



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 17, 2021 – 05:49 AM EDT

PDB ID : 1JC0  
Title : CRYSTAL STRUCTURE ANALYSIS OF A REDOX-SENSITIVE GREEN FLUORESCENT PROTEIN VARIANT IN A REDUCED FORM  
Authors : Hanson, G.T.; Aggeler, R.; Oglesbee, D.; Cannon, M.; Capaldi, R.A.; Tsien, R.Y.; Remington, S.J.  
Deposited on : 2001-06-07  
Resolution : 2.00 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.

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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 : 2.23.2  
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) : 2.23.2

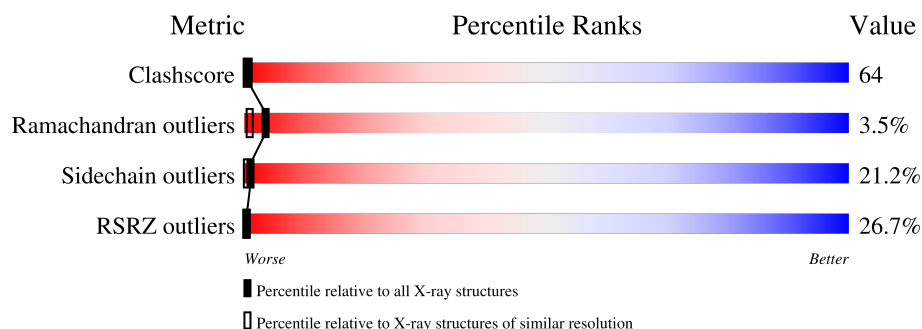
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	236	
1	B	236	
1	C	236	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5348 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 GREEN FLUORESCENT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1763	1124	292	339	8			
1	B	226	Total	C	N	O	S	0	0	0
			1732	1105	286	333	8			
1	C	226	Total	C	N	O	S	0	0	0
			1721	1102	282	330	7			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	48	SER	CYS	engineered mutation	UNP P42212
A	66	CRO	SER	chromophore	UNP P42212
A	66	CRO	TYR	chromophore	UNP P42212
A	66	CRO	GLY	chromophore	UNP P42212
A	64	LEU	TYR	engineered mutation	UNP P42212
A	80	ARG	GLN	engineered mutation	UNP P42212
A	147	CYS	SER	engineered mutation	UNP P42212
A	204	CYS	GLN	engineered mutation	UNP P42212
B	48	SER	CYS	engineered mutation	UNP P42212
B	66	CRO	SER	chromophore	UNP P42212
B	66	CRO	TYR	chromophore	UNP P42212
B	66	CRO	GLY	chromophore	UNP P42212
B	80	ARG	GLN	engineered mutation	UNP P42212
B	147	CYS	SER	engineered mutation	UNP P42212
B	204	CYS	GLN	engineered mutation	UNP P42212
C	48	SER	CYS	engineered mutation	UNP P42212
C	66	CRO	SER	chromophore	UNP P42212
C	66	CRO	TYR	chromophore	UNP P42212
C	66	CRO	GLY	chromophore	UNP P42212
C	80	ARG	GLN	engineered mutation	UNP P42212
C	147	CYS	SER	engineered mutation	UNP P42212
C	204	CYS	GLN	engineered mutation	UNP P42212

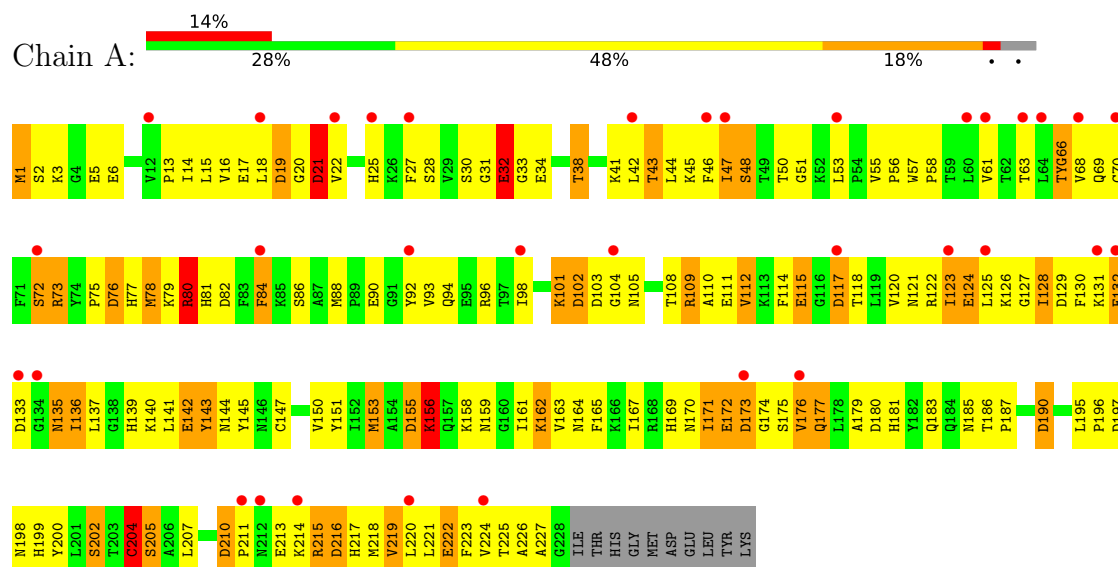
- Molecule 2 is water.

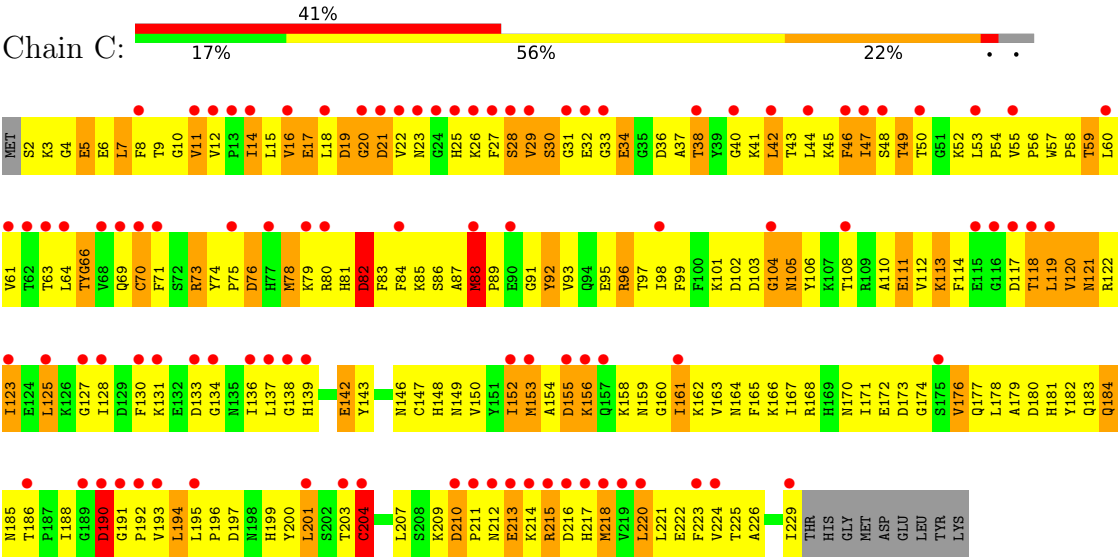
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	58	Total 58	O 58	0	0
2	B	36	Total 36	O 36	0	0
2	C	38	Total 38	O 38	0	0

### 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: GREEN FLUORESCENT PROTEIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	185.63Å 67.86Å 56.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 28.72 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.00) 78.1 (28.72-2.00)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.36 (at 2.00Å)	Xtriage
Refinement program	TNT	Depositor
R, $R_{free}$	0.223 , (Not available) 0.237 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	30.5	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.23 , 112.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5348	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.02% 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: CRO

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	1.07	9/1781 (0.5%)	1.50	32/2412 (1.3%)
1	B	1.03	8/1750 (0.5%)	1.46	32/2375 (1.3%)
1	C	1.00	10/1739 (0.6%)	1.51	26/2361 (1.1%)
All	All	1.03	27/5270 (0.5%)	1.49	90/7148 (1.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	6	0
1	B	4	0
1	C	16	0
All	All	26	0

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	32	GLU	CD-OE2	7.74	1.34	1.25
1	A	172	GLU	CD-OE2	7.52	1.33	1.25
1	B	90	GLU	CD-OE2	7.28	1.33	1.25
1	A	32	GLU	CD-OE2	6.87	1.33	1.25
1	A	222	GLU	CD-OE2	6.86	1.33	1.25
1	B	95	GLU	CD-OE2	6.77	1.33	1.25
1	C	6	GLU	CD-OE2	6.58	1.32	1.25
1	B	34	GLU	CD-OE2	6.52	1.32	1.25
1	A	115	GLU	CD-OE2	6.50	1.32	1.25
1	C	111	GLU	CD-OE2	6.43	1.32	1.25
1	B	111	GLU	CD-OE2	6.28	1.32	1.25
1	B	222	GLU	CD-OE2	6.21	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	124	GLU	CD-OE2	6.05	1.32	1.25
1	C	142	GLU	CD-OE2	5.94	1.32	1.25
1	A	34	GLU	CD-OE2	5.85	1.32	1.25
1	B	17	GLU	CD-OE2	5.83	1.32	1.25
1	A	111	GLU	CD-OE2	5.80	1.32	1.25
1	A	5	GLU	CD-OE2	5.75	1.31	1.25
1	B	142	GLU	CD-OE2	5.66	1.31	1.25
1	C	172	GLU	CD-OE2	5.52	1.31	1.25
1	C	34	GLU	CD-OE2	5.50	1.31	1.25
1	A	142	GLU	CD-OE2	5.42	1.31	1.25
1	C	213	GLU	CD-OE2	5.31	1.31	1.25
1	C	5	GLU	CD-OE2	5.30	1.31	1.25
1	C	222	GLU	CD-OE2	5.26	1.31	1.25
1	C	17	GLU	CD-OE2	5.20	1.31	1.25
1	B	124	GLU	CD-OE2	5.12	1.31	1.25

All (90) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	191	GLY	C-N-CD	-10.31	97.92	120.60
1	C	96	ARG	NE-CZ-NH2	-10.06	115.27	120.30
1	B	109	ARG	NE-CZ-NH1	9.02	124.81	120.30
1	A	21	ASP	CB-CG-OD2	-8.10	111.01	118.30
1	A	21	ASP	CB-CG-OD1	7.82	125.33	118.30
1	A	48	SER	N-CA-CB	7.80	122.20	110.50
1	B	109	ARG	NE-CZ-NH2	-7.61	116.50	120.30
1	C	180	ASP	CB-CG-OD2	-7.61	111.45	118.30
1	C	117	ASP	CB-CG-OD2	-7.38	111.66	118.30
1	B	182	TYR	CB-CG-CD2	7.37	125.42	121.00
1	C	19	ASP	CB-CG-OD2	-7.33	111.71	118.30
1	A	102	ASP	CB-CG-OD2	-7.22	111.80	118.30
1	B	82	ASP	CB-CG-OD2	-7.21	111.81	118.30
1	A	82	ASP	CB-CG-OD2	-7.16	111.86	118.30
1	C	204	CYS	N-CA-CB	7.12	123.42	110.60
1	B	36	ASP	CB-CG-OD2	-7.11	111.90	118.30
1	B	182	TYR	CB-CG-CD1	-7.06	116.76	121.00
1	B	197	ASP	CB-CG-OD2	-7.00	112.00	118.30
1	A	109	ARG	NE-CZ-NH1	6.95	123.78	120.30
1	A	155	ASP	CB-CG-OD2	-6.92	112.08	118.30
1	C	197	ASP	CB-CG-OD2	-6.82	112.16	118.30
1	A	216	ASP	CB-CG-OD1	6.81	124.43	118.30
1	B	173	ASP	CB-CG-OD2	-6.81	112.17	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	96	ARG	NE-CZ-NH1	6.81	123.70	120.30
1	A	216	ASP	CB-CG-OD2	-6.77	112.21	118.30
1	C	180	ASP	CB-CG-OD1	6.44	124.10	118.30
1	C	190	ASP	CB-CG-OD2	-6.44	112.50	118.30
1	A	80	ARG	NE-CZ-NH1	6.44	123.52	120.30
1	C	21	ASP	CB-CG-OD2	-6.42	112.52	118.30
1	C	88	MET	C-N-CD	-6.40	106.52	120.60
1	A	173	ASP	CB-CG-OD1	6.40	124.06	118.30
1	B	180	ASP	CB-CG-OD2	-6.39	112.55	118.30
1	B	173	ASP	CB-CG-OD1	6.36	124.02	118.30
1	C	216	ASP	CB-CG-OD2	-6.35	112.58	118.30
1	C	19	ASP	CB-CG-OD1	6.35	124.02	118.30
1	C	117	ASP	CB-CG-OD1	6.32	123.99	118.30
1	A	103	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	C	21	ASP	CB-CG-OD1	6.27	123.94	118.30
1	A	197	ASP	CB-CG-OD2	-6.25	112.67	118.30
1	B	129	ASP	CB-CG-OD2	-6.22	112.70	118.30
1	A	180	ASP	CB-CG-OD1	6.21	123.89	118.30
1	B	36	ASP	CB-CG-OD1	6.21	123.89	118.30
1	C	173	ASP	CB-CG-OD2	-6.20	112.72	118.30
1	B	19	ASP	CB-CG-OD2	-6.20	112.72	118.30
1	A	109	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	A	173	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	C	210	ASP	CB-CG-OD2	-6.12	112.80	118.30
1	A	197	ASP	CB-CG-OD1	6.08	123.77	118.30
1	B	155	ASP	CB-CG-OD2	-6.06	112.84	118.30
1	A	190	ASP	CB-CG-OD2	-6.06	112.85	118.30
1	A	180	ASP	CB-CG-OD2	-5.99	112.91	118.30
1	B	190	ASP	CB-CG-OD2	-5.95	112.95	118.30
1	A	143	TYR	CB-CG-CD2	-5.92	117.45	121.00
1	A	102	ASP	CB-CG-OD1	5.90	123.61	118.30
1	B	210	ASP	CB-CG-OD1	5.89	123.60	118.30
1	B	129	ASP	CB-CG-OD1	5.87	123.59	118.30
1	C	155	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	A	117	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	B	155	ASP	CB-CG-OD1	5.78	123.50	118.30
1	C	102	ASP	CB-CG-OD1	5.75	123.47	118.30
1	B	197	ASP	CB-CG-OD1	5.73	123.45	118.30
1	C	155	ASP	CB-CG-OD1	5.70	123.43	118.30
1	B	133	ASP	CB-CG-OD1	5.69	123.42	118.30
1	C	102	ASP	CB-CG-OD2	-5.69	113.18	118.30
1	C	210	ASP	CB-CG-OD1	5.68	123.41	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	133	ASP	CB-CG-OD2	-5.67	113.19	118.30
1	B	102	ASP	CB-CG-OD2	-5.61	113.25	118.30
1	A	204	CYS	N-CA-CB	5.58	120.65	110.60
1	A	155	ASP	CB-CG-OD1	5.56	123.30	118.30
1	C	21	ASP	N-CA-CB	5.53	120.55	110.60
1	C	190	ASP	CB-CG-OD1	5.43	123.19	118.30
1	A	210	ASP	CB-CG-OD1	5.43	123.19	118.30
1	B	21	ASP	CB-CG-OD1	5.39	123.16	118.30
1	A	80	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	A	129	ASP	CB-CG-OD1	5.34	123.11	118.30
1	B	190	ASP	CB-CG-OD1	5.33	123.10	118.30
1	A	19	ASP	CB-CG-OD1	5.32	123.08	118.30
1	C	197	ASP	CB-CG-OD1	5.32	123.08	118.30
1	B	82	ASP	CB-CG-OD1	5.31	123.08	118.30
1	B	210	ASP	CB-CG-OD2	-5.26	113.56	118.30
1	B	102	ASP	N-CA-CB	5.25	120.06	110.60
1	A	117	ASP	CB-CG-OD1	5.25	123.03	118.30
1	C	82	ASP	CB-CG-OD1	5.24	123.02	118.30
1	A	225	THR	CA-CB-CG2	-5.22	105.08	112.40
1	A	43	THR	N-CA-CB	5.12	120.03	110.30
1	B	129	ASP	N-CA-CB	5.12	119.82	110.60
1	B	21	ASP	CB-CG-OD2	-5.12	113.69	118.30
1	B	103	ASP	CB-CG-OD2	-5.10	113.71	118.30
1	B	225	THR	CA-CB-CG2	-5.07	105.31	112.40
1	A	76	ASP	CB-CG-OD1	5.01	122.81	118.30

All (26) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	38	THR	CB,CA
1	A	78	MET	CA
1	A	98	ILE	CB
1	A	123	ILE	CB
1	A	184	GLN	CA
1	B	9	THR	CB
1	B	101	LYS	CA
1	B	128	ILE	CB
1	B	155	ASP	CA
1	C	2	SER	CA
1	C	9	THR	CA,CB
1	C	18	LEU	CA
1	C	21	ASP	CA

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Mol	Chain	Res	Type	Atom
1	C	45	LYS	CA
1	C	46	PHE	CA
1	C	82	ASP	CA
1	C	94	GLN	CA
1	C	109	ARG	CA
1	C	121	ASN	CA
1	C	137	LEU	CA
1	C	154	ALA	CA
1	C	159	ASN	CA
1	C	186	THR	CB
1	C	215	ARG	CA

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1763	0	1664	162	0
1	B	1732	0	1607	170	0
1	C	1721	0	1582	313	0
2	A	58	0	0	3	0
2	B	36	0	0	7	0
2	C	38	0	0	11	0
All	All	5348	0	4853	642	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 64.

All (642) 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:B:18:LEU:HD12	1:B:123:ILE:HB	1.21	1.16
1:B:170:ASN:HA	1:B:176:VAL:HG12	1.25	1.14
1:C:112:VAL:HB	1:C:121:ASN:HB3	1.30	1.09
1:C:21:ASP:HB3	1:C:26:LYS:HG2	1.34	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:111:GLU:HG2	1:C:188:ILE:HD11	1.27	1.08
1:C:130:PHE:HB3	1:C:137:LEU:HD11	1.35	1.08
1:C:7:LEU:HD21	1:C:89:PRO:HD3	1.39	1.01
1:C:28:SER:HB3	1:C:49:THR:HB	1.41	1.00
1:B:16:VAL:HG13	1:B:121:ASN:HB3	1.41	0.99
1:C:91:GLY:HA3	1:C:113:LYS:HB3	1.43	0.98
1:C:4:GLY:HA2	1:C:7:LEU:HD13	1.41	0.97
1:B:171:ILE:HG12	1:B:176:VAL:HA	1.48	0.95
1:C:18:LEU:HD23	1:C:29:VAL:HG23	1.48	0.94
1:B:81:HIS:CE1	1:B:197:ASP:HB2	2.05	0.92
1:B:56:PRO:HG2	1:B:141:LEU:HD22	1.52	0.91
1:B:132:GLU:HA	1:B:137:LEU:HD12	1.50	0.90
1:B:170:ASN:HA	1:B:176:VAL:CG1	2.01	0.90
1:C:21:ASP:CB	1:C:26:LYS:HG2	2.01	0.90
1:C:110:ALA:HB2	1:C:123:ILE:HG23	1.53	0.90
1:B:171:ILE:HG12	1:B:176:VAL:CA	2.02	0.90
1:A:213:GLU:HB3	1:A:217:HIS:CE1	2.07	0.89
1:C:203:THR:HG23	1:C:224:VAL:HG22	1.51	0.89
1:C:22:VAL:HG13	1:C:127:GLY:HA3	1.51	0.89
1:A:153:MET:CE	1:A:162:LYS:HD2	2.04	0.88
1:C:18:LEU:HD23	1:C:29:VAL:CG2	2.03	0.87
1:C:166:LYS:HB3	1:C:178:LEU:HD11	1.54	0.87
1:A:153:MET:HB2	1:A:198:ASN:ND2	1.90	0.87
1:C:112:VAL:HB	1:C:121:ASN:CB	2.03	0.87
1:C:28:SER:HB2	1:C:50:THR:HG23	1.55	0.86
1:C:4:GLY:CA	1:C:7:LEU:HD13	2.06	0.85
1:C:28:SER:HB3	1:C:49:THR:CB	2.05	0.85
1:B:42:LEU:HD11	1:B:68:VAL:HG23	1.59	0.85
1:C:108:THR:CG2	1:C:125:LEU:HD12	2.06	0.84
1:C:163:VAL:HG21	1:C:183:GLN:NE2	1.92	0.84
1:C:20:GLY:HA2	1:C:27:PHE:CE2	2.12	0.83
1:A:153:MET:HE1	1:A:162:LYS:HD2	1.58	0.83
1:C:161:ILE:HG21	1:C:196:PRO:HG2	1.57	0.83
1:B:115:GLU:HB2	1:B:120:VAL:CG1	2.09	0.83
1:B:18:LEU:CD1	1:B:123:ILE:HB	2.07	0.82
1:C:23:ASN:HD21	1:C:130:PHE:H	1.22	0.82
1:C:8:PHE:CE2	1:C:85:LYS:HG2	2.15	0.81
1:C:44:LEU:HB2	1:C:220:LEU:HD22	1.61	0.81
1:A:220:LEU:HD12	1:A:221:LEU:H	1.44	0.81
1:C:150:VAL:HB	1:C:201:LEU:HD12	1.64	0.80
1:A:135:ASN:HD22	1:A:140:LYS:HD2	1.45	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:130:PHE:CB	1:C:137:LEU:HD11	2.11	0.80
1:A:221:LEU:HD11	1:A:223:PHE:CZ	2.17	0.79
1:B:71:PHE:HE2	1:B:119:LEU:HD22	1.47	0.79
1:C:171:ILE:HD12	1:C:176:VAL:HA	1.62	0.79
1:B:18:LEU:HB3	1:B:29:VAL:HG12	1.63	0.79
1:C:147:CYS:SG	1:C:204:CYS:HB3	2.23	0.79
1:B:109:ARG:HH11	1:B:109:ARG:HG2	1.45	0.78
1:B:170:ASN:CA	1:B:176:VAL:HG12	2.11	0.78
1:C:18:LEU:CD1	1:C:123:ILE:HB	2.13	0.78
1:C:63:THR:HG22	2:C:265:HOH:O	1.84	0.77
1:C:91:GLY:CA	1:C:113:LYS:HB3	2.14	0.77
1:B:42:LEU:HD12	1:B:222:GLU:OE2	1.85	0.76
1:C:163:VAL:HB	1:C:183:GLN:HB3	1.67	0.76
1:B:71:PHE:CE2	1:B:119:LEU:HD22	2.21	0.75
1:C:31:GLY:HA2	1:C:45:LYS:O	1.86	0.75
1:C:33:GLY:HA3	1:C:44:LEU:HD23	1.67	0.75
1:C:86:SER:OG	1:C:193:VAL:HG13	1.86	0.75
1:C:167:ILE:HB	1:C:179:ALA:HB3	1.67	0.75
1:A:42:LEU:HD12	1:A:222:GLU:HB2	1.69	0.75
1:B:90:GLU:HG3	2:B:261:HOH:O	1.85	0.74
1:A:66:CRO:HG11	1:A:220:LEU:HD21	1.66	0.74
1:A:75:PRO:HG2	1:A:78:MET:HG3	1.69	0.74
1:C:207:LEU:HD22	1:C:218:MET:SD	2.27	0.73
1:A:47:ILE:HD12	1:A:47:ILE:H	1.51	0.73
1:A:141:LEU:HD22	1:A:171:ILE:CD1	2.18	0.73
1:B:81:HIS:HE1	1:B:197:ASP:HB2	1.50	0.73
1:C:3:LYS:HG2	1:C:4:GLY:N	2.02	0.73
1:C:2:SER:HB3	1:C:5:GLU:HB2	1.71	0.72
1:B:82:ASP:OD2	1:B:85:LYS:HE3	1.89	0.72
1:B:93:VAL:HG22	1:B:111:GLU:HG2	1.70	0.72
1:A:1:MET:HE3	2:A:256:HOH:O	1.90	0.71
1:B:132:GLU:HA	1:B:137:LEU:CD1	2.20	0.71
1:A:28:SER:N	1:A:50:THR:HG21	2.05	0.71
1:C:111:GLU:HG2	1:C:188:ILE:CD1	2.16	0.71
1:C:83:PHE:CD1	1:C:193:VAL:HG11	2.25	0.71
1:C:108:THR:HG22	1:C:125:LEU:HD12	1.72	0.71
1:C:210:ASP:HB3	1:C:213:GLU:HB3	1.73	0.71
1:B:53:LEU:HB2	1:B:216:ASP:OD2	1.91	0.70
1:B:70:CYS:O	1:B:85:LYS:HE2	1.91	0.70
1:B:203:THR:HG23	1:B:224:VAL:HG22	1.71	0.70
1:C:8:PHE:CD2	1:C:85:LYS:HG2	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:ASP:HA	1:B:25:HIS:O	1.91	0.70
1:C:3:LYS:HG2	1:C:4:GLY:H	1.54	0.70
1:C:20:GLY:O	1:C:26:LYS:HA	1.92	0.70
1:B:39:TYR:CE1	1:C:147:CYS:HB3	2.25	0.70
1:C:21:ASP:HB2	1:C:25:HIS:O	1.91	0.70
1:C:96:ARG:HG3	1:C:183:GLN:HG3	1.74	0.70
1:C:153:MET:SD	1:C:162:LYS:HB3	2.32	0.70
1:A:141:LEU:HD22	1:A:171:ILE:HD11	1.74	0.69
1:C:21:ASP:O	1:C:127:GLY:N	2.25	0.69
1:C:154:ALA:HB2	1:C:161:ILE:HG22	1.74	0.69
1:A:167:ILE:HB	1:A:179:ALA:HB3	1.73	0.69
1:A:21:ASP:HA	1:A:25:HIS:O	1.92	0.69
1:A:66:CRO:N2	1:A:66:CRO:HG12	2.07	0.69
1:B:18:LEU:HD12	1:B:123:ILE:CB	2.12	0.69
1:C:171:ILE:HD12	1:C:176:VAL:CA	2.21	0.69
1:C:18:LEU:O	1:C:28:SER:HA	1.93	0.69
1:C:30:SER:O	1:C:46:PHE:HB3	1.93	0.68
1:C:213:GLU:HG2	1:C:217:HIS:ND1	2.08	0.68
1:C:55:VAL:HG12	1:C:136:ILE:CG2	2.23	0.68
1:A:47:ILE:CG2	1:A:217:HIS:HB3	2.24	0.68
1:B:171:ILE:HB	1:B:175:SER:C	2.12	0.68
1:C:63:THR:HG23	2:C:262:HOH:O	1.94	0.68
1:C:170:ASN:HA	1:C:176:VAL:HG23	1.75	0.68
1:B:115:GLU:HB2	1:B:120:VAL:HG13	1.75	0.67
1:A:31:GLY:HA2	1:A:45:LYS:O	1.93	0.67
1:A:42:LEU:O	1:A:221:LEU:HD12	1.95	0.67
1:A:147:CYS:SG	1:A:204:CYS:HB3	2.34	0.67
1:C:23:ASN:OD1	1:C:128:ILE:HA	1.94	0.67
1:C:171:ILE:HD11	1:C:177:GLN:HB2	1.77	0.67
1:A:28:SER:H	1:A:50:THR:HG21	1.59	0.67
1:A:175:SER:HB2	2:A:292:HOH:O	1.95	0.67
1:B:167:ILE:O	1:B:178:LEU:HD12	1.94	0.67
1:C:150:VAL:HG13	1:C:165:PHE:CD1	2.29	0.67
1:C:215:ARG:O	1:C:217:HIS:ND1	2.27	0.67
1:C:8:PHE:CD2	1:C:85:LYS:HD3	2.29	0.67
1:C:104:GLY:HA3	1:C:130:PHE:CD2	2.29	0.67
1:B:8:PHE:CZ	1:B:114:PHE:HE2	2.13	0.66
1:C:61:VAL:O	1:C:66:CRO:HG13	1.96	0.66
1:A:47:ILE:HG22	1:A:217:HIS:HB3	1.77	0.66
1:C:18:LEU:O	1:C:29:VAL:N	2.27	0.66
1:C:20:GLY:HA3	1:C:27:PHE:O	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:GLY:HA2	1:C:7:LEU:CD1	2.21	0.66
1:C:56:PRO:O	1:C:59:THR:HG23	1.96	0.66
1:C:213:GLU:OE2	1:C:215:ARG:N	2.27	0.66
1:B:213:GLU:OE2	1:B:214:LYS:N	2.29	0.66
1:C:15:LEU:CB	1:C:120:VAL:HG23	2.26	0.66
1:C:21:ASP:HB3	1:C:26:LYS:CG	2.21	0.66
1:A:176:VAL:HG13	1:A:177:GLN:N	2.07	0.66
1:B:15:LEU:HG	1:B:118:THR:HG21	1.76	0.66
1:C:20:GLY:HA2	1:C:27:PHE:CD2	2.30	0.66
1:C:101:LYS:O	1:C:177:GLN:NE2	2.29	0.66
1:C:153:MET:O	1:C:161:ILE:HG22	1.96	0.66
1:A:220:LEU:HD12	1:A:221:LEU:N	2.09	0.66
1:B:68:VAL:N	2:B:272:HOH:O	2.29	0.66
1:C:213:GLU:HG3	1:C:215:ARG:N	2.10	0.66
1:A:30:SER:O	1:A:46:PHE:HA	1.97	0.65
1:B:75:PRO:O	1:B:78:MET:N	2.28	0.65
1:C:150:VAL:HB	1:C:201:LEU:CD1	2.25	0.65
1:B:53:LEU:HD22	1:B:57:TRP:CE2	2.31	0.65
1:C:18:LEU:HD12	1:C:123:ILE:HB	1.76	0.65
1:B:154:ALA:HB2	1:B:196:PRO:O	1.97	0.65
1:B:19:ASP:OD2	1:B:19:ASP:N	2.29	0.64
1:B:25:HIS:ND1	1:B:25:HIS:N	2.39	0.64
1:B:147:CYS:SG	1:B:204:CYS:HB3	2.36	0.64
1:B:164:ASN:ND2	2:B:251:HOH:O	2.29	0.64
1:C:93:VAL:HG12	1:C:186:THR:HG22	1.78	0.64
1:C:99:PHE:HE1	1:C:182:TYR:CD2	2.14	0.64
1:C:66:CRO:N2	1:C:66:CRO:HG12	2.11	0.64
1:A:75:PRO:HG2	1:A:78:MET:SD	2.37	0.64
1:C:19:ASP:O	1:C:125:LEU:N	2.27	0.64
1:B:23:ASN:ND2	1:B:128:ILE:HA	2.12	0.64
1:C:85:LYS:O	1:C:88:MET:HB2	1.98	0.64
1:C:209:LYS:NZ	1:C:217:HIS:O	2.30	0.64
1:C:18:LEU:HD13	1:C:123:ILE:HB	1.78	0.64
1:A:45:LYS:NZ	1:A:210:ASP:OD2	2.31	0.64
1:C:80:ARG:HA	1:C:194:LEU:CD1	2.28	0.64
1:C:213:GLU:HG3	1:C:215:ARG:H	1.63	0.64
1:C:152:ILE:HD11	1:C:201:LEU:HD11	1.79	0.64
1:B:128:ILE:HG22	1:B:129:ASP:N	2.13	0.64
1:A:104:GLY:HA3	1:A:130:PHE:CD2	2.33	0.64
1:C:110:ALA:HB2	1:C:123:ILE:CG2	2.28	0.64
1:B:197:ASP:O	1:B:198:ASN:C	2.35	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:175:SER:O	1:B:176:VAL:HG13	1.98	0.63
1:B:20:GLY:HA3	1:B:27:PHE:CZ	2.33	0.63
1:C:103:ASP:OD1	1:C:104:GLY:N	2.29	0.63
1:A:135:ASN:HA	1:A:140:LYS:HB2	1.81	0.63
1:C:168:ARG:NH1	2:C:249:HOH:O	2.29	0.63
1:B:142:GLU:HG2	1:B:170:ASN:O	1.99	0.63
1:C:148:HIS:CD2	1:C:168:ARG:HH12	2.17	0.63
1:B:135:ASN:ND2	2:B:270:HOH:O	2.29	0.63
1:A:75:PRO:O	1:A:78:MET:N	2.29	0.62
1:C:7:LEU:CD2	1:C:89:PRO:HD3	2.22	0.62
1:A:142:GLU:HG3	1:A:144:ASN:OD1	1.98	0.62
1:C:131:LYS:O	1:C:134:GLY:N	2.29	0.62
1:C:14:ILE:HA	1:C:119:LEU:O	2.00	0.61
1:B:36:ASP:OD1	1:B:39:TYR:HB2	2.01	0.61
1:C:155:ASP:O	1:C:156:LYS:C	2.36	0.61
1:B:215:ARG:O	1:B:217:HIS:HB3	2.01	0.61
1:A:47:ILE:HD12	1:A:47:ILE:N	2.11	0.61
1:A:53:LEU:HD22	1:A:57:TRP:CE2	2.36	0.61
1:C:4:GLY:O	1:C:5:GLU:C	2.39	0.61
1:C:28:SER:HB3	1:C:49:THR:OG1	2.00	0.61
1:C:29:VAL:HG12	1:C:47:ILE:O	2.00	0.61
1:C:149:ASN:HB3	1:C:200:TYR:CD1	2.35	0.61
1:B:62:THR:OG1	1:B:181:HIS:HE1	1.83	0.61
1:B:186:THR:CG2	1:B:187:PRO:HD2	2.31	0.61
1:C:161:ILE:HG21	1:C:196:PRO:CG	2.30	0.61
1:B:17:GLU:OE1	1:B:17:GLU:HA	2.00	0.61
1:B:18:LEU:HA	1:B:123:ILE:O	2.00	0.61
1:C:203:THR:HG23	1:C:224:VAL:CG2	2.26	0.61
1:C:22:VAL:HG13	1:C:127:GLY:CA	2.28	0.61
1:C:28:SER:O	1:C:49:THR:N	2.27	0.61
1:A:221:LEU:HG	1:A:223:PHE:CE2	2.36	0.60
1:C:16:VAL:HG13	1:C:121:ASN:HA	1.82	0.60
1:A:199:HIS:HB2	1:A:227:ALA:O	2.02	0.60
1:C:58:PRO:HA	1:C:61:VAL:HG23	1.82	0.60
1:C:128:ILE:HD12	1:C:128:ILE:O	2.00	0.60
1:C:152:ILE:HD11	1:C:201:LEU:CD1	2.31	0.60
1:C:28:SER:HB2	1:C:50:THR:CG2	2.29	0.60
1:A:123:ILE:HG23	1:A:124:GLU:N	2.17	0.60
1:B:210:ASP:O	1:B:212:ASN:N	2.35	0.60
1:C:44:LEU:HB2	1:C:220:LEU:CD2	2.29	0.60
1:C:220:LEU:HG	1:C:221:LEU:N	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:ASN:ND2	1:B:170:ASN:HD21	1.99	0.59
1:B:14:ILE:HG22	1:B:15:LEU:N	2.18	0.59
1:B:179:ALA:O	1:B:181:HIS:HD2	1.85	0.59
1:B:198:ASN:O	1:B:199:HIS:HB3	2.02	0.59
1:C:210:ASP:OD1	1:C:211:PRO:HD2	2.03	0.59
1:A:28:SER:H	1:A:50:THR:CG2	2.15	0.59
1:A:151:TYR:HB2	1:A:164:ASN:OD1	2.03	0.59
1:B:56:PRO:HD3	1:B:136:ILE:O	2.02	0.59
1:B:71:PHE:HE2	1:B:119:LEU:CD2	2.13	0.59
1:A:33:GLY:HA3	1:A:44:LEU:HD23	1.85	0.59
1:C:87:ALA:C	1:C:88:MET:HE2	2.24	0.58
1:C:210:ASP:O	1:C:211:PRO:C	2.36	0.58
1:A:38:THR:O	1:A:73:ARG:HD2	2.03	0.58
1:A:75:PRO:HG2	1:A:78:MET:CG	2.32	0.58
1:A:153:MET:HB2	1:A:198:ASN:HD21	1.67	0.58
1:C:16:VAL:HA	1:C:121:ASN:O	2.03	0.58
1:C:28:SER:CB	1:C:49:THR:HB	2.23	0.58
1:C:42:LEU:CD1	1:C:44:LEU:HD11	2.33	0.58
1:A:207:LEU:HD22	1:A:218:MET:SD	2.44	0.58
1:A:77:HIS:CD2	1:A:78:MET:HG2	2.38	0.58
1:B:29:VAL:HG21	1:B:57:TRP:CZ3	2.39	0.58
1:C:55:VAL:HG11	1:C:106:TYR:OH	2.03	0.58
1:C:96:ARG:HG2	1:C:183:GLN:HB2	1.84	0.58
1:A:63:THR:CG2	1:A:108:THR:HG21	2.34	0.58
1:C:28:SER:CB	1:C:50:THR:HG23	2.30	0.57
1:C:92:TYR:HA	1:C:188:ILE:HG13	1.85	0.57
1:A:13:PRO:O	1:A:118:THR:HG23	2.04	0.57
1:B:161:ILE:CG1	1:B:185:ASN:HB2	2.34	0.57
1:C:7:LEU:N	1:C:7:LEU:HD12	2.20	0.57
1:C:21:ASP:N	1:C:125:LEU:O	2.36	0.57
1:A:171:ILE:N	1:A:175:SER:O	2.30	0.57
1:B:47:ILE:CD1	1:B:49:THR:HG22	2.35	0.57
1:A:156:LYS:O	1:A:159:ASN:N	2.38	0.57
1:C:96:ARG:HA	1:C:182:TYR:O	2.04	0.57
1:A:96:ARG:HG2	1:A:183:GLN:HB2	1.87	0.57
1:A:48:SER:OG	1:A:51:GLY:O	2.23	0.57
1:A:171:ILE:HB	1:A:175:SER:O	2.05	0.57
1:A:48:SER:HB3	1:A:53:LEU:CD1	2.35	0.56
1:B:169:HIS:O	1:B:177:GLN:N	2.36	0.56
1:C:148:HIS:HD2	1:C:168:ARG:HH12	1.53	0.56
1:B:172:GLU:O	1:B:174:GLY:N	2.30	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:5:GLU:HA	1:C:85:LYS:HD2	1.88	0.56
1:C:154:ALA:HB2	1:C:161:ILE:CG2	2.35	0.56
1:A:205:SER:HA	1:A:221:LEU:O	2.05	0.56
1:B:186:THR:HG22	1:B:187:PRO:HD2	1.88	0.56
1:C:14:ILE:HG13	1:C:34:GLU:HA	1.85	0.56
1:A:92:TYR:CZ	1:A:112:VAL:HG21	2.40	0.56
1:C:10:GLY:O	1:C:12:VAL:HG23	2.06	0.56
1:C:154:ALA:CB	1:C:161:ILE:HG22	2.36	0.56
1:B:9:THR:HG23	1:B:10:GLY:H	1.69	0.56
1:A:61:VAL:O	1:A:66:CRO:HG13	2.06	0.56
1:B:41:LYS:HG3	1:B:223:PHE:CE1	2.40	0.56
1:B:98:ILE:HD12	1:B:106:TYR:HD2	1.71	0.56
1:C:85:LYS:O	1:C:88:MET:N	2.28	0.56
1:B:42:LEU:HB2	1:B:222:GLU:HG2	1.88	0.56
1:C:74:TYR:CG	1:C:82:ASP:HB3	2.41	0.56
1:A:81:HIS:HB3	1:A:196:PRO:HB3	1.88	0.56
1:C:95:GLU:N	1:C:184:GLN:O	2.28	0.56
1:C:220:LEU:HD23	1:C:220:LEU:O	2.05	0.56
1:B:57:TRP:HB2	1:B:58:PRO:HD3	1.88	0.56
1:C:2:SER:OG	1:C:3:LYS:N	2.39	0.56
1:C:18:LEU:HD23	1:C:29:VAL:HG21	1.85	0.56
1:C:80:ARG:HA	1:C:194:LEU:HD13	1.88	0.56
1:C:213:GLU:CG	1:C:215:ARG:H	2.19	0.55
1:B:169:HIS:O	1:B:176:VAL:HG12	2.07	0.55
1:C:31:GLY:HA3	1:C:46:PHE:CD2	2.42	0.55
1:A:41:LYS:HG3	1:A:223:PHE:CE1	2.41	0.55
1:B:51:GLY:O	1:B:52:LYS:C	2.45	0.55
1:C:88:MET:C	2:C:270:HOH:O	2.45	0.55
1:B:39:TYR:CD1	1:C:147:CYS:HB3	2.42	0.55
1:B:42:LEU:CD1	1:B:68:VAL:HG23	2.34	0.55
1:C:88:MET:HE2	1:C:88:MET:N	2.22	0.55
1:C:92:TYR:CA	1:C:188:ILE:HG13	2.36	0.55
1:A:3:LYS:O	1:A:6:GLU:HB2	2.07	0.55
1:A:63:THR:HG21	1:A:108:THR:HG21	1.89	0.55
1:C:18:LEU:N	1:C:29:VAL:O	2.29	0.55
1:A:42:LEU:HD12	1:A:222:GLU:CB	2.37	0.55
1:C:18:LEU:HA	1:C:29:VAL:HG23	1.89	0.55
1:C:148:HIS:CD2	1:C:168:ARG:NH1	2.75	0.54
1:B:57:TRP:N	1:B:58:PRO:HD2	2.22	0.54
1:C:136:ILE:HD12	1:C:136:ILE:N	2.22	0.54
1:C:160:GLY:HA3	1:C:185:ASN:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:MET:HE1	1:A:226:ALA:HB1	1.89	0.54
1:C:213:GLU:CD	1:C:215:ARG:H	2.10	0.54
1:C:82:ASP:OD2	1:C:85:LYS:HE2	2.08	0.54
1:C:150:VAL:O	1:C:200:TYR:HB2	2.08	0.54
1:B:164:ASN:HB2	2:B:239:HOH:O	2.08	0.54
1:C:112:VAL:CB	1:C:121:ASN:HB3	2.21	0.54
1:C:150:VAL:HG23	1:C:201:LEU:O	2.08	0.54
1:C:89:PRO:N	2:C:270:HOH:O	2.40	0.54
1:B:221:LEU:HB2	2:B:274:HOH:O	2.07	0.54
1:C:101:LYS:N	1:C:177:GLN:HE21	2.06	0.54
1:A:161:ILE:CG1	1:A:185:ASN:HB2	2.37	0.53
1:B:95:GLU:HA	1:B:108:THR:O	2.08	0.53
1:C:183:GLN:NE2	1:C:185:ASN:OD1	2.31	0.53
1:A:22:VAL:O	1:A:25:HIS:N	2.28	0.53
1:A:150:VAL:O	1:A:200:TYR:HA	2.08	0.53
1:C:46:PHE:C	1:C:47:ILE:HG13	2.29	0.53
1:A:155:ASP:O	1:A:159:ASN:N	2.39	0.53
1:B:93:VAL:HG22	1:B:111:GLU:CG	2.38	0.53
1:B:171:ILE:O	1:B:172:GLU:C	2.45	0.53
1:C:146:ASN:ND2	1:C:168:ARG:O	2.38	0.53
1:A:2:SER:O	1:A:3:LYS:C	2.45	0.53
1:A:16:VAL:HG22	1:A:121:ASN:HB3	1.90	0.53
1:B:214:LYS:O	1:B:215:ARG:O	2.26	0.53
1:C:95:GLU:O	1:C:184:GLN:N	2.26	0.53
1:C:16:VAL:O	1:C:17:GLU:OE1	2.27	0.53
1:C:114:PHE:HA	1:C:118:THR:O	2.09	0.53
1:B:171:ILE:HG12	1:B:176:VAL:C	2.29	0.53
1:C:55:VAL:HG12	1:C:136:ILE:HG23	1.91	0.53
1:C:171:ILE:HD11	1:C:177:GLN:CB	2.39	0.53
1:A:115:GLU:OE1	1:A:122:ARG:NH1	2.39	0.53
1:B:89:PRO:O	1:B:90:GLU:C	2.47	0.53
1:A:43:THR:HG22	1:A:221:LEU:HD13	1.91	0.52
1:A:53:LEU:N	1:A:216:ASP:OD2	2.31	0.52
1:B:9:THR:HG23	1:B:10:GLY:N	2.24	0.52
1:C:73:ARG:O	1:C:75:PRO:HD3	2.08	0.52
1:C:146:ASN:HB2	1:C:148:HIS:CE1	2.45	0.52
1:B:20:GLY:HA3	1:B:27:PHE:CE1	2.45	0.52
1:C:170:ASN:HA	1:C:176:VAL:CG2	2.39	0.52
1:A:15:LEU:HD23	1:A:32:GLU:HA	1.92	0.52
1:B:203:THR:HG23	1:B:224:VAL:CG2	2.40	0.52
1:C:4:GLY:C	1:C:7:LEU:HD13	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:69:GLN:HB2	1:C:84:PHE:CE1	2.45	0.52
1:C:96:ARG:HG2	1:C:183:GLN:CB	2.38	0.52
1:A:101:LYS:NZ	1:A:102:ASP:OD2	2.27	0.52
1:B:171:ILE:HD11	1:B:177:GLN:CB	2.40	0.52
1:C:95:GLU:O	1:C:183:GLN:HA	2.10	0.52
1:B:4:GLY:O	1:B:7:LEU:HB2	2.11	0.51
1:C:74:TYR:CD1	1:C:82:ASP:HB3	2.45	0.51
1:C:153:MET:HG2	1:C:154:ALA:N	2.25	0.51
1:A:28:SER:HB3	2:A:259:HOH:O	2.10	0.51
1:A:48:SER:C	1:A:50:THR:H	2.12	0.51
1:B:4:GLY:HA3	1:B:85:LYS:O	2.10	0.51
1:A:219:VAL:HG12	1:A:219:VAL:O	2.10	0.51
1:C:55:VAL:O	1:C:139:HIS:HE1	1.92	0.51
1:B:173:ASP:OD1	1:B:175:SER:N	2.43	0.51
1:C:96:ARG:NE	1:C:183:GLN:OE1	2.41	0.51
1:B:223:PHE:CE2	1:C:223:PHE:CE2	2.98	0.51
1:B:175:SER:C	1:B:176:VAL:HG22	2.30	0.51
1:B:214:LYS:O	1:B:215:ARG:C	2.49	0.51
1:C:7:LEU:HD22	1:C:88:MET:HB3	1.92	0.51
1:C:96:ARG:NH2	1:C:183:GLN:OE1	2.41	0.51
1:A:69:GLN:O	1:A:72:SER:OG	2.28	0.51
1:A:141:LEU:N	1:A:141:LEU:HD23	2.24	0.51
1:B:62:THR:HG23	1:B:145:TYR:OH	2.11	0.51
1:C:66:CRO:N2	1:C:66:CRO:CG1	2.74	0.51
1:C:111:GLU:CG	1:C:188:ILE:HD11	2.20	0.51
1:C:112:VAL:CG2	1:C:119:LEU:HD21	2.41	0.51
1:B:197:ASP:O	1:B:198:ASN:O	2.28	0.51
1:A:32:GLU:HG3	1:A:32:GLU:O	2.10	0.50
1:C:210:ASP:O	1:C:212:ASN:N	2.44	0.50
1:A:171:ILE:HG22	1:A:173:ASP:H	1.75	0.50
1:A:171:ILE:N	1:A:171:ILE:HD13	2.25	0.50
1:B:17:GLU:O	1:B:123:ILE:N	2.29	0.50
1:C:110:ALA:HB2	1:C:123:ILE:HA	1.93	0.50
1:C:36:ASP:OD1	1:C:38:THR:OG1	2.28	0.50
1:C:150:VAL:HG13	1:C:165:PHE:CE1	2.47	0.50
1:A:128:ILE:O	1:A:128:ILE:HG12	2.06	0.50
1:A:214:LYS:O	1:A:215:ARG:O	2.30	0.50
1:B:30:SER:O	1:B:46:PHE:HA	2.12	0.50
1:B:73:ARG:O	1:B:225:THR:HG23	2.12	0.50
1:C:96:ARG:CG	1:C:183:GLN:HB2	2.42	0.50
1:B:101:LYS:O	1:B:102:ASP:C	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:61:VAL:HG22	1:C:218:MET:CE	2.42	0.49
1:B:27:PHE:CD1	1:B:27:PHE:N	2.80	0.49
1:B:197:ASP:C	1:B:198:ASN:O	2.49	0.49
1:B:30:SER:HB2	1:B:47:ILE:CD1	2.42	0.49
1:B:171:ILE:HB	1:B:175:SER:O	2.12	0.49
1:C:37:ALA:O	1:C:40:GLY:N	2.43	0.49
1:B:36:ASP:OD1	1:B:36:ASP:O	2.29	0.49
1:B:96:ARG:HB2	1:B:108:THR:OG1	2.12	0.49
1:C:92:TYR:N	1:C:92:TYR:CD2	2.80	0.49
1:C:111:GLU:O	1:C:121:ASN:HB2	2.12	0.49
1:A:18:LEU:HD12	1:A:19:ASP:N	2.27	0.49
1:B:147:CYS:HA	1:B:203:THR:O	2.12	0.49
1:B:164:ASN:O	1:B:165:PHE:HB3	2.12	0.49
1:C:29:VAL:CG1	1:C:57:TRP:CH2	2.96	0.49
1:A:55:VAL:HG12	1:A:136:ILE:HG22	1.94	0.49
1:C:83:PHE:CE1	1:C:193:VAL:HG11	2.48	0.49
1:A:58:PRO:O	1:A:169:HIS:HE1	1.96	0.48
1:A:115:GLU:OE2	1:A:120:VAL:HG11	2.13	0.48
1:A:214:LYS:O	1:A:215:ARG:C	2.50	0.48
1:C:110:ALA:CB	1:C:123:ILE:HG23	2.34	0.48
1:A:125:LEU:C	1:A:125:LEU:HD23	2.33	0.48
1:A:135:ASN:HB2	1:A:141:LEU:HD21	1.94	0.48
1:C:127:GLY:O	1:C:128:ILE:HG23	2.13	0.48
1:A:221:LEU:HD21	1:A:223:PHE:CZ	2.48	0.48
1:B:51:GLY:O	1:B:52:LYS:O	2.31	0.48
1:B:109:ARG:HH11	1:B:109:ARG:CG	2.20	0.48
1:B:92:TYR:HB2	1:B:186:THR:O	2.14	0.48
1:B:173:ASP:C	1:B:175:SER:H	2.16	0.48
1:C:93:VAL:HG12	1:C:93:VAL:O	2.13	0.48
1:C:93:VAL:CG1	1:C:186:THR:HG22	2.43	0.48
1:C:27:PHE:HA	1:C:50:THR:HG21	1.95	0.48
1:C:7:LEU:CD1	1:C:7:LEU:N	2.77	0.48
1:C:17:GLU:OE1	1:C:30:SER:OG	2.29	0.48
1:C:28:SER:N	1:C:50:THR:CG2	2.77	0.48
1:C:215:ARG:C	1:C:217:HIS:HD1	2.16	0.48
1:C:3:LYS:CG	1:C:4:GLY:N	2.75	0.48
1:C:74:TYR:HD2	1:C:78:MET:O	1.97	0.48
1:A:56:PRO:HG3	1:A:139:HIS:HA	1.95	0.47
1:A:135:ASN:HB3	1:A:140:LYS:HB2	1.96	0.47
1:A:169:HIS:CD2	1:A:179:ALA:HB2	2.48	0.47
1:B:128:ILE:CG2	1:B:129:ASP:N	2.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:7:LEU:HD21	1:C:89:PRO:CD	2.27	0.47
1:C:147:CYS:HA	1:C:203:THR:O	2.14	0.47
1:A:131:LYS:O	1:A:133:ASP:N	2.47	0.47
1:C:78:MET:HE3	1:C:78:MET:HB3	1.62	0.47
1:C:98:ILE:CG2	1:C:181:HIS:CE1	2.98	0.47
1:A:17:GLU:O	1:A:123:ILE:HD12	2.14	0.47
1:A:47:ILE:HG23	1:A:217:HIS:HB3	1.96	0.47
1:C:45:LYS:CG	1:C:46:PHE:N	2.76	0.47
1:C:99:PHE:CE1	1:C:182:TYR:CD2	3.00	0.47
1:B:57:TRP:O	1:B:58:PRO:C	2.51	0.47
1:C:60:LEU:CB	1:C:64:LEU:HD12	2.45	0.47
1:C:128:ILE:HD12	1:C:128:ILE:C	2.35	0.47
1:C:76:ASP:O	1:C:79:LYS:HG3	2.15	0.47
1:C:171:ILE:CD1	1:C:177:GLN:N	2.78	0.47
1:A:47:ILE:HG23	1:A:217:HIS:CB	2.44	0.47
1:A:131:LYS:C	1:A:137:LEU:HD12	2.35	0.47
1:B:143:TYR:O	1:B:144:ASN:HB3	2.15	0.47
1:C:3:LYS:CG	1:C:4:GLY:H	2.23	0.47
1:C:88:MET:N	1:C:88:MET:CE	2.77	0.47
1:A:16:VAL:HG12	1:A:17:GLU:N	2.29	0.47
1:A:68:VAL:O	1:A:68:VAL:HG23	2.14	0.47
1:A:102:ASP:O	1:A:131:LYS:HE3	2.14	0.47
1:B:167:ILE:HB	1:B:179:ALA:HB3	1.96	0.47
1:C:131:LYS:C	1:C:134:GLY:H	2.17	0.47
1:C:225:THR:HG22	1:C:226:ALA:N	2.29	0.47
1:A:213:GLU:OE1	1:A:213:GLU:HA	2.14	0.47
1:B:15:LEU:O	1:B:120:VAL:HA	2.14	0.47
1:B:36:ASP:OD1	1:B:39:TYR:N	2.47	0.47
1:C:18:LEU:HG	1:C:19:ASP:N	2.30	0.47
1:A:20:GLY:HA2	1:A:125:LEU:O	2.15	0.47
1:C:8:PHE:CD2	1:C:85:LYS:CG	2.98	0.47
1:C:61:VAL:HG22	1:C:218:MET:HE1	1.97	0.47
1:B:215:ARG:O	1:B:216:ASP:C	2.53	0.47
1:C:78:MET:HE1	1:C:199:HIS:CD2	2.50	0.47
1:C:161:ILE:CG2	1:C:196:PRO:HG2	2.37	0.47
1:A:57:TRP:N	1:A:58:PRO:CD	2.77	0.46
1:A:66:CRO:N2	1:A:66:CRO:CG1	2.77	0.46
1:C:174:GLY:HA2	2:C:256:HOH:O	2.15	0.46
1:C:47:ILE:HG23	1:C:217:HIS:HB3	1.97	0.46
1:B:45:LYS:HE3	1:B:47:ILE:HG23	1.98	0.46
1:C:170:ASN:ND2	2:C:271:HOH:O	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:213:GLU:CD	1:C:215:ARG:HA	2.36	0.46
1:B:57:TRP:N	1:B:58:PRO:CD	2.78	0.46
1:C:27:PHE:CD1	1:C:54:PRO:HG2	2.49	0.46
1:A:56:PRO:HD3	1:A:136:ILE:O	2.14	0.46
1:A:92:TYR:CZ	1:A:112:VAL:CG2	2.99	0.46
1:C:19:ASP:HA	1:C:27:PHE:O	2.16	0.46
1:C:44:LEU:HD12	1:C:220:LEU:CD2	2.46	0.46
1:A:165:PHE:O	1:A:181:HIS:HB2	2.16	0.46
1:B:132:GLU:CA	1:B:137:LEU:HD12	2.36	0.46
1:C:22:VAL:CG1	1:C:130:PHE:CE1	2.98	0.46
1:C:194:LEU:N	1:C:194:LEU:HD23	2.31	0.46
1:C:48:SER:O	1:C:48:SER:OG	2.29	0.46
1:B:1:MET:HE3	2:B:257:HOH:O	2.15	0.46
1:C:143:TYR:CZ	1:C:209:LYS:HE2	2.51	0.46
1:A:43:THR:CG2	1:A:221:LEU:HD13	2.45	0.46
1:C:23:ASN:O	1:C:25:HIS:HD2	1.99	0.46
1:A:221:LEU:CG	1:A:223:PHE:CE2	2.99	0.45
1:B:81:HIS:HB3	1:B:196:PRO:HB3	1.98	0.45
1:B:220:LEU:C	1:B:220:LEU:HD23	2.37	0.45
1:A:73:ARG:HG2	1:A:73:ARG:HH11	1.80	0.45
1:A:125:LEU:HD23	1:A:126:LYS:N	2.31	0.45
1:A:163:VAL:HB	1:A:183:GLN:HG2	1.98	0.45
1:C:4:GLY:O	1:C:7:LEU:N	2.47	0.45
1:C:75:PRO:O	1:C:78:MET:N	2.49	0.45
1:C:103:ASP:OD1	1:C:131:LYS:N	2.48	0.45
1:C:152:ILE:HG21	1:C:161:ILE:HD13	1.98	0.45
1:A:16:VAL:CG1	1:A:17:GLU:N	2.79	0.45
1:B:142:GLU:CD	1:B:144:ASN:HD21	2.20	0.45
1:C:37:ALA:HB2	1:C:71:PHE:HA	1.98	0.45
1:C:81:HIS:O	1:C:83:PHE:N	2.49	0.45
1:A:202:SER:O	1:A:224:VAL:HA	2.17	0.45
1:B:47:ILE:HD13	1:B:49:THR:HG22	1.97	0.45
1:B:75:PRO:HD2	1:B:78:MET:HG3	1.98	0.45
1:A:14:ILE:HG22	1:A:15:LEU:N	2.32	0.45
1:B:13:PRO:HB2	1:B:118:THR:HG23	1.99	0.45
1:B:142:GLU:OE1	1:B:170:ASN:HB3	2.17	0.45
1:B:167:ILE:HG22	1:B:168:ARG:N	2.31	0.45
1:B:220:LEU:HG	1:B:221:LEU:N	2.32	0.45
1:B:3:LYS:O	1:B:6:GLU:HB2	2.16	0.45
1:B:14:ILE:CG2	1:B:15:LEU:N	2.80	0.45
1:B:128:ILE:HG22	1:B:129:ASP:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:PHE:CD2	1:C:85:LYS:CD	2.98	0.45
1:C:28:SER:H	1:C:50:THR:CG2	2.29	0.45
1:C:75:PRO:HD2	1:C:226:ALA:HB3	1.99	0.45
1:C:103:ASP:OD1	1:C:130:PHE:HA	2.16	0.45
1:A:112:VAL:HA	1:A:120:VAL:O	2.16	0.45
1:A:215:ARG:H	1:A:215:ARG:HG3	1.57	0.45
1:B:186:THR:HA	1:B:187:PRO:HD3	1.66	0.45
1:C:23:ASN:O	1:C:25:HIS:N	2.41	0.45
1:C:74:TYR:CD2	1:C:82:ASP:HB3	2.52	0.45
1:C:214:LYS:N	1:C:214:LYS:CD	2.79	0.45
1:A:15:LEU:HD23	1:A:15:LEU:HA	1.85	0.45
1:A:171:ILE:HD12	1:A:171:ILE:HA	1.73	0.45
1:C:91:GLY:HA3	1:C:112:VAL:O	2.17	0.45
1:C:225:THR:CG2	1:C:226:ALA:N	2.80	0.45
1:A:172:GLU:C	1:A:174:GLY:H	2.20	0.45
1:B:161:ILE:HG13	1:B:185:ASN:HB2	1.99	0.45
1:C:80:ARG:O	1:C:194:LEU:HD13	2.17	0.45
1:C:113:LYS:N	1:C:113:LYS:CD	2.80	0.44
1:A:205:SER:HB3	1:A:222:GLU:HG2	2.00	0.44
1:C:29:VAL:HG12	1:C:57:TRP:HH2	1.81	0.44
1:C:81:HIS:ND1	1:C:81:HIS:N	2.63	0.44
1:B:23:ASN:N	1:B:23:ASN:HD22	2.15	0.44
1:C:70:CYS:HA	1:C:84:PHE:CB	2.47	0.44
1:C:88:MET:HG3	1:C:114:PHE:CD2	2.52	0.44
1:C:91:GLY:N	1:C:113:LYS:HB3	2.33	0.44
1:A:88:MET:CE	1:A:112:VAL:HG23	2.48	0.44
1:A:186:THR:HA	1:A:187:PRO:HD3	1.67	0.44
1:C:110:ALA:CB	1:C:123:ILE:HG12	2.47	0.44
1:C:42:LEU:HD12	1:C:44:LEU:CD1	2.48	0.44
1:C:92:TYR:C	1:C:188:ILE:HG13	2.38	0.44
1:C:171:ILE:HD11	1:C:177:GLN:N	2.32	0.44
1:A:55:VAL:HG12	1:A:136:ILE:CG2	2.47	0.44
1:B:96:ARG:HA	1:B:182:TYR:O	2.18	0.44
1:B:210:ASP:O	1:B:213:GLU:N	2.29	0.44
1:C:193:VAL:CG1	1:C:194:LEU:N	2.80	0.44
1:B:30:SER:HB2	1:B:47:ILE:HD11	2.00	0.44
1:C:104:GLY:CA	1:C:130:PHE:CD2	2.99	0.44
1:C:213:GLU:CG	1:C:217:HIS:ND1	2.79	0.44
1:A:142:GLU:HG2	1:A:170:ASN:O	2.18	0.44
1:C:110:ALA:HB2	1:C:123:ILE:CB	2.48	0.44
1:A:80:ARG:HD2	1:A:80:ARG:HA	1.69	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:ILE:CG2	1:A:217:HIS:CB	2.95	0.43
1:C:56:PRO:HD2	1:C:59:THR:HG21	1.99	0.43
1:C:110:ALA:HB2	1:C:123:ILE:CA	2.48	0.43
1:C:154:ALA:HB2	1:C:161:ILE:HA	2.00	0.43
1:A:151:TYR:CD1	1:A:200:TYR:HB3	2.54	0.43
1:C:11:VAL:HG13	1:C:12:VAL:N	2.33	0.43
1:C:22:VAL:HA	1:C:127:GLY:O	2.18	0.43
1:C:56:PRO:O	1:C:57:TRP:C	2.53	0.43
1:C:163:VAL:HG12	1:C:164:ASN:N	2.34	0.43
1:A:132:GLU:HA	1:A:137:LEU:HD13	2.00	0.43
1:B:29:VAL:HG21	1:B:57:TRP:HZ3	1.81	0.43
1:C:42:LEU:HD22	1:C:42:LEU:HA	1.75	0.43
1:C:92:TYR:HB2	1:C:186:THR:O	2.17	0.43
1:A:76:ASP:O	1:A:79:LYS:HG2	2.19	0.43
1:A:221:LEU:CD1	1:A:223:PHE:CZ	2.98	0.43
1:B:7:LEU:HD23	1:B:7:LEU:HA	1.80	0.43
1:B:206:ALA:HB3	1:B:221:LEU:HB2	2.01	0.43
1:B:215:ARG:H	1:B:215:ARG:HG3	1.42	0.43
1:C:88:MET:SD	1:C:91:GLY:HA2	2.58	0.43
1:C:98:ILE:HG23	1:C:181:HIS:CE1	2.54	0.43
1:C:213:GLU:HG2	1:C:217:HIS:CG	2.53	0.43
1:B:53:LEU:HD12	1:B:53:LEU:HA	1.89	0.43
1:B:171:ILE:HD11	1:B:177:GLN:HB3	2.01	0.43
1:C:66:CRO:N2	1:C:66:CRO:HD1	2.34	0.43
1:A:161:ILE:HG12	1:A:185:ASN:HB2	2.01	0.43
1:B:41:LYS:HG3	1:B:223:PHE:CD1	2.53	0.43
1:B:210:ASP:O	1:B:211:PRO:C	2.57	0.43
1:C:29:VAL:HG11	1:C:57:TRP:CH2	2.54	0.43
1:A:94:GLN:N	1:A:110:ALA:O	2.35	0.42
1:B:73:ARG:O	1:B:75:PRO:HD3	2.19	0.42
1:B:149:ASN:HA	1:B:201:LEU:O	2.19	0.42
1:B:171:ILE:HD11	1:B:177:GLN:HB2	1.99	0.42
1:C:7:LEU:CD1	1:C:7:LEU:H	2.32	0.42
1:C:83:PHE:CD1	1:C:193:VAL:CG1	2.99	0.42
1:C:96:ARG:HG2	1:C:183:GLN:CA	2.49	0.42
1:B:1:MET:HA	1:B:5:GLU:OE1	2.18	0.42
1:B:173:ASP:O	1:B:175:SER:N	2.52	0.42
1:C:57:TRP:CD2	1:C:218:MET:HB3	2.54	0.42
1:C:191:GLY:O	1:C:192:PRO:C	2.58	0.42
1:C:73:ARG:HB2	1:C:224:VAL:O	2.20	0.42
1:C:98:ILE:HG21	1:C:181:HIS:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:99:PHE:HB3	2:C:269:HOH:O	2.19	0.42
1:A:114:PHE:HA	1:A:118:THR:O	2.19	0.42
1:C:113:LYS:HD3	1:C:113:LYS:C	2.40	0.42
1:A:75:PRO:CG	1:A:78:MET:SD	3.08	0.42
1:A:210:ASP:HA	1:A:211:PRO:HD3	1.80	0.42
1:C:23:ASN:OD1	1:C:23:ASN:N	2.53	0.42
1:A:13:PRO:C	1:A:118:THR:HG23	2.40	0.42
1:A:53:LEU:HB2	1:A:216:ASP:OD2	2.20	0.42
1:A:130:PHE:HB3	1:A:137:LEU:HD11	2.01	0.42
1:B:74:TYR:HA	1:B:226:ALA:HB3	2.01	0.42
1:B:207:LEU:HD23	1:B:207:LEU:HA	1.82	0.42
1:A:135:ASN:CB	1:A:140:LYS:HB2	2.50	0.42
1:C:70:CYS:HA	2:C:260:HOH:O	2.18	0.42
1:A:14:ILE:CG2	1:A:15:LEU:N	2.82	0.41
1:A:63:THR:HG23	1:A:108:THR:HG21	2.02	0.41
1:A:78:MET:CE	1:A:226:ALA:HB1	2.50	0.41
1:C:60:LEU:HB2	1:C:64:LEU:HD12	2.01	0.41
1:C:138:GLY:O	1:C:139:HIS:HB2	2.20	0.41
1:C:148:HIS:N	1:C:203:THR:O	2.50	0.41
1:B:147:CYS:HG	1:B:204:CYS:HB3	1.84	0.41
1:B:152:ILE:HD11	1:B:201:LEU:HD11	2.03	0.41
1:C:195:LEU:HD23	1:C:195:LEU:HA	1.79	0.41
1:A:22:VAL:HG22	1:A:127:GLY:HA3	2.02	0.41
1:B:14:ILE:CD1	1:B:42:LEU:CD2	2.98	0.41
1:C:70:CYS:C	2:C:260:HOH:O	2.57	0.41
1:A:70:CYS:HA	1:A:84:PHE:HB2	2.03	0.41
1:A:22:VAL:O	1:A:25:HIS:HB2	2.20	0.41
1:A:204:CYS:O	1:A:222:GLU:HA	2.21	0.41
1:C:74:TYR:CE1	1:C:82:ASP:CB	3.04	0.41
1:C:96:ARG:CG	1:C:183:GLN:CB	2.98	0.41
1:B:12:VAL:HA	1:B:13:PRO:HD2	1.77	0.41
1:C:121:ASN:HB2	1:C:122:ARG:H	1.76	0.41
1:C:190:ASP:OD2	1:C:190:ASP:N	2.54	0.41
1:A:41:LYS:HG3	1:A:223:PHE:HE1	1.82	0.41
1:A:93:VAL:O	1:A:185:ASN:HA	2.21	0.41
1:A:135:ASN:CA	1:A:140:LYS:HB2	2.50	0.41
1:B:115:GLU:HB2	1:B:120:VAL:HG11	1.95	0.41
1:B:186:THR:HG22	1:B:187:PRO:CD	2.49	0.41
1:A:73:ARG:NH1	1:A:73:ARG:CG	2.81	0.41
1:A:131:LYS:O	1:A:132:GLU:C	2.59	0.41
1:B:206:ALA:HB3	1:B:221:LEU:CB	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:131:LYS:O	1:C:137:LEU:HD12	2.21	0.41
1:A:96:ARG:HB2	1:A:108:THR:OG1	2.22	0.40
1:B:173:ASP:C	1:B:175:SER:N	2.75	0.40
1:B:186:THR:CG2	1:B:187:PRO:CD	2.99	0.40
1:C:4:GLY:O	1:C:7:LEU:HD13	2.21	0.40
1:C:8:PHE:CG	1:C:85:LYS:HD3	2.57	0.40
1:C:60:LEU:HA	2:C:262:HOH:O	2.21	0.40
1:C:130:PHE:HB3	1:C:137:LEU:CD1	2.26	0.40
1:C:210:ASP:H	1:C:217:HIS:CD2	2.39	0.40
1:A:105:ASN:O	1:A:127:GLY:HA2	2.21	0.40
1:C:103:ASP:CG	1:C:104:GLY:H	2.22	0.40
1:C:154:ALA:CB	1:C:161:ILE:CG2	2.98	0.40
1:A:169:HIS:O	1:A:177:GLN:N	2.53	0.40
1:A:221:LEU:HD21	1:A:223:PHE:CE2	2.57	0.40
1:B:171:ILE:N	1:B:175:SER:O	2.47	0.40
1:C:14:ILE:HG23	1:C:119:LEU:O	2.22	0.40
1:A:158:LYS:O	1:A:159:ASN:HB3	2.21	0.40
1:C:99:PHE:HE1	1:C:182:TYR:HD2	1.68	0.40
1:C:99:PHE:HA	1:C:105:ASN:HB2	2.03	0.40
1:A:44:LEU:HD23	1:A:44:LEU:HA	1.85	0.40
1:B:167:ILE:CG2	1:B:168:ARG:N	2.84	0.40
1:C:23:ASN:HD21	1:C:130:PHE:N	2.02	0.40
1:C:31:GLY:HA3	1:C:46:PHE:HD2	1.86	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	221/236 (94%)	200 (90%)	17 (8%)	4 (2%)	8	3
1	B	221/236 (94%)	190 (86%)	20 (9%)	11 (5%)	2	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	221/236 (94%)	182 (82%)	31 (14%)	8 (4%)	3	1
All	All	663/708 (94%)	572 (86%)	68 (10%)	23 (4%)	3	1

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	21	ASP
1	B	52	LYS
1	B	135	ASN
1	B	173	ASP
1	B	215	ARG
1	C	82	ASP
1	A	132	GLU
1	A	215	ARG
1	B	76	ASP
1	B	211	PRO
1	C	52	LYS
1	C	104	GLY
1	C	158	LYS
1	C	159	ASN
1	A	156	LYS
1	B	199	HIS
1	A	143	TYR
1	B	198	ASN
1	C	76	ASP
1	C	156	LYS
1	B	84	PHE
1	B	192	PRO
1	C	20	GLY

### 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	184/206 (89%)	150 (82%)	34 (18%)	1	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	177/206 (86%)	144 (81%)	33 (19%)	1	0
1	C	172/206 (84%)	126 (73%)	46 (27%)	0	0
All	All	533/618 (86%)	420 (79%)	113 (21%)	1	0

All (113) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	21	ASP
1	A	27	PHE
1	A	32	GLU
1	A	47	ILE
1	A	72	SER
1	A	73	ARG
1	A	78	MET
1	A	80	ARG
1	A	84	PHE
1	A	86	SER
1	A	90	GLU
1	A	98	ILE
1	A	101	LYS
1	A	109	ARG
1	A	112	VAL
1	A	117	ASP
1	A	123	ILE
1	A	128	ILE
1	A	135	ASN
1	A	136	ILE
1	A	145	TYR
1	A	153	MET
1	A	156	LYS
1	A	162	LYS
1	A	171	ILE
1	A	176	VAL
1	A	177	GLN
1	A	190	ASP
1	A	195	LEU
1	A	202	SER
1	A	204	CYS
1	A	205	SER
1	A	219	VAL

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Mol	Chain	Res	Type
1	B	16	VAL
1	B	17	GLU
1	B	19	ASP
1	B	25	HIS
1	B	26	LYS
1	B	28	SER
1	B	29	VAL
1	B	32	GLU
1	B	36	ASP
1	B	38	THR
1	B	41	LYS
1	B	45	LYS
1	B	46	PHE
1	B	72	SER
1	B	78	MET
1	B	95	GLU
1	B	103	ASP
1	B	109	ARG
1	B	120	VAL
1	B	122	ARG
1	B	123	ILE
1	B	124	GLU
1	B	129	ASP
1	B	137	LEU
1	B	153	MET
1	B	155	ASP
1	B	175	SER
1	B	176	VAL
1	B	197	ASP
1	B	204	CYS
1	B	213	GLU
1	B	215	ARG
1	B	222	GLU
1	C	7	LEU
1	C	11	VAL
1	C	14	ILE
1	C	16	VAL
1	C	28	SER
1	C	29	VAL
1	C	30	SER
1	C	38	THR
1	C	41	LYS

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Mol	Chain	Res	Type
1	C	42	LEU
1	C	43	THR
1	C	46	PHE
1	C	47	ILE
1	C	49	THR
1	C	53	LEU
1	C	59	THR
1	C	70	CYS
1	C	73	ARG
1	C	78	MET
1	C	82	ASP
1	C	88	MET
1	C	92	TYR
1	C	97	THR
1	C	105	ASN
1	C	113	LYS
1	C	118	THR
1	C	119	LEU
1	C	120	VAL
1	C	121	ASN
1	C	123	ILE
1	C	125	LEU
1	C	133	ASP
1	C	142	GLU
1	C	152	ILE
1	C	153	MET
1	C	161	ILE
1	C	176	VAL
1	C	184	GLN
1	C	190	ASP
1	C	194	LEU
1	C	201	LEU
1	C	204	CYS
1	C	215	ARG
1	C	218	MET
1	C	220	LEU
1	C	229	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	135	ASN

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Mol	Chain	Res	Type
1	A	169	HIS
1	A	198	ASN
1	B	146	ASN
1	B	149	ASN
1	B	181	HIS
1	C	25	HIS
1	C	105	ASN
1	C	139	HIS
1	C	149	ASN
1	C	177	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues 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
1	CRO	A	66	1	23,23,24	2.65	8 (34%)	30,32,34	2.22	10 (33%)
1	CRO	C	66	1	23,23,24	2.55	10 (43%)	30,32,34	1.52	8 (26%)
1	CRO	B	66	1	23,23,24	2.33	8 (34%)	30,32,34	2.20	10 (33%)

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
1	CRO	A	66	1	-	0/12/31/32	0/2/2/2
1	CRO	C	66	1	-	1/12/31/32	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CRO	B	66	1	-	3/12/31/32	0/2/2/2

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	66	CRO	CB2-CA2	7.50	1.41	1.35
1	C	66	CRO	CE1-CZ	5.93	1.50	1.38
1	A	66	CRO	OH-CZ	-5.49	1.24	1.37
1	B	66	CRO	CE1-CZ	4.71	1.47	1.38
1	B	66	CRO	CB2-CA2	4.57	1.38	1.35
1	C	66	CRO	CG2-CB2	-4.55	1.38	1.46
1	B	66	CRO	OH-CZ	-4.51	1.26	1.37
1	A	66	CRO	C1-N3	4.37	1.44	1.37
1	B	66	CRO	CD1-CG2	4.21	1.47	1.39
1	C	66	CRO	OH-CZ	-4.12	1.27	1.37
1	C	66	CRO	CE2-CZ	4.08	1.46	1.38
1	A	66	CRO	CE1-CZ	3.98	1.46	1.38
1	C	66	CRO	C1-N3	3.77	1.43	1.37
1	B	66	CRO	CA3-N3	-3.49	1.40	1.47
1	C	66	CRO	CB2-CA2	3.30	1.37	1.35
1	B	66	CRO	CE2-CZ	2.80	1.44	1.38
1	C	66	CRO	CD2-CG2	2.79	1.44	1.39
1	B	66	CRO	CD2-CG2	2.69	1.44	1.39
1	A	66	CRO	CG2-CB2	-2.56	1.41	1.46
1	C	66	CRO	OG1-CB1	-2.49	1.36	1.43
1	A	66	CRO	CE2-CZ	2.46	1.43	1.38
1	C	66	CRO	CD1-CG2	2.43	1.44	1.39
1	C	66	CRO	CA3-N3	-2.37	1.42	1.47
1	B	66	CRO	C1-N3	2.33	1.41	1.37
1	A	66	CRO	CA2-C2	2.31	1.50	1.48
1	A	66	CRO	CD1-CG2	2.08	1.43	1.39

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	CRO	O2-C2-CA2	6.61	134.67	130.96
1	A	66	CRO	O2-C2-CA2	5.14	133.85	130.96
1	B	66	CRO	CA1-C1-N3	-4.58	119.26	124.75
1	A	66	CRO	CA2-C2-N3	4.40	105.45	103.37
1	A	66	CRO	CG2-CB2-CA2	4.39	135.33	129.94
1	C	66	CRO	C2-N3-C1	-3.93	105.98	107.97
1	A	66	CRO	C1-CA1-N1	-3.76	103.86	109.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	CRO	CE2-CZ-CE1	-2.93	114.83	119.77
1	A	66	CRO	C2-N3-C1	-2.86	106.52	107.97
1	B	66	CRO	CE2-CZ-CE1	-2.85	114.97	119.77
1	C	66	CRO	CE2-CZ-CE1	-2.83	114.99	119.77
1	B	66	CRO	CD1-CE1-CZ	2.75	122.89	119.88
1	B	66	CRO	CA2-C2-N3	2.70	104.65	103.37
1	A	66	CRO	OG1-CB1-CA1	2.70	114.81	109.04
1	B	66	CRO	CA1-C1-N2	2.55	127.46	123.89
1	B	66	CRO	CG2-CB2-CA2	2.54	133.06	129.94
1	A	66	CRO	CA2-N2-C1	2.52	107.63	105.77
1	C	66	CRO	CD1-CE1-CZ	2.42	122.53	119.88
1	A	66	CRO	CE2-CD2-CG2	2.36	124.33	121.25
1	C	66	CRO	CA2-C2-N3	2.35	104.48	103.37
1	B	66	CRO	N3-C1-N2	2.35	113.08	111.45
1	C	66	CRO	CG2-CB2-CA2	2.28	132.74	129.94
1	C	66	CRO	N3-C1-N2	2.24	113.01	111.45
1	B	66	CRO	CE2-CD2-CG2	2.20	124.11	121.25
1	B	66	CRO	O3-C3-CA3	-2.19	119.77	126.39
1	C	66	CRO	CA2-N2-C1	2.17	107.37	105.77
1	A	66	CRO	CA3-N3-C1	2.14	129.73	127.16
1	C	66	CRO	CA1-C1-N3	-2.09	122.23	124.75

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	66	CRO	C3-CA3-N3-C2
1	B	66	CRO	C1-CA1-CB1-CG1
1	B	66	CRO	N1-CA1-CB1-CG1
1	B	66	CRO	N1-CA1-CB1-OG1

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	66	CRO	4	0
1	C	66	CRO	4	0

## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 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	225/236 (95%)	1.17	34 (15%) 2 1	27, 42, 59, 71	0
1	B	225/236 (95%)	1.31	49 (21%) 0 0	30, 48, 67, 79	0
1	C	225/236 (95%)	2.06	97 (43%) 0 0	30, 56, 82, 98	0
All	All	675/708 (95%)	1.51	180 (26%) 0 0	27, 48, 72, 98	0

All (180) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	211	PRO	11.0
1	B	171	ILE	7.7
1	C	64	LEU	7.0
1	C	192	PRO	6.4
1	C	24	GLY	6.2
1	B	173	ASP	5.6
1	C	133	ASP	5.4
1	C	116	GLY	5.3
1	C	29	VAL	5.3
1	A	211	PRO	5.3
1	C	191	GLY	5.1
1	A	64	LEU	4.9
1	B	176	VAL	4.8
1	C	28	SER	4.7
1	C	128	ILE	4.7
1	C	190	ASP	4.6
1	C	27	PHE	4.5
1	C	130	PHE	4.5
1	C	212	ASN	4.4
1	C	137	LEU	4.4
1	C	134	GLY	4.4
1	C	50	THR	4.4
1	A	47	ILE	4.2

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Mol	Chain	Res	Type	RSRZ
1	C	23	ASN	4.2
1	C	63	THR	4.2
1	C	215	ARG	4.2
1	C	123	ILE	4.1
1	C	213	GLU	4.1
1	C	214	LYS	4.1
1	C	22	VAL	4.0
1	C	217	HIS	4.0
1	C	229	ILE	3.9
1	B	12	VAL	3.9
1	B	40	GLY	3.9
1	B	64	LEU	3.9
1	C	14	ILE	3.9
1	C	71	PHE	3.8
1	C	104	GLY	3.8
1	C	68	VAL	3.8
1	C	220	LEU	3.8
1	C	46	PHE	3.8
1	A	25	HIS	3.8
1	B	53	LEU	3.7
1	C	138	GLY	3.7
1	C	193	VAL	3.7
1	A	220	LEU	3.6
1	A	133	ASP	3.6
1	C	61	VAL	3.6
1	C	84	PHE	3.5
1	B	175	SER	3.5
1	C	26	LYS	3.4
1	A	117	ASP	3.4
1	B	197	ASP	3.4
1	C	186	THR	3.3
1	C	21	ASP	3.3
1	A	53	LEU	3.3
1	C	42	LEU	3.2
1	C	155	ASP	3.2
1	C	70	CYS	3.1
1	C	117	ASP	3.1
1	C	210	ASP	3.1
1	B	118	THR	3.1
1	C	119	LEU	3.1
1	A	68	VAL	3.1
1	B	220	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	8	PHE	3.1
1	B	76	ASP	3.1
1	C	125	LEU	3.1
1	B	128	ILE	3.1
1	B	212	ASN	3.0
1	C	20	GLY	3.0
1	C	175	SER	3.0
1	C	47	ILE	3.0
1	C	18	LEU	3.0
1	A	131	LYS	3.0
1	B	133	ASP	3.0
1	B	174	GLY	3.0
1	C	77	HIS	3.0
1	A	63	THR	2.9
1	C	98	ILE	2.9
1	B	63	THR	2.9
1	C	80	ARG	2.9
1	C	152	ILE	2.9
1	A	176	VAL	2.8
1	C	157	GLN	2.8
1	C	189	GLY	2.8
1	B	11	VAL	2.8
1	A	42	LEU	2.8
1	C	153	MET	2.8
1	C	218	MET	2.8
1	A	212	ASN	2.8
1	B	60	LEU	2.8
1	C	16	VAL	2.8
1	A	60	LEU	2.8
1	C	195	LEU	2.8
1	A	27	PHE	2.7
1	A	70	CYS	2.7
1	C	11	VAL	2.7
1	B	201	LEU	2.7
1	C	53	LEU	2.7
1	A	104	GLY	2.7
1	C	44	LEU	2.7
1	C	48	SER	2.6
1	A	98	ILE	2.6
1	C	88	MET	2.6
1	A	61	VAL	2.6
1	C	31	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	216	ASP	2.6
1	A	134	GLY	2.6
1	A	46	PHE	2.6
1	C	33	GLY	2.6
1	B	98	ILE	2.6
1	B	210	ASP	2.6
1	B	77	HIS	2.6
1	B	46	PHE	2.6
1	A	125	LEU	2.6
1	A	123	ILE	2.5
1	C	90	GLU	2.5
1	C	118	THR	2.5
1	A	214	LYS	2.5
1	C	25	HIS	2.5
1	B	140	LYS	2.5
1	B	61	VAL	2.5
1	A	173	ASP	2.5
1	B	22	VAL	2.5
1	A	224	VAL	2.5
1	C	40	GLY	2.5
1	B	42	LEU	2.4
1	B	78	MET	2.4
1	C	75	PRO	2.4
1	B	68	VAL	2.4
1	C	224	VAL	2.4
1	A	84	PHE	2.4
1	B	14	ILE	2.4
1	B	62	THR	2.4
1	C	55	VAL	2.4
1	C	13	PRO	2.4
1	B	38	THR	2.4
1	C	219	VAL	2.3
1	A	132	GLU	2.3
1	B	172	GLU	2.3
1	B	203	THR	2.3
1	C	156	LYS	2.3
1	A	18	LEU	2.3
1	B	18	LEU	2.3
1	B	211	PRO	2.3
1	C	127	GLY	2.3
1	B	223	PHE	2.3
1	C	136	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	108	THR	2.2
1	C	223	PHE	2.2
1	C	131	LYS	2.2
1	B	9	THR	2.2
1	C	62	THR	2.2
1	C	12	VAL	2.2
1	B	198	ASN	2.2
1	C	60	LEU	2.2
1	B	25	HIS	2.2
1	B	44	LEU	2.2
1	A	12	VAL	2.2
1	C	115	GLU	2.2
1	C	161	ILE	2.1
1	C	69	GLN	2.1
1	B	70	CYS	2.1
1	C	38	THR	2.1
1	A	22	VAL	2.1
1	A	92	TYR	2.1
1	C	79	LYS	2.1
1	C	204	CYS	2.1
1	C	32	GLU	2.1
1	B	143	TYR	2.1
1	B	51	GLY	2.1
1	A	72	SER	2.0
1	C	139	HIS	2.0
1	B	27	PHE	2.0
1	B	208	SER	2.0
1	C	201	LEU	2.0
1	C	203	THR	2.0
1	B	224	VAL	2.0
1	B	134	GLY	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CRO	C	66	22/23	0.88	0.29	26,43,56,56	0
1	CRO	B	66	22/23	0.92	0.26	23,33,54,77	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
1	CRO	A	66	22/23	0.94	0.27	21,32,43,49	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.