



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 01:21 PM GMT

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 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 <http://wwpdb.org/ValidationPDFNotes.html>

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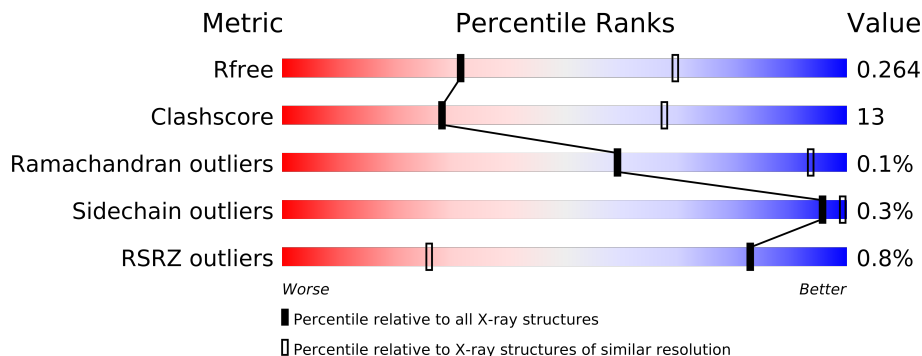
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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))
$R_{free}$	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

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

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

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

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Mol	Type	Chain	Res	Geometry	Electron density
3	GOL	C	602	-	X
3	GOL	C	603	-	X
3	GOL	E	602	-	X
3	GOL	F	603	-	X

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22274 atoms, of which 0 are hydrogen and 0 are deuterium.

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
1	A	461	Total	C	N	O	S	0	0	0
			3664	2323	623	703	15			
1	B	461	Total	C	N	O	S	0	0	0
			3664	2323	623	703	15			
1	C	482	Total	C	N	O	S	0	0	0
			3807	2406	651	732	18			
1	D	461	Total	C	N	O	S	0	0	0
			3664	2323	623	703	15			
1	E	461	Total	C	N	O	S	0	0	0
			3664	2323	623	703	15			
1	F	461	Total	C	N	O	S	0	0	0
			3664	2323	623	703	15			

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

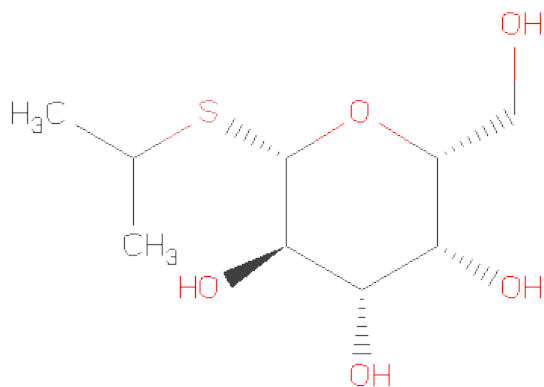
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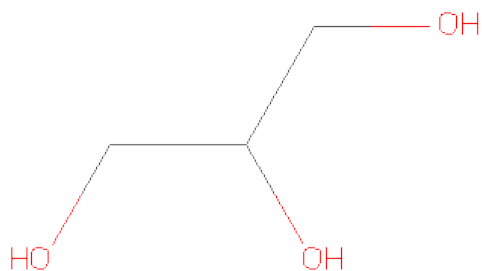
Chain	Residue	Modelled	Actual	Comment	Reference
F	-30	HIS	-	EXPRESSION TAG	UNP A3DD67
F	-29	HIS	-	EXPRESSION TAG	UNP A3DD67
F	-28	HIS	-	EXPRESSION TAG	UNP A3DD67
F	-27	HIS	-	EXPRESSION TAG	UNP A3DD67
F	-26	HIS	-	EXPRESSION TAG	UNP A3DD67
F	-25	SER	-	EXPRESSION TAG	UNP A3DD67
F	-24	SER	-	EXPRESSION TAG	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 ISOPROPYL-1-BETA-D-THIOGALACTOSIDE (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		

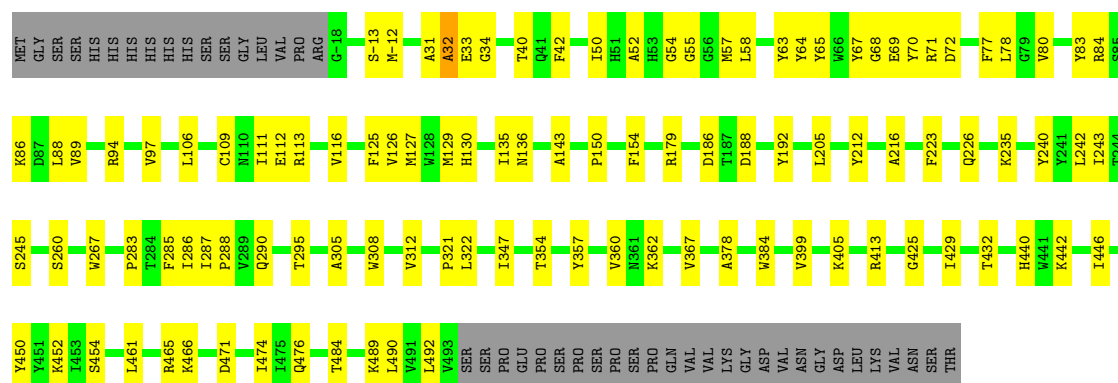
- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

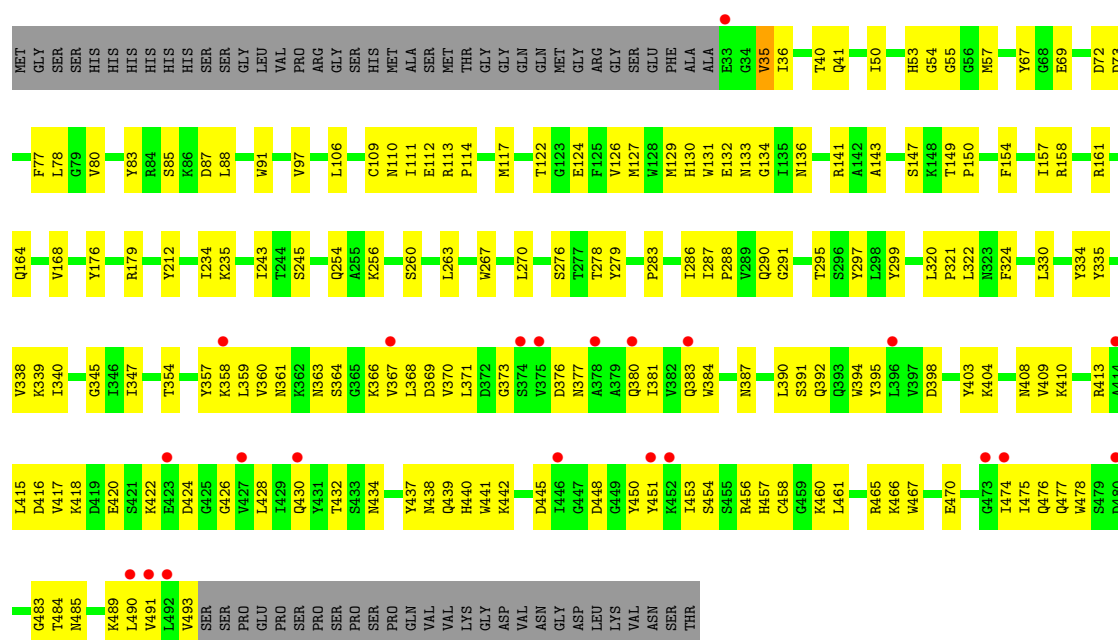


## Chain C:



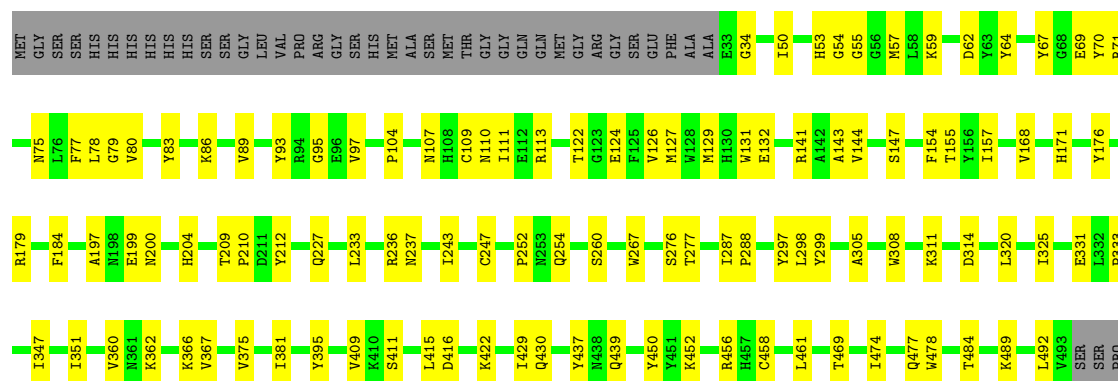
- Molecule 1: Ricin B lectin

## Chain D:



- Molecule 1: Ricin B lectin

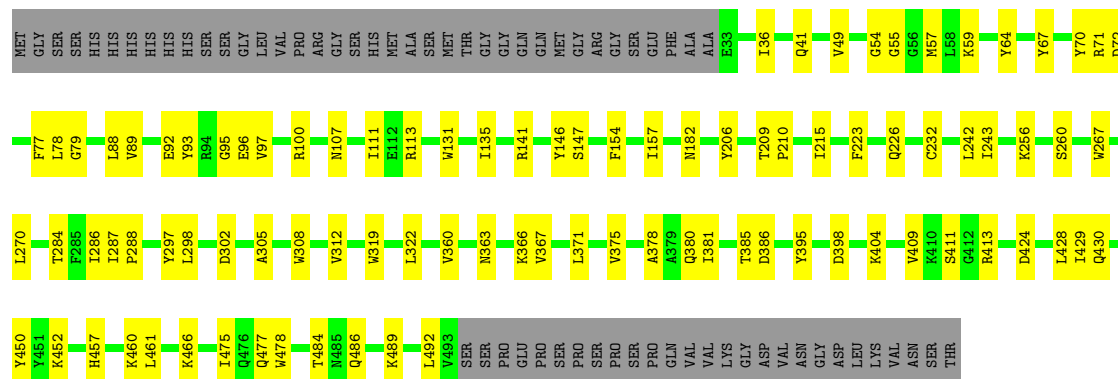
Chain E:



GLU PRO SER PRO SER PRO SER PRO GLN VAL VAL LYS GLY ASP VAL ASN GLY ASP LEU LYS VAL ASN SER THR

- Molecule 1: Ricin B lectin

Chain F: 



## 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)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.245 , 0.271 0.236 , 0.264	Depositor DCC
$R_{free}$ test set	1581 reflections (1.78%)	DCC
Wilson B-factor (Å <sup>2</sup> )	66.5	Xtriage
Anisotropy	0.601	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 33.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 88879 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	22274	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	82.0	wwPDB-VP

Xtriage'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.

## 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 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	15	0	18	0	0
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

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

All (546) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(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
1:F:371:LEU:HD12	1:F:380:GLN:HB3	1.72	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:E:54:GLY:O	1:E:113:ARG:HA	1.95	0.67
1:D:403:TYR:HB3	1:D:440:HIS:HB3	1.75	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:F:182:ASN:HD22	1:F:232:CYS:HA	1.61	0.66
1:B:364:SER:HA	1:B:469:THR:HG23	1.77	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:E:416:ASP:CB	1:E:439:GLN:HG2	2.27	0.64
1:B:378:ALA:HA	1:B:429:ILE:HD12	1.78	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
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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:358:LYS:HE3	1:D:493:VAL:HG21	1.81	0.62
1:B:122:THR:HG23	1:B:124:GLU:H	1.65	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:223:PHE:HE2	1:B:242:LEU:HD23	1.63	0.61
1:B:97:VAL:HB	1:B:154:PHE:CD2	2.35	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:D:321:PRO:HD3	1:D:338:VAL:HG11	1.82	0.60
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:F:450:TYR:CE1	1:F:489:LYS:HB2	2.37	0.60
1:D:245:SER:HB3	1:D:283:PRO:HD2	1.82	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:370:VAL:HG22	1:D:391:SER:HB3	1.83	0.60
1:D:72:ASP:CG	1:D:73:ASP:H	2.05	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:D:426:GLY:O	1:D:476:GLN:HB2	2.03	0.58
1:A:84:ARG:HD3	1:A:94:ARG:HH11	1.66	0.58
1:F:286:ILE:HD13	1:F:322:LEU:HD22	1.83	0.58
1:F:57:MET:HE2	1:F:287:ILE:HD13	1.85	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:F:375:VAL:HG12	1:F:411:SER:HB3	1.85	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:284:THR:HG21	1:F:302:ASP:OD2	2.03	0.58
1:B:171:HIS:CE1	1:B:199:GLU:HB2	2.39	0.58
1:D:408:ASN:HD22	1:D:430:GLN:NE2	2.01	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:467:TRP:HA	1:D:485:ASN:ND2	2.19	0.57
1:D:366:LYS:HB2	1:D:383:GLN:OE1	2.04	0.57
1:F:366:LYS:HE3	1:F:385:THR:HG22	1.87	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:D:260:SER:HB2	1:D:267:TRP:HA	1.87	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:D:450:TYR:HB3	1:D:489:LYS:HG2	1.86	0.57
1:A:157:ILE:HG22	1:A:158:ARG:HG2	1.87	0.57
1:D:359:LEU:HD22	1:D:490:LEU:HA	1.86	0.57
1:A:228:ARG:NH1	1:A:256:LYS:HD2	2.20	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:D:129:MET:HG3	1:D:143:ALA:HB3	1.87	0.56
1:C:54:GLY:O	1:C:113:ARG:HA	2.05	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:A:67:TYR:HE1	1:A:82:CYS:HG	1.53	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:D:454:SER:HA	1:D:461:LEU:HD22	1.88	0.56
1:B:182:ASN:HB2	1:B:231:PRO:HG2	1.87	0.56
1:A:288:PRO:HG3	1:A:297:TYR:CE1	2.41	0.56
1:D:340:ILE:HG22	1:D:347:ILE:HG23	1.87	0.56
1:A:71:ARG:NH1	1:A:312:VAL:HG11	2.21	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:381:ILE:HD11	1:D:430:GLN:CD	2.26	0.55
1:D:377:ASN:HA	1:D:413:ARG:NH2	2.21	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
1:F:59:LYS:HD3	1:F:64:TYR:CE1	2.42	0.55
1:C:106:LEU:HD22	1:C:111:ILE:HD11	1.89	0.55
1:F:395:TYR:CE2	1:F:409:VAL:HG22	2.42	0.55
1:E:366:LYS:HE2	1:E:469:THR:O	2.06	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:F:100:ARG:HD2	1:F:107:ASN:O	2.07	0.54
1:D:417:VAL:HG21	1:D:477:GLN:NE2	2.23	0.54
1:D:448:ASP:HB2	1:D:450:TYR:CD2	2.43	0.54
1:B:97:VAL:HB	1:B:154:PHE:HD2	1.72	0.54
1:A:110:ASN:HB2	1:A:132:GLU:HB2	1.89	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: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: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: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:F:54:GLY:O	1:F:113:ARG:HA	2.08	0.53
1:A:116:VAL:HG22	1:A:127:MET:HB2	1.90	0.53
1:B:368:LEU:CD1	1:B:475:ILE:HD12	2.38	0.53
1:A:129:MET:HG2	1:A:143:ALA:HB3	1.90	0.53
1:D:437:TYR:O	1:D:456:ARG:HB3	2.09	0.53
1:A:118:TYR:CD1	1:A:125:PHE:HE1	2.26	0.53
1:D:110:ASN:HB2	1:D:132:GLU:HB2	1.89	0.53
1:B:230:ALA:O	1:B:244:THR:HA	2.08	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:106:LEU:HD11	1:B:156:TYR:CD2	2.44	0.53
1:B:41:GLN:HB3	1:B:49:VAL:HG23	1.89	0.53
1:B:284:THR:HG21	1:B:302:ASP:OD2	2.08	0.53
1:B:146:TYR:HD2	1:B:157:ILE:HD11	1.74	0.53
1:A:97:VAL:HB	1:A:154:PHE:CD2	2.44	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: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:B:55:GLY:HA3	1:B:67:TYR:O	2.09	0.52
1:A:395:TYR:CE2	1:A:409:VAL:HG22	2.44	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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:77:PHE:CD1	1:A:111:ILE:HB	2.45	0.52
1:C:63:TYR:CG	1:C:84:ARG:HD2	2.44	0.52
1:A:118:TYR:CD1	1:A:125:PHE:CE1	2.96	0.52
1:B:484:THR:HA	1:B:487:HIS:HD2	1.73	0.52
1:B:156:TYR:OH	1:B:159:SER:HB3	2.10	0.52
1:B:125:PHE:CZ	1:B:150:PRO:HG3	2.44	0.52
1:C:442:LYS:HE3	1:F:100:ARG:CZ	2.39	0.52
1:C:55:GLY:HA3	1:C:67:TYR:O	2.09	0.52
1:D:448:ASP:HB2	1:D:450:TYR:CE2	2.45	0.52
1:D:291:GLY:HA3	1:D:345:GLY:HA3	1.90	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:F:41:GLN:HB3	1:F:49:VAL:HG13	1.91	0.51
1:C:69:GLU:OE1	1:C:112:GLU:HA	2.10	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:321:PRO:HB3	1:B:347:ILE:HG22	1.92	0.51
1:B:41:GLN:HG3	1:B:316:GLN:HG2	1.93	0.51
1:B:363:ASN:HD22	1:B:467:TRP:HE3	1.58	0.51
1:D:363:ASN:OD1	1:D:484:THR:HB	2.11	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: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:D:394:TRP:HH2	1:D:430:GLN:HE21	1.59	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: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:D:110:ASN:OD1	1:D:134:GLY:HA2	2.11	0.50
1:E:478:TRP:CZ3	3:E:602:GOL:H31	2.46	0.50
1:A:253:ASN:C	1:A:253:ASN:HD22	2.14	0.50
1:B:356:ARG:HG2	1:B:393:GLN:OE1	2.11	0.50
1:C:399:VAL:O	1:C:399:VAL:HG12	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

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:381:ILE:HD11	1:D:430:GLN:NE2	2.27	0.50
1:D:358:LYS:O	1:D:491:VAL:HB	2.11	0.50
1:B:283:PRO:HB3	1:B:299:TYR:HE1	1.76	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:B:157:ILE:HD12	1:B:157:ILE:N	2.27	0.49
1:A:54:GLY:O	1:A:113:ARG:HA	2.12	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:256:LYS:HE2	1:A:272:ASN:HD21	1.76	0.49
1:A:125:PHE:HE2	1:A:150:PRO:HB3	1.78	0.49
1:D:234:ILE:HD11	1:D:286:ILE:C	2.33	0.49
1:D:445:ASP:HA	1:D:451:TYR:HB3	1.93	0.49
1:C:129:MET:HG2	1:C:143:ALA:HB3	1.94	0.49
1:E:236:ARG:HG2	1:E:237:ASN:OD1	2.13	0.49
1:E:375:VAL:HG12	1:E:411:SER:HB3	1.95	0.49
1:B:200:ASN:O	1:B:227:GLN:HA	2.12	0.49
1:D:442:LYS:HB3	1:D:454:SER:OG	2.12	0.49
1:A:245:SER:CB	1:A:283:PRO:HD2	2.40	0.49
1:D:361:ASN:HB3	1:D:364:SER:OG	2.13	0.49
1:C:223:PHE:HE2	1:C:242:LEU:HD23	1.77	0.49
1:D:465:ARG:O	1:D:466:LYS:HG2	2.11	0.49
1:A:55:GLY:HA3	1:A:67:TYR:O	2.13	0.49
1:E:131:TRP:CE3	1:E:141:ARG:HD2	2.48	0.49
1:F:70:TYR:HD1	1:F:96:GLU:OE2	1.96	0.48
1:A:196:ALA:HB1	1:A:200:ASN:HA	1.95	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:F:223:PHE:CE2	1:F:242:LEU:HD23	2.47	0.48
1:E:299:TYR:HB3	1:E:320:LEU:O	2.13	0.48
1:D:338:VAL:O	1:D:340:ILE:HG23	2.13	0.48
1:F:430:GLN:O	1:F:430:GLN:HG3	2.14	0.48
1:D:114:PRO:HB2	1:D:127:MET:HE3	1.94	0.48
1:F:55:GLY:HA3	1:F:67:TYR:O	2.13	0.48
1:E:260:SER:HB2	1:E:267:TRP:HA	1.96	0.48
1:A:110:ASN:OD1	1:A:134:GLY:HA2	2.14	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:156:TYR:OH	1:A:159:SER:HB3	2.13	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:298:LEU:HD11	1:F:319:TRP:HB3	1.96	0.48
1:F:71:ARG:HD3	1:F:312:VAL:HG11	1.96	0.48
1:D:416:ASP:CG	1:D:439:GLN:HG3	2.34	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:A:53:HIS:HD2	1:A:312:VAL:HG12	1.79	0.48
1:D:364:SER:HB2	1:D:383:GLN:OE1	2.14	0.47
1:C:378:ALA:HA	1:C:429:ILE:HD12	1.96	0.47
1:C:40:THR:HB	1:F:92:GLU:OE2	2.14	0.47
1:D:149:THR:HG23	1:D:150:PRO:HD2	1.96	0.47
1:A:381:ILE:HD13	1:A:429:ILE:HA	1.94	0.47
1:D:131:TRP:CE3	1:D:141:ARG:HD2	2.49	0.47
1:B:286:ILE:HD13	1:B:322:LEU:HD22	1.95	0.47
1:A:360:VAL:CG2	1:A:489:LYS:HB3	2.43	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:B:109:CYS:HB2	1:B:132:GLU:O	2.15	0.47
1:C:80:VAL:HG21	1:C:127:MET:HE1	1.97	0.47
1:F:147:SER:HB2	1:F:154:PHE:HA	1.96	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: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:71:ARG:HH11	1:A:312:VAL:HG11	1.79	0.47
1:F:182:ASN:ND2	1:F:232:CYS:HA	2.27	0.47
1:A:53:HIS:HE2	1:A:313:ASN:HA	1.79	0.47
1:E:70:TYR:O	1:E:78:LEU:HB3	2.15	0.47
1:D:106:LEU:HA	1:D:109:CYS:SG	2.55	0.47
1:C:71:ARG:NH1	1:C:312:VAL:HG11	2.30	0.47
1:B:339:LYS:HB2	1:B:350:TYR:HB2	1.97	0.47
1:D:387:ASN:N	1:D:392:GLN:HE22	2.05	0.47
1:A:413:ARG:HE	1:A:430:GLN:HG3	1.79	0.47
1:B:453:ILE:N	1:B:453:ILE:HD12	2.30	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:D:278:THR:O	1:D:278:THR:HG22	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:D:321:PRO:HB3	1:D:347:ILE:CG2	2.45	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:77:PHE:HB2	1:D:111:ILE:H	1.80	0.46
1:E:70:TYR:HB3	1:E:79:GLY:O	2.16	0.46
1:C:354:THR:O	1:C:354:THR:HG22	2.16	0.46
1:A:131:TRP:CE3	1:A:141:ARG:HD2	2.51	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:F:72:ASP:HB3	1:F:78:LEU:HD11	1.97	0.46
1:F:70:TYR:CD1	1:F:96:GLU:OE2	2.69	0.46
1:B:335:TYR:HB2	1:B:338:VAL:HG22	1.98	0.46
1:A:254:GLN:OE1	1:A:276:SER:HA	2.16	0.46
1:C:106:LEU:HA	1:C:109:CYS:SG	2.56	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:C:192:TYR:HB3	1:C:205:LEU:HD11	1.98	0.46
1:D:390:LEU:O	1:D:410:LYS:HB2	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:F:64:TYR:CG	1:F:88:LEU:HD21	2.51	0.45
1:B:226:GLN:HB3	1:B:228:ARG:HG2	1.98	0.45
1:F:461:LEU:CD1	1:F:486:GLN:HB3	2.43	0.45
1:E:57:MET:CE	1:E:287:ILE:HG21	2.46	0.45
1:C:77:PHE:HB2	1:C:111:ILE:H	1.81	0.45
1:E:122:THR:OG1	1:E:124:GLU:HG2	2.15	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:E:325:ILE:HD11	1:E:331:GLU:OE2	2.16	0.45
1:F:413:ARG:HB2	1:F:430:GLN:HB2	1.99	0.45
1:E:381:ILE:HG12	1:E:429:ILE:HA	1.97	0.45
1:E:351:ILE:N	1:E:351:ILE:HD12	2.32	0.45
1:E:34:GLY:HA2	1:E:89:VAL:HG21	1.97	0.45
1:C:77:PHE:CZ	1:C:111:ILE:HD12	2.51	0.45
1:A:97:VAL:HB	1:A:154:PHE:HD2	1.81	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:403:TYR:CE1	1:B:442:LYS:HG2	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:288:PRO:HG3	1:B:297:TYR:CE1	2.52	0.45
1:F:492:LEU:HD12	1:F:492:LEU:N	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:D:161:ARG:O	1:D:164:GLN:HB3	2.16	0.45
1:C:-13:SER:HA	1:C:492:LEU:CD1	2.47	0.45
1:A:194:ILE:HD12	1:A:204:HIS:O	2.17	0.45
1:B:359:LEU:HD12	1:B:368:LEU:HD22	1.98	0.45
1:B:145:ALA:HA	1:B:157:ILE:CD1	2.47	0.45
1:B:119:ASN:HB2	1:B:212:TYR:CD2	2.52	0.45
1:E:252:PRO:HB2	1:E:277:THR:CG2	2.47	0.45
1:D:87:ASP:O	1:D:88:LEU:HB2	2.16	0.45
1:C:126:VAL:HG21	1:C:212:TYR:HB2	1.98	0.45
1:D:376:ASP:C	1:D:413:ARG:HH12	2.21	0.44
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:E:277:THR:HG22	1:E:277:THR:O	2.17	0.44
1:B:463:ASP:OD1	3:B:602:GOL:H11	2.18	0.44
1:B:257:TYR:CE2	1:B:330:LEU:HD13	2.52	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:C:57:MET:HE2	1:C:287:ILE:HG21	2.00	0.44
1:E:474:ILE:N	1:E:474:ILE:HD12	2.31	0.44
1:E:62:ASP:O	1:E:86:LYS:HG2	2.17	0.44
1:D:243:ILE:N	1:D:243:ILE:HD12	2.32	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:B:230:ALA:CB	1:B:283:PRO:HG2	2.48	0.44
1:B:218:LEU:HD12	1:B:218:LEU:O	2.17	0.44
1:B:209:THR:OG1	1:B:210:PRO:HD2	2.17	0.44
1:B:484:THR:HA	1:B:487:HIS:CD2	2.52	0.44
1:D:168:VAL:HG21	1:D:176:TYR:CE1	2.52	0.44
1:A:279:TYR:CE2	1:A:334:TYR:HB2	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:E:59:LYS:HD3	1:E:64:TYR:CE1	2.52	0.44
1:D:263:LEU:HD12	1:D:263:LEU:H	1.83	0.44
1:B:129:MET:CG	1:B:143:ALA:HB3	2.48	0.44
1:D:111:ILE:HD11	1:D:131:TRP:HD1	1.81	0.44
1:B:278:THR:O	1:B:278:THR:HG22	2.18	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:125:PHE:HD2	1:A:150:PRO:HA	1.83	0.44
1:C:399:VAL:HG11	1:C:440:HIS:CE1	2.53	0.44
1:E:109:CYS:HB2	1:E:132:GLU:O	2.17	0.44
1:C:245:SER:HB3	1:C:283:PRO:HD2	2.00	0.44
1:D:297:TYR:CD2	1:D:324:PHE:CE2	3.06	0.44
1:A:57:MET:HA	1:A:65:TYR:O	2.18	0.44
1:C:42:PHE:CE2	1:C:50:ILE:HD12	2.53	0.43
1:A:129:MET:CG	1:A:143:ALA:HB3	2.47	0.43
1:C:126:VAL:HG11	1:C:212:TYR:O	2.18	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:D:451:TYR:OH	1:D:490:LEU:HD13	2.18	0.43
1:D:359:LEU:O	1:D:367:VAL:HG13	2.18	0.43
1:B:115:LYS:HG3	1:B:182:ASN:HA	2.00	0.43
1:F:70:TYR:O	1:F:78:LEU:HB2	2.18	0.43
1:E:362:LYS:HG2	1:E:484:THR:HB	1.99	0.43
1:D:288:PRO:HG3	1:D:297:TYR:CE1	2.52	0.43
1:E:452:LYS:HG2	1:E:461:LEU:HD22	2.00	0.43
1:C:223:PHE:CE2	1:C:242:LEU:HD23	2.52	0.43
1:A:279:TYR:CD2	1:A:334:TYR:HB2	2.52	0.43
1:F:288:PRO:HB3	1:F:297:TYR:CE1	2.54	0.43
1:C:135:ILE:HG13	1:C:136:ASN:ND2	2.34	0.43
1:B:131:TRP:CE3	1:B:141:ARG:HD2	2.54	0.43
1:D:83:TYR:HB3	1:D:91:TRP:HB3	2.00	0.43
1:C:399:VAL:HG21	1:C:405:LYS:HB2	2.00	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:D:340:ILE:CG2	1:D:347:ILE:HG23	2.47	0.43
1:B:321:PRO:HB3	1:B:347:ILE:CG2	2.48	0.43
1:C:287:ILE:HA	1:C:288:PRO:HD3	1.88	0.43
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:C:58:LEU:HD22	1:C:116:VAL:HG12	2.00	0.43
1:D:369:ASP:OD1	1:D:391:SER:HB2	2.19	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:E:197:ALA:HB3	1:E:204:HIS:CE1	2.54	0.43
1:A:50:ILE:HG23	1:A:83:TYR:CE1	2.53	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:E:147:SER:HB2	1:E:154:PHE:HA	2.01	0.43
1:B:240:TYR:CZ	1:B:263:LEU:HD11	2.54	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:256:LYS:HD3	1:D:270:LEU:HB3	2.00	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:D:413:ARG:HG2	1:D:432:THR:HA	2.00	0.42
1:D:50:ILE:HG23	1:D:83:TYR:CE1	2.54	0.42
1:C:466:LYS:H	3:C:602:GOL:C1	2.32	0.42
1:D:354:THR:O	1:D:354:THR:HG22	2.19	0.42
1:D:40:THR:HG22	1:D:41:GLN:N	2.34	0.42
1:A:370:VAL:HG11	1:A:430:GLN:NE2	2.34	0.42
1:E:144:VAL:HG22	1:E:157:ILE:HD12	2.02	0.42
1:C:285:PHE:HE2	1:C:287:ILE:HB	1.85	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: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:E:227:GLN:OE1	1:E:247:CYS:HB3	2.19	0.42
1:A:215:ILE:N	1:A:215:ILE:HD12	2.35	0.42
1:D:441:TRP:HB3	1:D:453:ILE:HG22	2.01	0.42
1:D:130:HIS:NE2	1:D:179:ARG:HA	2.35	0.42
1:F:77:PHE:CZ	1:F:79:GLY:HA2	2.55	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:B:492:LEU:HD12	1:B:492:LEU:N	2.34	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:C:305:ALA:HA	1:C:308:TRP:CZ2	2.54	0.42
1:F:466:LYS:H	3:F:603:GOL:C3	2.33	0.42
1:F:209:THR:HB	1:F:210:PRO:HD2	2.02	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:C:57:MET:CE	1:C:287:ILE:HG21	2.50	0.42
1:B:182:ASN:HD22	1:B:232:CYS:HA	1.85	0.42
1:E:254:GLN:OE1	1:E:276:SER:HA	2.19	0.42
1:B:77:PHE:CE2	1:B:111:ILE:HD12	2.54	0.42
1:E:362:LYS:HB2	1:E:450:TYR:CE1	2.55	0.42
1:F:378:ALA:HA	1:F:429:ILE:HD12	2.01	0.42
1:E:461:LEU:O	1:E:477:GLN:HA	2.20	0.42
1:F:97:VAL:HB	1:F:154:PHE:HD2	1.80	0.41
1:E:57:MET:HE2	1:E:287:ILE:HG21	2.00	0.41
1:B:236:ARG:HB2	1:B:297:TYR:OH	2.20	0.41
1:A:186:ASP:HB3	1:A:188:ASP:OD1	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:243:ILE:N	1:A:243:ILE:HD12	2.36	0.41
1:A:41:GLN:HG3	1:A:316:GLN:HG2	2.02	0.41
1:D:394:TRP:CZ3	1:D:408:ASN:HB3	2.55	0.41
1:B:194:ILE:HG23	1:B:231:PRO:HB2	2.02	0.41
1:D:85:SER:HB2	1:D:91:TRP:HA	2.02	0.41
1:B:162:PRO:HD2	1:B:176:TYR:O	2.20	0.41
1:F:36:ILE:HD11	1:F:89:VAL:HG22	2.01	0.41
1:C:52:ALA:HB1	1:C:68:GLY:HA3	2.01	0.41
1:B:126:VAL:HG21	1:B:212:TYR:HB2	2.02	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:C:243:ILE:N	1:C:243:ILE:HD12	2.35	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: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:D:279:TYR:CD2	1:D:334:TYR:HB2	2.56	0.41
1:F:57:MET:HE1	1:F:287:ILE:HG21	2.02	0.41
1:C:384:TRP:CZ3	1:C:471:ASP:HB3	2.55	0.41
1:B:305:ALA:HA	1:B:308:TRP:CH2	2.56	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:E:104:PRO:HA	1:E:107:ASN:OD1	2.21	0.41
1:E:437:TYR:CG	1:E:456:ARG:HD3	2.56	0.41
1:E:298:LEU:HB2	1:E:347:ILE:CD1	2.51	0.41
1:D:290:GLN:OE1	1:D:295:THR:HB	2.21	0.41
1:B:454:SER:HB2	1:B:459:GLY:O	2.20	0.41
1:D:366:LYS:HB3	1:D:384:TRP:C	2.41	0.41
1:C:-13:SER:OG	1:C:490:LEU:HB3	2.20	0.41
1:B:419:ASP:OD1	2:B:601:IPT:H3'2	2.21	0.41
1:E:243:ILE:HD12	1:E:243:ILE:N	2.36	0.41
1:A:403:TYR:CD1	1:A:442:LYS:HB2	2.56	0.41
1:B:359:LEU:O	1:B:367:VAL:HA	2.20	0.40
1:D:467:TRP:CH2	1:D:483:GLY:HA2	2.56	0.40
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: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:B:209:THR:HG22	1:B:214:ASN:O	2.22	0.40
1:C:186:ASP:HB3	1:C:188:ASP:OD1	2.21	0.40
1:C:450:TYR:CE1	1:C:489:LYS:HB2	2.57	0.40
1:B:385:THR:HG23	1:B:471:ASP:OD1	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
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:F:452:LYS:HB2	1:F:461:LEU:HD22	2.04	0.40
1:A:84:ARG:NE	1:A:94:ARG:HD3	2.36	0.40
1:D:360:VAL:HG22	1:D:361:ASN:N	2.37	0.40
1:F:70:TYR:HB3	1:F:79:GLY:O	2.22	0.40
1:C:64:TYR:CG	1:C:88:LEU:HD21	2.56	0.40
1:E:311:LYS:HG2	1:E:314:ASP:OD2	2.21	0.40
1:F:398:ASP:HA	1:F:404:LYS:HG2	2.04	0.40
1:C:425:GLY:HA2	1:C:476:GLN:CD	2.42	0.40
1:B:119:ASN:HB2	1:B:212:TYR:CE2	2.57	0.40
1:F:57:MET:CE	1:F:287:ILE:HG21	2.51	0.40
1:B:156:TYR:HH	1:B:159:SER:HB3	1.87	0.40
1:C:446:ILE:HG12	1:C:450:TYR:O	2.21	0.40
1:B:287:ILE:HA	1:B:288:PRO:HD3	1.91	0.40
1:F:460:LYS:HB2	1:F:477:GLN:HG2	2.03	0.40
1:F:243:ILE:N	1:F:243:ILE:HD12	2.37	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%)	56	92
1	C	480/526 (91%)	453 (94%)	26 (5%)	1 (0%)	56	92
1	D	459/526 (87%)	423 (92%)	35 (8%)	1 (0%)	56	92
1	E	459/526 (87%)	439 (96%)	20 (4%)	0	100	100
1	F	459/526 (87%)	439 (96%)	19 (4%)	1 (0%)	56	92
All	All	2775/3156 (88%)	2609 (94%)	162 (6%)	4 (0%)	59	93

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 ⓘ

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%)	94	99
1	B	389/442 (88%)	387 (100%)	2 (0%)	94	99
1	C	402/442 (91%)	402 (100%)	0	100	100
1	D	389/442 (88%)	388 (100%)	1 (0%)	96	99
1	E	389/442 (88%)	389 (100%)	0	100	100
1	F	389/442 (88%)	388 (100%)	1 (0%)	96	99
All	All	2347/2652 (88%)	2341 (100%)	6 (0%)	96	99

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

Some 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

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Mol	Chain	Res	Type
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 ⓘ

There are no RNA chains in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	A	601	-	15,15,15	0.84	1 (6%)	21,21,21	1.04	1 (4%)
3	GOL	A	602	-	5,5,5	0.33	0	5,5,5	0.26	0
2	IPT	B	601	-	15,15,15	0.84	1 (6%)	21,21,21	1.13	2 (9%)
3	GOL	B	602	-	5,5,5	0.33	0	5,5,5	0.28	0
2	IPT	C	601	-	15,15,15	0.85	1 (6%)	21,21,21	1.24	4 (19%)
3	GOL	C	602	-	5,5,5	0.33	0	5,5,5	0.27	0
3	GOL	C	603	-	5,5,5	0.32	0	5,5,5	0.24	0
2	IPT	D	601	-	15,15,15	0.83	1 (6%)	21,21,21	1.16	2 (9%)
2	IPT	E	601	-	15,15,15	0.85	1 (6%)	21,21,21	1.37	4 (19%)
3	GOL	E	602	-	5,5,5	0.35	0	5,5,5	0.24	0
3	GOL	E	603	-	5,5,5	0.33	0	5,5,5	0.25	0
2	IPT	F	601	-	15,15,15	0.86	1 (6%)	21,21,21	1.16	2 (9%)
2	IPT	F	602	-	15,15,15	0.85	1 (6%)	21,21,21	1.42	4 (19%)
3	GOL	F	603	-	5,5,5	0.33	0	5,5,5	0.21	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	A	601	-	-	0/6/26/26	0/1/1/1
3	GOL	A	602	-	-	0/4/4/4	0/0/0/0
2	IPT	B	601	-	-	0/6/26/26	0/1/1/1
3	GOL	B	602	-	-	0/4/4/4	0/0/0/0
2	IPT	C	601	-	-	0/6/26/26	0/1/1/1
3	GOL	C	602	-	-	0/4/4/4	0/0/0/0
3	GOL	C	603	-	-	0/4/4/4	0/0/0/0
2	IPT	D	601	-	-	0/6/26/26	0/1/1/1
2	IPT	E	601	-	-	0/6/26/26	0/1/1/1
3	GOL	E	602	-	-	0/4/4/4	0/0/0/0
3	GOL	E	603	-	-	0/4/4/4	0/0/0/0
2	IPT	F	601	-	-	0/6/26/26	0/1/1/1
2	IPT	F	602	-	-	0/6/26/26	0/1/1/1
3	GOL	F	603	-	-	0/4/4/4	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	601	IPT	C1-S1	-2.77	1.77	1.81
2	C	601	IPT	C1-S1	-2.74	1.77	1.81
2	B	601	IPT	C1-S1	-2.73	1.77	1.81
2	A	601	IPT	C1-S1	-2.73	1.77	1.81
2	E	601	IPT	C1-S1	-2.70	1.77	1.81
2	D	601	IPT	C1-S1	-2.69	1.77	1.81
2	F	602	IPT	C1-S1	-2.64	1.77	1.81

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	602	IPT	C1-S1-C1'	3.44	110.55	100.94
2	C	601	IPT	C1-S1-C1'	3.31	110.19	100.94
2	F	602	IPT	C1-O5-C5	3.30	119.22	112.70
2	B	601	IPT	C1-S1-C1'	3.30	110.17	100.94
2	E	601	IPT	O5-C1-C2	3.28	114.64	110.42
2	D	601	IPT	C1-S1-C1'	3.26	110.05	100.94
2	E	601	IPT	C1-S1-C1'	3.25	110.02	100.94
2	F	601	IPT	C1-S1-C1'	3.11	109.64	100.94
2	A	601	IPT	C1-S1-C1'	3.11	109.63	100.94
2	F	602	IPT	O5-C1-C2	2.66	113.84	110.42
2	C	601	IPT	C1-O5-C5	2.34	117.32	112.70
2	E	601	IPT	C1-O5-C5	2.26	117.17	112.70
2	E	601	IPT	C2-C1-S1	-2.25	108.27	110.97
2	B	601	IPT	C1-O5-C5	2.17	116.97	112.70
2	F	601	IPT	C1-O5-C5	2.16	116.97	112.70
2	D	601	IPT	C1-O5-C5	2.15	116.95	112.70
2	C	601	IPT	C2-C1-S1	-2.03	108.52	110.97
2	F	602	IPT	O5-C5-C4	2.00	113.47	109.76
2	C	601	IPT	O5-C1-C2	2.00	113.00	110.42

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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%)	-0.10	0	100	100	55, 84, 107, 140	0
1	B	461/526 (87%)	-0.02	0	100	100	64, 94, 120, 138	0
1	C	482/526 (91%)	-0.19	0	100	100	45, 62, 84, 132	0
1	D	461/526 (87%)	0.32	22 (4%)	29	6	54, 97, 178, 183	0
1	E	461/526 (87%)	-0.13	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%)	-0.05	22 (0%)	83	26	43, 78, 135, 183	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	380	GLN	4.6
1	D	430	GLN	4.2
1	D	383	GLN	3.9
1	D	490	LEU	3.7
1	D	414	ALA	2.9
1	D	492	LEU	2.9
1	D	423	GLU	2.7
1	D	396	LEU	2.7
1	D	473	GLY	2.7
1	D	452	LYS	2.6
1	D	491	VAL	2.5
1	D	427	VAL	2.5
1	D	474	ILE	2.4
1	D	358	LYS	2.3
1	D	375	VAL	2.3
1	D	480	ASP	2.3
1	D	367	VAL	2.2
1	D	451	TYR	2.2
1	D	374	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	378	ALA	2.1
1	D	446	ILE	2.0
1	D	33	GLU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	IPT	F	602	15/15	0.46	4.84	81,98,118,123	0
3	GOL	F	603	6/6	0.35	3.75	66,71,77,78	0
3	GOL	C	603	6/6	0.32	3.51	57,69,71,73	0
3	GOL	E	602	6/6	0.31	2.39	66,75,77,80	0
3	GOL	C	602	6/6	0.30	2.26	62,66,74,77	0
2	IPT	F	601	15/15	0.26	2.04	61,66,73,81	0
3	GOL	A	602	6/6	0.27	1.69	58,63,71,81	0
2	IPT	A	601	15/15	0.23	1.32	62,68,85,86	0
3	GOL	B	602	6/6	0.28	0.78	74,77,79,79	0
2	IPT	C	601	15/15	0.22	0.34	57,64,80,90	0
3	GOL	E	603	6/6	0.23	0.27	71,73,78,80	0
2	IPT	D	601	15/15	0.41	0.19	121,133,141,143	0
2	IPT	B	601	15/15	0.19	-0.17	75,81,88,100	0
2	IPT	E	601	15/15	0.15	-1.11	63,74,82,88	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.