	2.07	0.52
1:A:77:PHE:CD1	1:A:111:ILE:HB	2.45	0.52
1:B:403:TYR:HE1	1:B:442:LYS:HE2	1.74	0.52
1:C:235:LYS:HD2	1:C:240:TYR:CE2	2.44	0.52
1:F:93:TYR:CZ	1:F:95:GLY:HA2	2.44	0.52
1:A:118:TYR:CD1	1:A:125:PHE:CE1	2.96	0.52
1:C:63:TYR:CG	1:C:84:ARG:HD2	2.44	0.52
1:B:484:THR:HA	1:B:487:HIS:HD2	1.73	0.52
1:B:125:PHE:CZ	1:B:150:PRO:HG3	2.44	0.52
1:B:156:TYR:OH	1:B:159:SER:HB3	2.10	0.52
1:C:55:GLY:HA3	1:C:67:TYR:O	2.09	0.52
1:C:442:LYS:HE3	1:F:100:ARG:CZ	2.39	0.52
1:D:291:GLY:HA3	1:D:345:GLY:HA3	1.90	0.52
1:D:448:ASP:HB2	1:D:450:TYR:CE2	2.45	0.52
1:F:428:LEU:HD12	1:F:475:ILE:HG22	1.90	0.52
1:C:50:ILE:HG23	1:C:83:TYR:CE1	2.45	0.51
1:C:69:GLU:OE1	1:C:112:GLU:HA	2.10	0.51
1:F:41:GLN:HB3	1:F:49:VAL:HG13	1.91	0.51
1:A:379:ALA:HB3	1:A:430:GLN:HE21	1.75	0.51
1:B:363:ASN:ND2	1:B:467:TRP:HE3	2.09	0.51
1:B:41:GLN:HG3	1:B:316:GLN:HG2	1.93	0.51
1:B:321:PRO:HB3	1:B:347:ILE:HG22	1.92	0.51
1:B:363:ASN:HD22	1:B:467:TRP:HE3	1.58	0.51
1:C:290:GLN:HG3	1:C:295:THR:HG22	1.91	0.51
1:D:55:GLY:HA3	1:D:67:TYR:O	2.10	0.51
1:D:363:ASN:OD1	1:D:484:THR:HB	2.11	0.51
1:A:146:TYR:CD2	1:A:157:ILE:HD11	2.46	0.51
1:A:72:ASP:CG	1:A:73:ASP:H	2.13	0.51
1:C:-13:SER:HA	1:C:492:LEU:HD11	1.93	0.51
1:A:254:GLN:NE2	1:A:272:ASN:HB3	2.26	0.51
1:B:113:ARG:NH1	1:B:284:THR:HG22	2.26	0.51
1:D:77:PHE:CD1	1:D:111:ILE:HB	2.46	0.51
1:D:394:TRP:HH2	1:D:430:GLN:HE21	1.59	0.51
1:E:97:VAL:HB	1:E:154:PHE:CD2	2.46	0.51
1:C:454:SER:HB3	1:C:461:LEU:HD23	1.92	0.51
1:A:253:ASN:C	1:A:253:ASN:HD22	2.14	0.50
1:D:110:ASN:OD1	1:D:134:GLY:HA2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:478:TRP:CZ3	3:E:602:GOL:H31	2.46	0.50
1:B:356:ARG:HG2	1:B:393:GLN:OE1	2.11	0.50
1:C:399:VAL:HG12	1:C:399:VAL:O	2.11	0.50
1:E:331:GLU:HG2	1:E:333:PRO:HD3	1.94	0.50
1:A:109:CYS:HB2	1:A:132:GLU:O	2.10	0.50
1:C:130:HIS:CD2	1:C:179:ARG:HA	2.46	0.50
1:B:283:PRO:HB3	1:B:299:TYR:HE1	1.76	0.50
1:D:358:LYS:O	1:D:491:VAL:HB	2.11	0.50
1:D:381:ILE:HD11	1:D:430:GLN:NE2	2.27	0.50
1:D:157:ILE:HG22	1:D:158:ARG:HG2	1.93	0.50
1:C:77:PHE:CD1	1:C:111:ILE:HB	2.47	0.50
1:E:126:VAL:HG21	1:E:212:TYR:HB2	1.92	0.50
1:B:67:TYR:CE2	1:B:116:VAL:HG21	2.47	0.50
1:B:380:GLN:HE22	1:B:427:VAL:HG13	1.77	0.50
1:A:54:GLY:O	1:A:113:ARG:HA	2.12	0.49
1:B:157:ILE:N	1:B:157:ILE:HD12	2.27	0.49
1:A:369:ASP:OD1	1:A:370:VAL:N	2.44	0.49
1:B:33:GLU:HG2	1:B:35:VAL:HG12	1.95	0.49
1:B:381:ILE:HG12	1:B:429:ILE:HA	1.94	0.49
1:D:422:LYS:HA	1:D:458:CYS:HB3	1.95	0.49
1:A:125:PHE:HE2	1:A:150:PRO:HB3	1.78	0.49
1:A:256:LYS:HE2	1:A:272:ASN:HD21	1.76	0.49
1:D:234:ILE:HD11	1:D:286:ILE:C	2.33	0.49
1:C:129:MET:HG2	1:C:143:ALA:HB3	1.94	0.49
1:D:445:ASP:HA	1:D:451:TYR:HB3	1.93	0.49
1:E:236:ARG:HG2	1:E:237:ASN:OD1	2.13	0.49
1:B:200:ASN:O	1:B:227:GLN:HA	2.12	0.49
1:E:375:VAL:HG12	1:E:411:SER:HB3	1.95	0.49
1:A:245:SER:CB	1:A:283:PRO:HD2	2.40	0.49
1:C:223:PHE:HE2	1:C:242:LEU:HD23	1.77	0.49
1:D:361:ASN:HB3	1:D:364:SER:OG	2.13	0.49
1:D:442:LYS:HB3	1:D:454:SER:OG	2.12	0.49
1:A:55:GLY:HA3	1:A:67:TYR:O	2.13	0.49
1:D:465:ARG:O	1:D:466:LYS:HG2	2.11	0.49
1:E:131:TRP:CE3	1:E:141:ARG:HD2	2.48	0.49
1:A:196:ALA:HB1	1:A:200:ASN:HA	1.95	0.48
1:F:70:TYR:HD1	1:F:96:GLU:OE2	1.96	0.48
1:C:70:TYR:CE2	1:C:78:LEU:HD23	2.47	0.48
1:C:321:PRO:HB3	1:C:347:ILE:HG22	1.95	0.48
1:E:93:TYR:CZ	1:E:95:GLY:HA2	2.48	0.48
1:E:299:TYR:HB3	1:E:320:LEU:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:223:PHE:CE2	1:F:242:LEU:HD23	2.47	0.48
1:D:114:PRO:HB2	1:D:127:MET:HE3	1.94	0.48
1:D:338:VAL:O	1:D:340:ILE:HG23	2.13	0.48
1:E:260:SER:HB2	1:E:267:TRP:HA	1.96	0.48
1:F:55:GLY:HA3	1:F:67:TYR:O	2.13	0.48
1:F:430:GLN:O	1:F:430:GLN:HG3	2.14	0.48
1:A:110:ASN:OD1	1:A:134:GLY:HA2	2.14	0.48
1:A:156:TYR:OH	1:A:159:SER:HB3	2.13	0.48
1:A:424:ASP:O	1:C:136:ASN:HB2	2.14	0.48
1:E:450:TYR:CE1	1:E:489:LYS:HB2	2.49	0.48
1:F:135:ILE:HD12	1:F:135:ILE:N	2.29	0.48
1:A:284:THR:HG23	1:A:301:GLY:HA2	1.94	0.48
1:F:256:LYS:HD3	1:F:270:LEU:HB3	1.95	0.48
1:F:71:ARG:HD3	1:F:312:VAL:HG11	1.96	0.48
1:F:298:LEU:HD11	1:F:319:TRP:HB3	1.96	0.48
1:B:357:TYR:HB3	1:B:490:LEU:HD11	1.95	0.48
1:C:446:ILE:HG21	1:C:452:LYS:HG3	1.96	0.48
1:D:416:ASP:CG	1:D:439:GLN:HG3	2.34	0.48
1:A:53:HIS:HD2	1:A:312:VAL:HG12	1.79	0.48
1:C:40:THR:HB	1:F:92:GLU:OE2	2.14	0.47
1:C:378:ALA:HA	1:C:429:ILE:HD12	1.96	0.47
1:D:149:THR:HG23	1:D:150:PRO:HD2	1.96	0.47
1:D:364:SER:HB2	1:D:383:GLN:OE1	2.14	0.47
1:A:381:ILE:HD13	1:A:429:ILE:HA	1.94	0.47
1:B:286:ILE:HD13	1:B:322:LEU:HD22	1.95	0.47
1:D:131:TRP:CE3	1:D:141:ARG:HD2	2.49	0.47
1:A:360:VAL:CG2	1:A:489:LYS:HB3	2.43	0.47
1:B:109:CYS:HB2	1:B:132:GLU:O	2.15	0.47
1:E:305:ALA:HA	1:E:308:TRP:CZ2	2.49	0.47
1:F:206:TYR:HB3	1:F:215:ILE:HG23	1.96	0.47
1:C:80:VAL:HG21	1:C:127:MET:HE1	1.97	0.47
1:C:362:LYS:HE3	1:C:484:THR:HG22	1.96	0.47
1:D:147:SER:HB2	1:D:154:PHE:HA	1.96	0.47
1:F:147:SER:HB2	1:F:154:PHE:HA	1.96	0.47
1:A:71:ARG:HH11	1:A:312:VAL:HG11	1.79	0.47
1:D:363:ASN:HB2	1:D:485:ASN:HB3	1.96	0.47
1:D:437:TYR:HE1	1:D:457:HIS:CD2	2.33	0.47
1:A:53:HIS:HE2	1:A:313:ASN:HA	1.79	0.47
1:D:106:LEU:HA	1:D:109:CYS:SG	2.55	0.47
1:E:70:TYR:O	1:E:78:LEU:HB3	2.15	0.47
1:F:182:ASN:ND2	1:F:232:CYS:HA	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:LYS:HB2	1:B:350:TYR:HB2	1.97	0.47
1:C:71:ARG:NH1	1:C:312:VAL:HG11	2.30	0.47
1:A:413:ARG:HE	1:A:430:GLN:HG3	1.79	0.47
1:B:453:ILE:HD12	1:B:453:ILE:N	2.30	0.47
1:D:387:ASN:N	1:D:392:GLN:HE22	2.05	0.47
1:D:278:THR:HG22	1:D:278:THR:O	2.14	0.47
1:D:467:TRP:HA	1:D:485:ASN:HD21	1.78	0.47
1:F:363:ASN:HB2	1:F:484:THR:OG1	2.14	0.47
1:A:118:TYR:HD1	1:A:125:PHE:CE1	2.33	0.46
1:D:234:ILE:CG2	1:D:235:LYS:N	2.77	0.46
1:E:184:PHE:CG	1:E:233:LEU:HD22	2.50	0.46
1:C:31:ALA:O	1:C:32:ALA:C	2.54	0.46
1:D:234:ILE:HG22	1:D:235:LYS:N	2.31	0.46
1:D:321:PRO:HB3	1:D:347:ILE:CG2	2.45	0.46
1:D:77:PHE:HB2	1:D:111:ILE:H	1.80	0.46
1:A:131:TRP:CE3	1:A:141:ARG:HD2	2.51	0.46
1:C:354:THR:HG22	1:C:354:THR:O	2.16	0.46
1:E:70:TYR:HB3	1:E:79:GLY:O	2.16	0.46
1:C:80:VAL:HG21	1:C:127:MET:CE	2.45	0.46
1:A:169:MET:HE2	1:A:174:PRO:HA	1.97	0.46
1:B:335:TYR:HB2	1:B:338:VAL:HG22	1.98	0.46
1:F:70:TYR:CD1	1:F:96:GLU:OE2	2.69	0.46
1:F:72:ASP:HB3	1:F:78:LEU:HD11	1.97	0.46
1:A:254:GLN:OE1	1:A:276:SER:HA	2.16	0.46
1:A:286:ILE:HD13	1:A:322:LEU:HD22	1.98	0.46
1:B:384:TRP:CZ3	1:B:471:ASP:HB3	2.51	0.46
1:C:106:LEU:HA	1:C:109:CYS:SG	2.56	0.46
1:C:192:TYR:HB3	1:C:205:LEU:HD11	1.98	0.46
1:D:80:VAL:HG21	1:D:127:MET:HE1	1.98	0.46
1:D:97:VAL:HB	1:D:154:PHE:CD2	2.50	0.46
1:D:390:LEU:O	1:D:410:LYS:HB2	2.16	0.46
1:B:226:GLN:HB3	1:B:228:ARG:HG2	1.98	0.45
1:F:64:TYR:CG	1:F:88:LEU:HD21	2.51	0.45
1:A:58:LEU:HD13	1:A:59:LYS:N	2.32	0.45
1:B:192:TYR:HB3	1:B:205:LEU:HD11	1.98	0.45
1:C:77:PHE:HB2	1:C:111:ILE:H	1.81	0.45
1:E:57:MET:CE	1:E:287:ILE:HG21	2.46	0.45
1:E:122:THR:OG1	1:E:124:GLU:HG2	2.15	0.45
1:F:461:LEU:CD1	1:F:486:GLN:HB3	2.43	0.45
1:E:34:GLY:HA2	1:E:89:VAL:HG21	1.97	0.45
1:E:325:ILE:HD11	1:E:331:GLU:OE2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:351:ILE:N	1:E:351:ILE:HD12	2.32	0.45
1:E:381:ILE:HG12	1:E:429:ILE:HA	1.97	0.45
1:F:413:ARG:HB2	1:F:430:GLN:HB2	1.99	0.45
1:A:97:VAL:HB	1:A:154:PHE:HD2	1.81	0.45
1:C:77:PHE:CZ	1:C:111:ILE:HD12	2.51	0.45
1:D:434:ASN:HD21	2:D:601:IPT:H3	1.81	0.45
1:D:437:TYR:HE1	1:D:457:HIS:CG	2.35	0.45
1:E:55:GLY:HA3	1:E:67:TYR:O	2.16	0.45
1:B:288:PRO:HG3	1:B:297:TYR:CE1	2.52	0.45
1:B:403:TYR:CE1	1:B:442:LYS:HG2	2.52	0.45
1:F:492:LEU:N	1:F:492:LEU:HD12	2.32	0.45
1:A:72:ASP:CB	1:A:78:LEU:HD12	2.47	0.45
1:A:170:ASP:OD1	1:A:177:MET:HG3	2.16	0.45
1:A:194:ILE:HD12	1:A:204:HIS:O	2.17	0.45
1:C:-13:SER:HA	1:C:492:LEU:CD1	2.47	0.45
1:D:161:ARG:O	1:D:164:GLN:HB3	2.16	0.45
1:B:119:ASN:HB2	1:B:212:TYR:CD2	2.52	0.45
1:B:145:ALA:HA	1:B:157:ILE:CD1	2.47	0.45
1:B:359:LEU:HD12	1:B:368:LEU:HD22	1.98	0.45
1:C:126:VAL:HG21	1:C:212:TYR:HB2	1.98	0.45
1:D:87:ASP:O	1:D:88:LEU:HB2	2.16	0.45
1:E:252:PRO:HB2	1:E:277:THR:CG2	2.47	0.45
1:A:163:MET:SD	1:B:165:ASP:HB2	2.57	0.44
1:A:240:TYR:O	1:A:259:TYR:HA	2.16	0.44
1:D:376:ASP:C	1:D:413:ARG:HH12	2.21	0.44
1:B:257:TYR:CE2	1:B:330:LEU:HD13	2.52	0.44
1:B:463:ASP:OD1	3:B:602:GOL:H11	2.18	0.44
1:D:299:TYR:HB3	1:D:320:LEU:O	2.18	0.44
1:D:428:LEU:HD22	1:D:475:ILE:HG22	1.99	0.44
1:E:277:THR:HG22	1:E:277:THR:O	2.17	0.44
1:C:57:MET:HE2	1:C:287:ILE:HG21	2.00	0.44
1:D:243:ILE:N	1:D:243:ILE:HD12	2.32	0.44
1:E:62:ASP:O	1:E:86:LYS:HG2	2.17	0.44
1:E:474:ILE:HD12	1:E:474:ILE:N	2.31	0.44
1:B:209:THR:OG1	1:B:210:PRO:HD2	2.17	0.44
1:B:218:LEU:O	1:B:218:LEU:HD12	2.17	0.44
1:B:230:ALA:CB	1:B:283:PRO:HG2	2.48	0.44
1:D:358:LYS:HG3	1:D:392:GLN:HB3	2.00	0.44
1:E:129:MET:CG	1:E:143:ALA:HB3	2.47	0.44
1:A:279:TYR:CE2	1:A:334:TYR:HB2	2.52	0.44
1:B:484:THR:HA	1:B:487:HIS:CD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:168:VAL:HG21	1:D:176:TYR:CE1	2.52	0.44
1:D:321:PRO:HB3	1:D:347:ILE:HG22	1.99	0.44
1:D:367:VAL:HG12	1:D:368:LEU:N	2.32	0.44
1:F:381:ILE:HG12	1:F:429:ILE:HA	1.98	0.44
1:C:129:MET:CG	1:C:143:ALA:HB3	2.48	0.44
1:D:263:LEU:HD12	1:D:263:LEU:H	1.83	0.44
1:E:59:LYS:HD3	1:E:64:TYR:CE1	2.52	0.44
1:B:129:MET:CG	1:B:143:ALA:HB3	2.48	0.44
1:B:278:THR:HG22	1:B:278:THR:O	2.18	0.44
1:D:111:ILE:HD11	1:D:131:TRP:HD1	1.81	0.44
1:A:57:MET:HA	1:A:65:TYR:O	2.18	0.44
1:A:125:PHE:HD2	1:A:150:PRO:HA	1.83	0.44
1:C:245:SER:HB3	1:C:283:PRO:HD2	2.00	0.44
1:C:399:VAL:HG11	1:C:440:HIS:CE1	2.53	0.44
1:D:297:TYR:CD2	1:D:324:PHE:CE2	3.06	0.44
1:E:109:CYS:HB2	1:E:132:GLU:O	2.17	0.44
1:A:129:MET:CG	1:A:143:ALA:HB3	2.47	0.43
1:B:209:THR:HG23	1:B:211:ASP:OD1	2.18	0.43
1:B:419:ASP:HA	2:B:601:IPT:S1	2.57	0.43
1:C:42:PHE:CE2	1:C:50:ILE:HD12	2.53	0.43
1:C:126:VAL:HG11	1:C:212:TYR:O	2.18	0.43
1:D:451:TYR:OH	1:D:490:LEU:HD13	2.18	0.43
1:B:115:LYS:HG3	1:B:182:ASN:HA	2.00	0.43
1:D:288:PRO:HG3	1:D:297:TYR:CE1	2.52	0.43
1:D:359:LEU:O	1:D:367:VAL:HG13	2.18	0.43
1:E:362:LYS:HG2	1:E:484:THR:HB	1.99	0.43
1:E:452:LYS:HG2	1:E:461:LEU:HD22	2.00	0.43
1:F:70:TYR:O	1:F:78:LEU:HB2	2.18	0.43
1:A:279:TYR:CD2	1:A:334:TYR:HB2	2.52	0.43
1:C:223:PHE:CE2	1:C:242:LEU:HD23	2.52	0.43
1:F:288:PRO:HB3	1:F:297:TYR:CE1	2.54	0.43
1:B:131:TRP:CE3	1:B:141:ARG:HD2	2.54	0.43
1:C:135:ILE:HG13	1:C:136:ASN:ND2	2.34	0.43
1:A:252:PRO:HB2	1:A:277:THR:HB	2.01	0.43
1:C:286:ILE:HD13	1:C:322:LEU:HD22	2.00	0.43
1:C:399:VAL:HG21	1:C:405:LYS:HB2	2.00	0.43
1:D:83:TYR:HB3	1:D:91:TRP:HB3	2.00	0.43
1:B:321:PRO:HB3	1:B:347:ILE:CG2	2.48	0.43
1:C:58:LEU:HD22	1:C:116:VAL:HG12	2.00	0.43
1:C:287:ILE:HA	1:C:288:PRO:HD3	1.88	0.43
1:D:340:ILE:CG2	1:D:347:ILE:HG23	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:110:ASN:HB3	1:E:132:GLU:HB2	2.01	0.43
1:E:395:TYR:CE2	1:E:409:VAL:HG22	2.54	0.43
1:A:50:ILE:HG23	1:A:83:TYR:CE1	2.53	0.43
1:C:63:TYR:CE1	1:C:84:ARG:NH1	2.86	0.43
1:D:122:THR:OG1	1:D:124:GLU:HG2	2.17	0.43
1:D:369:ASP:OD1	1:D:391:SER:HB2	2.19	0.43
1:E:197:ALA:HB3	1:E:204:HIS:CE1	2.54	0.43
1:D:415:LEU:HD21	1:D:428:LEU:HD21	2.00	0.43
1:A:67:TYR:HE1	1:A:82:CYS:SG	2.41	0.43
1:B:240:TYR:CZ	1:B:263:LEU:HD11	2.54	0.43
1:D:256:LYS:HD3	1:D:270:LEU:HB3	2.00	0.43
1:E:147:SER:HB2	1:E:154:PHE:HA	2.01	0.43
1:F:146:TYR:HD2	1:F:157:ILE:HD11	1.84	0.43
1:A:125:PHE:CE2	1:A:150:PRO:HB3	2.54	0.42
1:C:466:LYS:H	3:C:602:GOL:C1	2.32	0.42
1:D:40:THR:HG22	1:D:41:GLN:N	2.34	0.42
1:D:50:ILE:HG23	1:D:83:TYR:CE1	2.54	0.42
1:D:354:THR:HG22	1:D:354:THR:O	2.19	0.42
1:D:413:ARG:HG2	1:D:432:THR:HA	2.00	0.42
1:A:370:VAL:HG11	1:A:430:GLN:NE2	2.34	0.42
1:B:335:TYR:CD2	1:B:349:GLU:HB2	2.54	0.42
1:B:375:VAL:HG12	1:B:411:SER:HB3	2.00	0.42
1:B:425:GLY:HA2	1:B:476:GLN:OE1	2.19	0.42
1:C:285:PHE:HE2	1:C:287:ILE:HB	1.85	0.42
1:E:144:VAL:HG22	1:E:157:ILE:HD12	2.02	0.42
1:A:122:THR:OG1	1:A:124:GLU:HG2	2.19	0.42
1:B:358:LYS:HE2	1:B:392:GLN:HB2	2.01	0.42
1:A:215:ILE:HD12	1:A:215:ILE:N	2.35	0.42
1:E:227:GLN:OE1	1:E:247:CYS:HB3	2.19	0.42
1:B:492:LEU:HD12	1:B:492:LEU:N	2.34	0.42
1:D:130:HIS:NE2	1:D:179:ARG:HA	2.35	0.42
1:D:441:TRP:HB3	1:D:453:ILE:HG22	2.01	0.42
1:E:209:THR:HB	1:E:210:PRO:HD2	2.02	0.42
1:E:430:GLN:O	1:E:430:GLN:HG3	2.19	0.42
1:F:77:PHE:CZ	1:F:79:GLY:HA2	2.55	0.42
1:C:305:ALA:HA	1:C:308:TRP:CZ2	2.54	0.42
1:D:72:ASP:CG	1:D:73:ASP:N	2.71	0.42
1:E:381:ILE:HG13	1:E:415:LEU:CD1	2.50	0.42
1:F:209:THR:HB	1:F:210:PRO:HD2	2.02	0.42
1:F:466:LYS:H	3:F:603:GOL:C3	2.33	0.42
1:B:77:PHE:CE2	1:B:111:ILE:HD12	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:182:ASN:HD22	1:B:232:CYS:HA	1.85	0.42
1:C:57:MET:CE	1:C:287:ILE:HG21	2.50	0.42
1:D:370:VAL:CG2	1:D:373:GLY:HA2	2.50	0.42
1:D:441:TRP:HB3	1:D:453:ILE:CG2	2.50	0.42
1:E:254:GLN:OE1	1:E:276:SER:HA	2.19	0.42
1:E:362:LYS:HB2	1:E:450:TYR:CE1	2.55	0.42
1:E:461:LEU:O	1:E:477:GLN:HA	2.20	0.42
1:F:378:ALA:HA	1:F:429:ILE:HD12	2.01	0.42
1:F:97:VAL:HB	1:F:154:PHE:HD2	1.80	0.41
1:A:41:GLN:HG3	1:A:316:GLN:HG2	2.02	0.41
1:A:186:ASP:HB3	1:A:188:ASP:OD1	2.20	0.41
1:A:243:ILE:N	1:A:243:ILE:HD12	2.36	0.41
1:B:236:ARG:HB2	1:B:297:TYR:OH	2.20	0.41
1:E:57:MET:HE2	1:E:287:ILE:HG21	2.00	0.41
1:B:162:PRO:HD2	1:B:176:TYR:O	2.20	0.41
1:B:194:ILE:HG23	1:B:231:PRO:HB2	2.02	0.41
1:C:52:ALA:HB1	1:C:68:GLY:HA3	2.01	0.41
1:D:85:SER:HB2	1:D:91:TRP:HA	2.02	0.41
1:D:394:TRP:CZ3	1:D:408:ASN:HB3	2.55	0.41
1:F:36:ILE:HD11	1:F:89:VAL:HG22	2.01	0.41
1:B:126:VAL:HG21	1:B:212:TYR:HB2	2.02	0.41
1:C:243:ILE:N	1:C:243:ILE:HD12	2.35	0.41
1:C:362:LYS:HB2	1:C:450:TYR:CE1	2.55	0.41
1:F:424:ASP:HB3	1:F:478:TRP:CE3	2.55	0.41
1:E:50:ILE:HG23	1:E:83:TYR:CE1	2.56	0.41
1:A:170:ASP:O	1:A:171:HIS:HB2	2.20	0.41
1:D:279:TYR:CD2	1:D:334:TYR:HB2	2.56	0.41
1:E:197:ALA:HB3	1:E:204:HIS:ND1	2.35	0.41
1:E:492:LEU:HD12	1:E:492:LEU:N	2.35	0.41
1:B:305:ALA:HA	1:B:308:TRP:CH2	2.56	0.41
1:C:384:TRP:CZ3	1:C:471:ASP:HB3	2.55	0.41
1:F:57:MET:HE1	1:F:287:ILE:HG21	2.02	0.41
1:B:119:ASN:HB3	1:B:122:THR:CG2	2.51	0.41
1:C:42:PHE:HD2	1:C:50:ILE:HD12	1.83	0.41
1:D:290:GLN:OE1	1:D:295:THR:HB	2.21	0.41
1:E:104:PRO:HA	1:E:107:ASN:OD1	2.21	0.41
1:E:298:LEU:HB2	1:E:347:ILE:CD1	2.51	0.41
1:E:437:TYR:CG	1:E:456:ARG:HD3	2.56	0.41
1:A:403:TYR:CD1	1:A:442:LYS:HB2	2.56	0.41
1:B:419:ASP:OD1	2:B:601:IPT:H3'2	2.21	0.41
1:B:454:SER:HB2	1:B:459:GLY:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:-13:SER:OG	1:C:490:LEU:HB3	2.20	0.41
1:D:366:LYS:HB3	1:D:384:TRP:C	2.41	0.41
1:E:243:ILE:HD12	1:E:243:ILE:N	2.36	0.41
1:A:125:PHE:O	1:A:146:TYR:HA	2.21	0.40
1:A:236:ARG:HG3	1:A:297:TYR:CZ	2.56	0.40
1:B:209:THR:HG22	1:B:214:ASN:O	2.22	0.40
1:B:359:LEU:O	1:B:367:VAL:HA	2.20	0.40
1:C:186:ASP:HB3	1:C:188:ASP:OD1	2.21	0.40
1:C:357:TYR:CD1	1:C:490:LEU:HG	2.56	0.40
1:C:399:VAL:HG11	1:C:440:HIS:NE2	2.36	0.40
1:D:467:TRP:CH2	1:D:483:GLY:HA2	2.56	0.40
1:B:385:THR:HG23	1:B:471:ASP:OD1	2.21	0.40
1:C:450:TYR:CE1	1:C:489:LYS:HB2	2.57	0.40
1:A:130:HIS:NE2	1:A:179:ARG:HA	2.36	0.40
1:C:223:PHE:HB3	1:C:226:GLN:HG3	2.03	0.40
1:E:288:PRO:HB3	1:E:297:TYR:CE1	2.57	0.40
1:A:84:ARG:NE	1:A:94:ARG:HD3	2.36	0.40
1:C:64:TYR:CG	1:C:88:LEU:HD21	2.56	0.40
1:C:425:GLY:HA2	1:C:476:GLN:CD	2.42	0.40
1:D:360:VAL:HG22	1:D:361:ASN:N	2.37	0.40
1:E:311:LYS:HG2	1:E:314:ASP:OD2	2.21	0.40
1:F:70:TYR:HB3	1:F:79:GLY:O	2.22	0.40
1:F:398:ASP:HA	1:F:404:LYS:HG2	2.04	0.40
1:F:452:LYS:HB2	1:F:461:LEU:HD22	2.04	0.40
1:B:119:ASN:HB2	1:B:212:TYR:CE2	2.57	0.40
1:B:156:TYR:HH	1:B:159:SER:HB3	1.87	0.40
1:B:287:ILE:HA	1:B:288:PRO:HD3	1.91	0.40
1:C:446:ILE:HG12	1:C:450:TYR:O	2.21	0.40
1:F:57:MET:CE	1:F:287:ILE:HG21	2.51	0.40
1:F:243:ILE:HD12	1:F:243:ILE:N	2.37	0.40
1:F:460:LYS:HB2	1:F:477:GLN:HG2	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	459/526 (87%)	431 (94%)	28 (6%)	0	100	100
1	B	459/526 (87%)	424 (92%)	34 (7%)	1 (0%)	47	82
1	C	480/526 (91%)	453 (94%)	26 (5%)	1 (0%)	47	82
1	D	459/526 (87%)	423 (92%)	35 (8%)	1 (0%)	47	82
1	E	459/526 (87%)	439 (96%)	20 (4%)	0	100	100
1	F	459/526 (87%)	439 (96%)	19 (4%)	1 (0%)	47	82
All	All	2775/3156 (88%)	2609 (94%)	162 (6%)	4 (0%)	51	85

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	32	ALA
1	D	35	VAL
1	F	386	ASP
1	B	231	PRO

### 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	389/442 (88%)	387 (100%)	2 (0%)	88	96
1	B	389/442 (88%)	387 (100%)	2 (0%)	88	96
1	C	402/442 (91%)	402 (100%)	0	100	100
1	D	389/442 (88%)	388 (100%)	1 (0%)	92	97
1	E	389/442 (88%)	389 (100%)	0	100	100
1	F	389/442 (88%)	388 (100%)	1 (0%)	92	97
All	All	2347/2652 (88%)	2341 (100%)	6 (0%)	92	97

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	ARG
1	A	253	ASN
1	B	180	ASP
1	B	209	THR
1	D	470	GLU
1	F	457	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	253	ASN
1	A	272	ASN
1	A	430	GLN
1	B	53	HIS
1	B	171	HIS
1	B	272	ASN
1	B	430	GLN
1	B	487	HIS
1	C	200	ASN
1	D	38	ASN
1	D	119	ASN
1	D	136	ASN
1	D	164	GLN
1	D	392	GLN
1	D	430	GLN
1	D	457	HIS
1	D	477	GLN
1	E	108	HIS
1	E	171	HIS
1	F	171	HIS
1	F	269	GLN
1	F	476	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](#)

14 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	IPT	B	601	-	14,15,15	0.49	0	18,21,21	1.22	2 (11%)
3	GOL	C	603	-	5,5,5	0.36	0	5,5,5	0.25	0
2	IPT	F	601	-	14,15,15	0.50	0	18,21,21	1.25	2 (11%)
3	GOL	E	603	-	5,5,5	0.37	0	5,5,5	0.27	0
2	IPT	A	601	-	14,15,15	0.49	0	18,21,21	1.13	1 (5%)
3	GOL	A	602	-	5,5,5	0.36	0	5,5,5	0.28	0
3	GOL	E	602	-	5,5,5	0.38	0	5,5,5	0.26	0
2	IPT	D	601	-	14,15,15	0.50	0	18,21,21	1.26	2 (11%)
2	IPT	F	602	-	14,15,15	0.54	0	18,21,21	1.58	4 (22%)
2	IPT	E	601	-	14,15,15	0.52	0	18,21,21	1.47	3 (16%)
3	GOL	F	603	-	5,5,5	0.36	0	5,5,5	0.29	0
2	IPT	C	601	-	14,15,15	0.51	0	18,21,21	1.33	3 (16%)
3	GOL	B	602	-	5,5,5	0.36	0	5,5,5	0.30	0
3	GOL	C	602	-	5,5,5	0.36	0	5,5,5	0.31	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IPT	B	601	-	-	1/6/26/26	0/1/1/1
3	GOL	C	603	-	-	2/4/4/4	-
2	IPT	F	601	-	-	1/6/26/26	0/1/1/1
3	GOL	E	603	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	IPT	A	601	-	-	0/6/26/26	0/1/1/1
3	GOL	A	602	-	-	2/4/4/4	-
3	GOL	E	602	-	-	2/4/4/4	-
2	IPT	D	601	-	-	0/6/26/26	0/1/1/1
2	IPT	F	602	-	-	1/6/26/26	0/1/1/1
2	IPT	E	601	-	-	2/6/26/26	0/1/1/1
3	GOL	F	603	-	-	4/4/4/4	-
2	IPT	C	601	-	-	1/6/26/26	0/1/1/1
3	GOL	B	602	-	-	2/4/4/4	-
3	GOL	C	602	-	-	2/4/4/4	-

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	602	IPT	C1-O5-C5	3.60	119.22	112.58
2	E	601	IPT	O5-C1-C2	3.44	114.64	110.31
2	F	602	IPT	C1-S1-C1'	3.36	110.55	100.26
2	C	601	IPT	C1-S1-C1'	3.24	110.19	100.26
2	B	601	IPT	C1-S1-C1'	3.24	110.17	100.26
2	D	601	IPT	C1-S1-C1'	3.20	110.05	100.26
2	E	601	IPT	C1-S1-C1'	3.19	110.02	100.26
2	F	601	IPT	C1-S1-C1'	3.06	109.64	100.26
2	A	601	IPT	C1-S1-C1'	3.06	109.63	100.26
2	F	602	IPT	O5-C1-C2	2.80	113.84	110.31
2	C	601	IPT	C1-O5-C5	2.57	117.32	112.58
2	E	601	IPT	C1-O5-C5	2.49	117.17	112.58
2	B	601	IPT	C1-O5-C5	2.38	116.97	112.58
2	F	601	IPT	C1-O5-C5	2.38	116.97	112.58
2	D	601	IPT	C1-O5-C5	2.37	116.95	112.58
2	C	601	IPT	O5-C1-C2	2.13	113.00	110.31
2	F	602	IPT	O5-C5-C4	2.08	113.47	109.69

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	601	IPT	C3'-C1'-S1-C1
2	F	601	IPT	C3'-C1'-S1-C1
2	F	602	IPT	C3'-C1'-S1-C1

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Mol	Chain	Res	Type	Atoms
3	B	602	GOL	O1-C1-C2-C3
3	C	603	GOL	O1-C1-C2-C3
3	E	602	GOL	O1-C1-C2-C3
3	E	603	GOL	O1-C1-C2-C3
3	F	603	GOL	O1-C1-C2-C3
3	A	602	GOL	O1-C1-C2-C3
3	C	602	GOL	O1-C1-C2-C3
3	F	603	GOL	C1-C2-C3-O3
3	A	602	GOL	O1-C1-C2-O2
3	B	602	GOL	O1-C1-C2-O2
3	C	603	GOL	O1-C1-C2-O2
3	F	603	GOL	O1-C1-C2-O2
3	C	602	GOL	O1-C1-C2-O2
3	E	602	GOL	O1-C1-C2-O2
3	E	603	GOL	O1-C1-C2-O2
3	F	603	GOL	O2-C2-C3-O3
2	E	601	IPT	C4-C5-C6-O6
2	E	601	IPT	O5-C5-C6-O6
2	B	601	IPT	C3'-C1'-S1-C1

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	IPT	2	0
3	E	602	GOL	1	0
2	D	601	IPT	2	0
3	F	603	GOL	1	0
3	B	602	GOL	1	0
3	C	602	GOL	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	461/526 (87%)	-0.04	1 (0%) 95 87	55, 84, 107, 140	0
1	B	461/526 (87%)	0.08	7 (1%) 73 46	64, 94, 120, 138	0
1	C	482/526 (91%)	-0.21	1 (0%) 95 87	45, 62, 84, 132	0
1	D	461/526 (87%)	0.71	84 (18%) 1 0	54, 97, 178, 183	0
1	E	461/526 (87%)	-0.11	0 100 100	50, 72, 91, 115	0
1	F	461/526 (87%)	-0.16	0 100 100	43, 67, 89, 113	0
All	All	2787/3156 (88%)	0.04	93 (3%) 46 20	43, 78, 135, 183	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	430	GLN	6.7
1	D	383	GLN	6.5
1	D	380	GLN	6.3
1	D	490	LEU	6.0
1	D	374	SER	5.5
1	D	491	VAL	5.4
1	D	427	VAL	5.0
1	D	473	GLY	4.9
1	D	414	ALA	4.7
1	D	367	VAL	4.6
1	D	471	ASP	4.5
1	D	474	ILE	4.5
1	D	480	ASP	4.4
1	D	446	ILE	4.3
1	D	375	VAL	4.3
1	D	382	VAL	4.3
1	D	396	LEU	4.2
1	D	492	LEU	4.2
1	D	444	THR	4.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	459	GLY	4.2
1	D	423	GLU	4.1
1	D	452	LYS	4.1
1	D	484	THR	4.1
1	D	390	LEU	3.8
1	D	387	ASN	3.8
1	D	451	TYR	3.8
1	D	493	VAL	3.8
1	D	384	TRP	3.5
1	D	448	ASP	3.4
1	D	487	HIS	3.3
1	D	450	TYR	3.3
1	D	467	TRP	3.3
1	D	358	LYS	3.3
1	D	470	GLU	3.3
1	D	479	SER	3.2
1	D	458	CYS	3.2
1	D	378	ALA	3.2
1	D	394	TRP	3.0
1	D	478	TRP	3.0
1	D	364	SER	3.0
1	D	482	GLY	3.0
1	D	457	HIS	2.9
1	D	472	GLY	2.9
1	D	426	GLY	2.9
1	D	381	ILE	2.9
1	B	63	TYR	2.9
1	D	429	ILE	2.9
1	D	424	ASP	2.9
1	D	365	GLY	2.9
1	D	422	LYS	2.8
1	D	376	ASP	2.8
1	D	462	ILE	2.8
1	D	360	VAL	2.8
1	D	481	ALA	2.7
1	D	371	LEU	2.7
1	D	392	GLN	2.7
1	D	431	TYR	2.6
1	D	466	LYS	2.6
1	D	437	TYR	2.6
1	D	469	THR	2.6
1	D	356	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	366	LYS	2.6
1	B	393	GLN	2.5
1	D	33	GLU	2.5
1	D	401	GLY	2.5
1	D	445	ASP	2.5
1	D	363	ASN	2.4
1	D	370	VAL	2.4
1	D	359	LEU	2.4
1	D	407	VAL	2.4
1	D	372	ASP	2.4
1	D	461	LEU	2.4
1	D	428	LEU	2.4
1	D	357	TYR	2.3
1	D	72	ASP	2.3
1	D	419	ASP	2.2
1	D	368	LEU	2.2
1	A	86	LYS	2.2
1	D	447	GLY	2.2
1	B	387	ASN	2.2
1	B	390	LEU	2.2
1	B	78	LEU	2.1
1	B	150	PRO	2.1
1	D	405	LYS	2.1
1	D	463	ASP	2.1
1	D	449	GLY	2.1
1	B	374	SER	2.1
1	D	455	SER	2.1
1	D	362	LYS	2.1
1	D	486	GLN	2.1
1	D	400	GLY	2.0
1	D	408	ASN	2.0
1	C	-18	GLY	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<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	IPT	F	602	15/15	0.74	0.42	81,98,118,123	0
3	GOL	C	603	6/6	0.76	0.31	57,69,71,73	0
2	IPT	D	601	15/15	0.78	0.40	121,133,141,143	0
3	GOL	E	603	6/6	0.83	0.22	71,73,78,80	0
3	GOL	B	602	6/6	0.86	0.32	74,77,79,79	0
3	GOL	A	602	6/6	0.89	0.29	58,63,71,81	0
3	GOL	C	602	6/6	0.91	0.33	62,66,74,77	0
3	GOL	E	602	6/6	0.92	0.34	66,75,77,80	0
2	IPT	B	601	15/15	0.92	0.19	75,81,88,100	0
2	IPT	C	601	15/15	0.94	0.22	57,64,80,90	0
2	IPT	E	601	15/15	0.95	0.17	63,74,82,88	0
2	IPT	F	601	15/15	0.96	0.27	61,66,73,81	0
2	IPT	A	601	15/15	0.96	0.26	62,68,85,86	0
3	GOL	F	603	6/6	0.96	0.36	66,71,77,78	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.