



# Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2WFF / pdb\_00002wff  
Title : Equine Rhinitis A Virus  
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Deposited on : 2009-04-05  
Resolution : 4.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

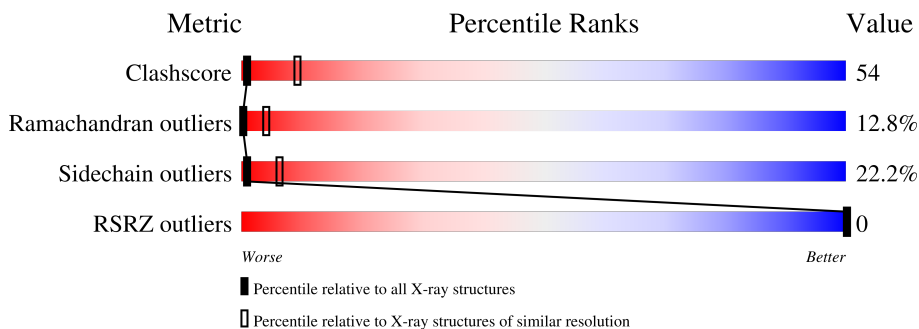
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.00 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	190562	1129 (4.20-3.80)
Ramachandran outliers	187476	1064 (4.20-3.80)
Sidechain outliers	187428	1055 (4.20-3.80)
RSRZ outliers	180081	1082 (4.20-3.80)

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	1	246	
2	2	230	
3	3	226	
4	4	80	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5506 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 P1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1	246	1929	1240	329	352	8	0	0	0

- Molecule 2 is a protein called P1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	2	219	1692	1081	290	314	7	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	21	VAL	ALA	conflict	UNP B9VV85
2	85	SER	GLY	conflict	UNP B9VV85

- Molecule 3 is a protein called P1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	3	226	1719	1107	280	326	6	0	0	0

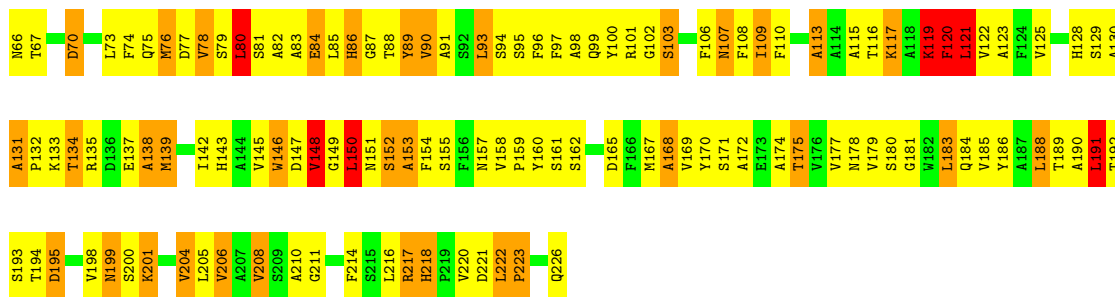
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	59	LYS	ARG	conflict	UNP B9VV85

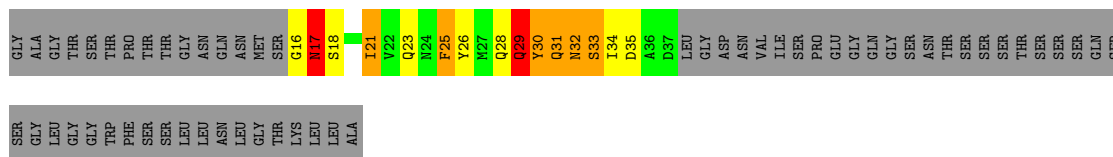
- Molecule 4 is a protein called P1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	4	22	166	101	29	35	1	0	0	1





- Molecule 4: P1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	314.00Å 497.80Å 556.50Å 90.00° 92.35° 90.00°	Depositor
Resolution (Å)	20.00 – 4.00 20.00 – 4.00	Depositor EDS
% Data completeness (in resolution range)	35.0 (20.00-4.00) 25.5 (20.00-4.00)	Depositor EDS
$R_{merge}$	0.44	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.33 (at 3.48Å)	Xtrriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.462 , (Not available) 0.449 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.4	Xtrriage
Anisotropy	0.097	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 349.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.35$ , $\langle L^2 \rangle = 0.17$	Xtrriage
Estimated twinning fraction	0.095 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.12	EDS
Total number of atoms	5506	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	10.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.87% 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 [i](#)

### 5.1 Standard geometry [i](#)

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	1	1.05	3/1993 (0.2%)	1.53	40/2721 (1.5%)
2	2	1.10	5/1746 (0.3%)	1.75	60/2397 (2.5%)
3	3	1.12	5/1769 (0.3%)	1.52	40/2420 (1.7%)
4	4	0.97	0/168	1.44	4/226 (1.8%)
All	All	1.08	13/5676 (0.2%)	1.60	144/7764 (1.9%)

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
3	3	0	2

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	3	120	PHE	N-CA	9.92	1.58	1.46
2	2	151	THR	CA-CB	6.99	1.64	1.53
1	1	225	PRO	CA-C	6.61	1.58	1.52
3	3	76	MET	SD-CE	-6.12	1.64	1.79
3	3	119	LYS	CE-NZ	6.06	1.67	1.49
3	3	139	MET	SD-CE	-5.75	1.65	1.79
1	1	116	THR	CA-CB	5.51	1.62	1.53
2	2	167	THR	CA-CB	5.37	1.62	1.53
1	1	218	MET	SD-CE	-5.34	1.66	1.79
2	2	148	PRO	CA-C	5.27	1.59	1.52
2	2	213	MET	SD-CE	-5.27	1.66	1.79
3	3	125	VAL	CA-C	-5.24	1.48	1.53
2	2	171	VAL	CA-C	-5.04	1.46	1.52

All (144) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	139	SER	CA-C-N	12.29	135.21	119.84
1	1	139	SER	C-N-CA	12.29	135.21	119.84
2	2	55	GLY	CA-C-N	11.10	131.38	119.05
2	2	55	GLY	C-N-CA	11.10	131.38	119.05
1	1	70	ARG	N-CA-C	-10.65	94.52	110.28
3	3	44	ILE	N-CA-C	-10.44	100.40	110.42
2	2	224	GLY	CA-C-N	10.36	130.28	120.03
2	2	224	GLY	C-N-CA	10.36	130.28	120.03
1	1	9	GLU	CA-C-N	10.28	132.69	119.84
1	1	9	GLU	C-N-CA	10.28	132.69	119.84
1	1	225	PRO	N-CA-C	10.12	123.04	110.70
1	1	242	ASN	N-CA-C	-9.88	100.47	111.14
3	3	96	PHE	N-CA-C	-9.57	101.61	113.28
3	3	149	GLY	N-CA-C	-9.54	90.58	113.18
2	2	216	ALA	CA-C-N	9.46	129.29	120.21
2	2	216	ALA	C-N-CA	9.46	129.29	120.21
2	2	138	LYS	N-CA-C	-9.32	99.23	111.71
1	1	20	SER	CA-C-N	9.03	131.13	119.84
1	1	20	SER	C-N-CA	9.03	131.13	119.84
1	1	235	THR	N-CA-C	8.95	123.69	110.17
1	1	191	HIS	N-CA-C	8.91	120.01	108.34
2	2	57	THR	N-CA-C	-8.80	98.20	110.35
2	2	62	TYR	N-CA-C	-8.61	96.13	108.96
2	2	46	THR	CB-CA-C	-8.56	100.36	111.40
2	2	184	THR	N-CA-C	8.39	121.33	108.42
3	3	120	PHE	CB-CA-C	-8.38	93.74	110.42
1	1	225	PRO	CA-C-N	8.16	130.04	119.84
1	1	225	PRO	C-N-CA	8.16	130.04	119.84
1	1	47	ASN	N-CA-C	-8.14	98.44	110.48
2	2	65	LYS	N-CA-C	-8.13	96.80	109.25
2	2	99	LYS	N-CA-C	-7.97	102.18	111.03
1	1	74	THR	N-CA-C	-7.95	102.86	114.39
4	4	25	PHE	N-CA-C	-7.91	102.65	111.28
2	2	48	SER	N-CA-C	-7.85	98.53	110.70
2	2	65	LYS	CA-C-N	7.84	130.50	120.70
2	2	65	LYS	C-N-CA	7.84	130.50	120.70
2	2	92	GLY	N-CA-C	7.77	131.60	113.18
2	2	158	PHE	CB-CA-C	-7.63	101.31	110.08
2	2	104	VAL	N-CA-C	7.57	118.98	107.77
1	1	156	PHE	N-CA-C	7.57	118.23	108.24
2	2	115	ASN	N-CA-C	7.49	122.03	108.17
2	2	129	VAL	N-CA-C	7.24	116.60	108.05
2	2	145	LEU	N-CA-C	-7.18	98.53	109.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	119	LYS	CA-C-O	-7.17	110.26	120.51
2	2	30	VAL	N-CA-C	-7.15	106.11	111.90
1	1	18	ALA	N-CA-C	7.10	125.93	110.80
3	3	208	VAL	N-CA-C	6.98	117.70	107.37
1	1	207	CYS	N-CA-C	6.95	125.60	110.80
2	2	204	GLY	CA-C-N	6.89	127.44	120.14
2	2	204	GLY	C-N-CA	6.89	127.44	120.14
1	1	167	VAL	N-CA-C	6.89	114.72	107.76
2	2	37	SER	N-CA-C	6.88	117.35	108.34
3	3	177	VAL	N-CA-C	6.83	121.63	113.22
3	3	180	SER	N-CA-C	-6.80	104.18	113.30
3	3	93	LEU	N-CA-C	-6.77	103.51	111.03
1	1	101	PHE	N-CA-C	-6.74	99.61	110.32
3	3	32	PRO	CA-C-N	6.74	127.13	119.92
3	3	32	PRO	C-N-CA	6.74	127.13	119.92
3	3	119	LYS	CB-CG-CD	6.71	126.73	111.30
3	3	168	ALA	N-CA-C	6.67	119.59	108.73
2	2	25	ASN	N-CA-C	-6.66	99.45	110.17
2	2	109	ASP	N-CA-C	-6.66	97.37	108.75
2	2	42	ARG	CA-C-N	6.65	127.22	120.38
2	2	42	ARG	C-N-CA	6.65	127.22	120.38
3	3	121	LEU	N-CA-C	6.63	119.20	108.32
3	3	70	ASP	N-CA-C	6.63	118.20	110.97
1	1	68	TRP	N-CA-C	-6.62	105.74	113.88
2	2	97	VAL	N-CA-C	6.60	116.73	110.53
2	2	175	MET	CA-C-N	6.58	128.06	119.84
2	2	175	MET	C-N-CA	6.58	128.06	119.84
3	3	183	LEU	N-CA-C	-6.55	97.68	108.76
3	3	119	LYS	CB-CA-C	6.54	123.43	110.42
2	2	46	THR	N-CA-C	6.41	120.34	111.55
2	2	226	LEU	CA-C-N	6.39	127.83	119.84
2	2	226	LEU	C-N-CA	6.39	127.83	119.84
1	1	43	LEU	N-CA-C	6.38	120.45	108.65
2	2	71	HIS	N-CA-C	6.34	120.81	112.13
2	2	73	GLN	N-CA-C	6.20	119.64	107.98
3	3	138	ALA	N-CA-C	6.20	118.12	111.36
3	3	55	SER	N-CA-C	6.17	119.20	109.39
1	1	56	VAL	N-CA-C	6.10	116.65	107.75
2	2	103	LEU	N-CA-C	6.08	119.44	109.72
1	1	21	PRO	N-CA-C	6.04	124.92	112.47
2	2	187	THR	N-CA-C	-5.99	105.28	112.59
3	3	125	VAL	CB-CA-C	-5.98	104.30	111.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	160	HIS	N-CA-C	5.96	115.88	108.19
2	2	24	ILE	CB-CA-C	-5.92	105.53	111.80
2	2	58	LEU	CA-CB-CG	5.91	136.99	116.30
2	2	100	ALA	N-CA-C	5.89	118.08	110.65
2	2	151	THR	N-CA-C	-5.88	104.21	111.33
3	3	11	SER	N-CA-C	5.88	123.33	110.80
3	3	21	ASN	N-CA-C	5.88	123.32	110.80
1	1	212	ARG	N-CA-C	-5.86	97.76	108.02
1	1	239	PHE	CB-CA-C	-5.80	102.18	109.31
4	4	32	ASN	CB-CA-C	-5.79	107.16	114.40
2	2	120	HIS	N-CA-C	5.78	117.81	108.34
3	3	117	LYS	N-CA-C	-5.78	100.28	109.23
3	3	80	LEU	N-CA-C	5.76	123.07	110.80
1	1	34	LEU	N-CA-C	5.65	120.29	113.17
2	2	23	ILE	N-CA-C	5.64	114.73	106.55
3	3	199	ASN	N-CA-C	5.63	118.70	107.62
2	2	106	ASN	N-CA-C	5.57	118.50	108.48
4	4	29	GLN	N-CA-C	-5.54	98.99	110.80
2	2	168	ASN	N-CA-C	5.54	122.59	110.80
3	3	56	ILE	CB-CA-C	-5.50	104.64	111.08
4	4	32	ASN	N-CA-C	5.50	117.05	109.29
1	1	203	ASP	N-CA-C	-5.49	102.06	110.14
2	2	116	ALA	N-CA-C	5.48	118.80	108.65
2	2	163	LEU	N-CA-C	-5.42	100.57	109.40
3	3	88	THR	N-CA-C	5.41	117.70	110.35
2	2	85	SER	N-CA-C	5.39	117.90	110.35
1	1	190	ALA	N-CA-C	-5.39	104.05	111.81
3	3	201	LYS	N-CA-C	5.37	118.46	110.14
1	1	237	HIS	N-CA-C	-5.36	100.97	109.76
3	3	119	LYS	CD-CE-NZ	5.35	129.02	111.90
1	1	224	ILE	CA-C-N	5.34	125.89	120.38
1	1	224	ILE	C-N-CA	5.34	125.89	120.38
2	2	151	THR	CB-CA-C	5.32	119.73	110.68
3	3	82	ALA	N-CA-C	-5.31	103.01	110.50
3	3	193	SER	N-CA-C	5.29	117.44	109.23
2	2	134	HIS	N-CA-C	5.29	122.06	110.80
1	1	232	ALA	N-CA-C	-5.27	100.65	109.24
1	1	52	PRO	N-CA-C	5.27	120.41	111.03
1	1	88	PHE	N-CA-C	5.26	122.01	110.80
2	2	104	VAL	CB-CA-C	-5.26	103.31	110.42
3	3	53	PHE	N-CA-C	5.25	117.30	109.59
3	3	64	VAL	CB-CA-C	-5.19	102.78	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	148	VAL	N-CA-C	-5.18	102.91	109.80
3	3	150	LEU	N-CA-C	5.18	121.83	110.80
2	2	126	VAL	CB-CA-C	5.18	118.07	110.98
3	3	89	TYR	N-CA-C	-5.13	105.38	110.97
2	2	181	GLY	CA-C-N	5.09	126.20	119.84
2	2	181	GLY	C-N-CA	5.09	126.20	119.84
2	2	88	LEU	N-CA-C	-5.08	105.39	112.45
3	3	191	LEU	N-CA-C	5.08	121.62	110.80
3	3	36	VAL	CA-C-N	5.06	126.89	120.51
3	3	36	VAL	C-N-CA	5.06	126.89	120.51
1	1	26	VAL	N-CA-C	5.05	119.84	109.34
1	1	241	THR	N-CA-C	5.02	117.83	109.94
3	3	48	LYS	N-CA-C	-5.02	104.81	112.04
1	1	87	GLN	N-CA-C	5.02	118.84	112.12
2	2	171	VAL	N-CA-C	-5.01	100.32	107.78
1	1	107	PHE	CA-C-N	5.00	126.82	120.51
1	1	107	PHE	C-N-CA	5.00	126.82	120.51

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	26	TYR	Sidechain
3	3	53	PHE	Sidechain

## 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	1	1929	0	1864	220	0
2	2	1692	0	1666	228	0
3	3	1719	0	1677	199	0
4	4	166	0	146	17	0
All	All	5506	0	5353	583	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 54.

All (583) 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)
3:3:119:LYS:CE	3:3:119:LYS:NZ	1.67	1.56
1:1:13:THR:HB	3:3:157:ASN:HB2	1.27	1.11
2:2:104:VAL:HG13	2:2:222:VAL:HG22	1.15	1.09
2:2:44:PRO:HB2	2:2:47:VAL:HG22	1.36	1.06
3:3:42:ASN:ND2	3:3:44:ILE:HG22	1.73	1.02
3:3:116:THR:HG23	3:3:191:LEU:HD21	1.44	0.98
3:3:191:LEU:HD22	3:3:192:THR:H	1.29	0.95
2:2:121:SER:HB2	2:2:203:THR:HG22	1.47	0.95
2:2:209:VAL:H	2:2:210:PRO:HD3	1.32	0.94
1:1:187:LEU:HD22	1:1:188:PRO:HD2	1.47	0.94
1:1:88:PHE:CE1	1:1:205:GLY:HA3	2.05	0.92
1:1:30:VAL:HG13	1:1:218:MET:HE3	1.53	0.91
3:3:117:LYS:HB3	3:3:119:LYS:HE3	1.50	0.91
1:1:164:TRP:CZ2	1:1:187:LEU:HD21	2.07	0.90
1:1:164:TRP:NE1	1:1:187:LEU:HD11	1.88	0.89
3:3:103:SER:HB3	3:3:159:PRO:HA	1.52	0.88
2:2:156:SER:HB3	3:3:51:TYR:HE1	1.40	0.87
1:1:82:LEU:HD11	1:1:211:TYR:HD2	1.37	0.87
3:3:8:VAL:HG12	3:3:9:PRO:HD2	1.56	0.87
3:3:222:LEU:HD13	3:3:223:PRO:HD2	1.56	0.87
2:2:82:PRO:HA	2:2:193:THR:HB	1.54	0.86
1:1:48:LEU:HD22	1:1:130:ILE:HA	1.56	0.86
2:2:73:GLN:HE21	2:2:73:GLN:HA	1.41	0.85
1:1:102:VAL:HG22	1:1:199:SER:HB2	1.58	0.85
2:2:58:LEU:HD13	2:2:94:PHE:HA	1.56	0.85
1:1:187:LEU:HD22	1:1:188:PRO:CD	2.06	0.84
1:1:83:GLU:HB2	1:1:212:ARG:HB3	1.60	0.83
3:3:191:LEU:HD22	3:3:192:THR:N	1.93	0.83
3:3:103:SER:O	3:3:211:GLY:HA3	1.79	0.83
1:1:13:THR:HB	3:3:157:ASN:CB	2.09	0.83
2:2:120:HIS:NE2	2:2:205:PRO:HD2	1.94	0.83
1:1:157:SER:HB2	3:3:24:PRO:HA	1.58	0.82
1:1:70:ARG:O	1:1:71:LEU:HB2	1.79	0.82
1:1:130:ILE:HD11	1:1:135:VAL:HG12	1.59	0.82
2:2:15:GLU:HG3	2:2:29:SER:HB3	1.61	0.82
1:1:75:CYS:HB3	1:1:218:MET:SD	2.20	0.81
3:3:53:PHE:HE1	3:3:205:LEU:HB3	1.43	0.81
2:2:156:SER:HB3	3:3:51:TYR:CE1	2.15	0.81
3:3:63:GLU:HG2	3:3:201:LYS:HD3	1.63	0.81
2:2:13:ARG:O	2:2:27:GLN:HA	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:122:GLY:HA2	2:2:200:SER:O	1.79	0.81
2:2:161:GLN:HB3	2:2:171:VAL:HG13	1.63	0.80
1:1:115:THR:HG23	1:1:133:LEU:H	1.45	0.79
1:1:170:PHE:HD1	1:1:222:ARG:CZ	1.96	0.79
2:2:109:ASP:HB2	2:2:218:ILE:HD11	1.64	0.79
3:3:103:SER:CB	3:3:159:PRO:HA	2.12	0.79
2:2:154:GLN:O	2:2:157:VAL:HG12	1.83	0.79
1:1:174:TRP:HB2	2:2:188:LEU:HD23	1.65	0.79
2:2:44:PRO:HB2	2:2:47:VAL:CG2	2.13	0.79
2:2:104:VAL:CG1	2:2:222:VAL:HG22	2.06	0.79
2:2:124:LEU:HD22	2:2:196:ILE:HG22	1.66	0.78
1:1:60:PHE:CE1	1:1:167:VAL:HG11	2.18	0.78
1:1:62:SER:HB2	1:1:73:ASN:HD21	1.49	0.77
1:1:86:ILE:N	1:1:86:ILE:HD12	2.00	0.77
2:2:121:SER:O	2:2:202:LEU:HD22	1.85	0.76
2:2:180:PRO:HD2	2:2:189:HIS:CE1	2.19	0.76
1:1:223:PRO:HB3	2:2:154:GLN:HB3	1.69	0.75
1:1:219:TYR:CD1	3:3:39:ARG:HB2	2.22	0.75
2:2:58:LEU:CD1	2:2:94:PHE:HA	2.17	0.75
2:2:213:MET:HE2	2:2:215:VAL:HG22	1.68	0.74
1:1:101:PHE:HD1	1:1:143:VAL:CG1	2.00	0.74
2:2:209:VAL:N	2:2:210:PRO:HD3	2.02	0.74
1:1:164:TRP:HE1	1:1:187:LEU:HD11	1.52	0.73
1:1:75:CYS:O	1:1:222:ARG:HD2	1.88	0.73
1:1:119:TRP:HB3	1:1:130:ILE:HG23	1.70	0.73
1:1:15:PRO:HG3	3:3:157:ASN:ND2	2.03	0.73
3:3:116:THR:HG23	3:3:191:LEU:CD2	2.17	0.73
1:1:106:TRP:HZ3	3:3:26:TYR:CD1	2.08	0.72
3:3:24:PRO:HB3	4:4:30:TYR:O	1.89	0.72
3:3:106:PHE:CE2	3:3:208:VAL:HG22	2.25	0.71
1:1:101:PHE:HD1	1:1:143:VAL:HG11	1.56	0.71
2:2:101:HIS:HB3	2:2:222:VAL:HG12	1.72	0.71
3:3:117:LYS:HB3	3:3:119:LYS:CE	2.20	0.71
3:3:19:PRO:HG3	4:4:17:ASN:HD21	1.56	0.71
2:2:88:LEU:HD23	2:2:91:MET:SD	2.30	0.70
2:2:13:ARG:HG3	2:2:29:SER:O	1.91	0.70
2:2:62:TYR:CD2	2:2:91:MET:HA	2.27	0.70
2:2:112:VAL:HG21	2:2:126:VAL:HG21	1.72	0.70
2:2:119:ALA:O	2:2:204:GLY:HA3	1.92	0.70
3:3:116:THR:CG2	3:3:191:LEU:HD21	2.21	0.70
1:1:186:TRP:CZ2	1:1:188:PRO:HA	2.27	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:239:PHE:CD1	3:3:170:TYR:HD2	2.10	0.70
2:2:208:THR:OG1	2:2:210:PRO:HD3	1.92	0.70
1:1:104:VAL:HG22	1:1:197:LEU:CD2	2.22	0.69
2:2:54:LEU:HD12	2:2:220:ALA:HB1	1.74	0.69
3:3:42:ASN:ND2	3:3:44:ILE:H	1.90	0.69
2:2:26:SER:O	2:2:28:GLY:N	2.25	0.69
2:2:58:LEU:HD13	2:2:94:PHE:CA	2.23	0.69
1:1:103:TRP:HB2	1:1:198:THR:CG2	2.23	0.68
3:3:119:LYS:HG2	3:3:147:ASP:OD2	1.93	0.68
1:1:88:PHE:CE2	1:1:146:ILE:HD13	2.28	0.68
3:3:99:GLN:OE1	3:3:217:ARG:HD2	1.93	0.68
1:1:76:THR:HB	1:1:220:CYS:HB2	1.74	0.68
1:1:82:LEU:HD11	1:1:211:TYR:CD2	2.26	0.68
1:1:88:PHE:HA	1:1:207:CYS:HA	1.74	0.68
2:2:20:GLY:HA2	2:2:56:PRO:O	1.94	0.68
1:1:43:LEU:HD23	1:1:43:LEU:N	2.07	0.68
2:2:152:TYR:CZ	3:3:60:PRO:HD3	2.28	0.68
2:2:209:VAL:H	2:2:210:PRO:CD	2.07	0.68
1:1:83:GLU:HG2	1:1:157:SER:HA	1.76	0.68
2:2:13:ARG:HB3	2:2:27:GLN:OE1	1.95	0.67
3:3:56:ILE:O	3:3:59:LYS:HG2	1.94	0.67
1:1:88:PHE:HE2	1:1:146:ILE:HG21	1.58	0.67
2:2:223:ASN:HD22	2:2:223:ASN:H	1.41	0.67
1:1:164:TRP:HZ2	1:1:187:LEU:HD21	1.58	0.67
3:3:8:VAL:HB	3:3:10:GLU:HG2	1.77	0.67
1:1:130:ILE:CD1	1:1:135:VAL:HG12	2.24	0.67
1:1:40:VAL:HB	1:1:68:TRP:CZ2	2.30	0.67
2:2:120:HIS:CD2	2:2:205:PRO:HD2	2.29	0.67
3:3:56:ILE:HG13	3:3:74:PHE:CE1	2.29	0.67
1:1:210:ARG:NH1	3:3:14:PHE:CE1	2.63	0.67
2:2:101:HIS:HB3	2:2:222:VAL:CG1	2.25	0.66
2:2:209:VAL:HG12	2:2:209:VAL:O	1.94	0.66
1:1:77:TYR:HD1	1:1:168:PRO:HA	1.60	0.66
1:1:88:PHE:CZ	1:1:205:GLY:HA3	2.30	0.66
3:3:83:ALA:O	3:3:86:HIS:HB3	1.96	0.66
2:2:126:VAL:CG1	2:2:171:VAL:HG21	2.25	0.66
3:3:19:PRO:O	3:3:20:ASP:HB2	1.94	0.66
1:1:57:LEU:HD21	1:1:195:ILE:HG12	1.76	0.65
1:1:187:LEU:CD2	1:1:188:PRO:HD2	2.25	0.65
2:2:58:LEU:HD22	2:2:93:SER:HB3	1.78	0.65
2:2:135:THR:HB	2:2:139:ALA:HA	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:42:ASN:O	3:3:45:ASP:HB2	1.96	0.65
3:3:66:ASN:HA	3:3:190:ALA:HB1	1.77	0.65
3:3:121:LEU:HD23	3:3:121:LEU:C	2.22	0.65
1:1:59:PRO:O	1:1:72:LEU:HD13	1.97	0.65
1:1:78:PHE:O	1:1:167:VAL:HB	1.96	0.65
3:3:132:PRO:HG2	3:3:184:GLN:HE22	1.62	0.64
2:2:120:HIS:HA	2:2:203:THR:O	1.98	0.64
1:1:209:LEU:HD13	1:1:210:ARG:H	1.61	0.64
2:2:22:THR:HG21	2:2:61:HIS:N	2.13	0.64
3:3:115:ALA:HB1	3:3:194:THR:OG1	1.98	0.64
3:3:101:ARG:NH1	3:3:165:ASP:HB3	2.13	0.64
3:3:119:LYS:HA	3:3:147:ASP:HA	1.79	0.63
3:3:110:PHE:CB	3:3:148:VAL:HG11	2.29	0.63
2:2:32:THR:HG23	2:2:172:HIS:CE1	2.33	0.63
2:2:110:VAL:HG11	2:2:213:MET:HE3	1.81	0.63
3:3:66:ASN:HB3	3:3:191:LEU:O	1.99	0.63
1:1:87:GLN:O	1:1:88:PHE:HB3	1.98	0.63
3:3:27:PRO:HB3	4:4:30:TYR:HA	1.82	0.62
1:1:19:LEU:CD1	3:3:160:TYR:HB3	2.29	0.62
2:2:15:GLU:HG3	2:2:29:SER:CB	2.30	0.62
1:1:104:VAL:HG22	1:1:197:LEU:HD23	1.80	0.62
1:1:230:ARG:NH2	3:3:83:ALA:HB1	2.14	0.62
3:3:42:ASN:HD22	3:3:44:ILE:H	1.46	0.62
3:3:53:PHE:CE1	3:3:205:LEU:HB3	2.31	0.62
2:2:208:THR:O	2:2:209:VAL:HG23	1.99	0.62
1:1:74:THR:HG21	3:3:43:PHE:CZ	2.35	0.62
1:1:88:PHE:CE1	1:1:205:GLY:CA	2.81	0.62
2:2:213:MET:CE	2:2:215:VAL:HG22	2.30	0.62
2:2:69:TRP:CZ3	2:2:124:LEU:HG	2.34	0.61
2:2:113:GLN:HA	2:2:169:SER:O	2.01	0.61
2:2:23:ILE:HD12	2:2:23:ILE:N	2.15	0.61
2:2:61:HIS:HA	2:2:216:ALA:HB2	1.81	0.61
4:4:25:PHE:HD2	4:4:26:TYR:CE1	2.19	0.60
2:2:18:VAL:HG13	2:2:23:ILE:HG13	1.82	0.60
2:2:100:ALA:O	2:2:101:HIS:CD2	2.54	0.60
2:2:54:LEU:HD12	2:2:220:ALA:CB	2.31	0.60
1:1:102:VAL:HG22	1:1:199:SER:CB	2.30	0.60
1:1:86:ILE:N	1:1:86:ILE:CD1	2.65	0.60
1:1:209:LEU:CD1	1:1:210:ARG:H	2.15	0.60
2:2:110:VAL:HG12	2:2:215:VAL:HA	1.83	0.60
3:3:160:TYR:OH	3:3:167:MET:HG2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:5:GLY:O	1:1:6:GLU:HB3	2.01	0.60
1:1:223:PRO:HD3	2:2:158:PHE:CZ	2.37	0.60
3:3:42:ASN:HD22	3:3:44:ILE:HG22	1.65	0.60
1:1:209:LEU:O	1:1:210:ARG:HG2	2.01	0.59
1:1:224:ILE:HG13	3:3:89:TYR:CE2	2.37	0.59
2:2:27:GLN:HG3	2:2:28:GLY:N	2.17	0.59
3:3:56:ILE:N	3:3:56:ILE:HD12	2.18	0.59
1:1:115:THR:HG22	1:1:131:GLN:OE1	2.02	0.59
1:1:88:PHE:CE2	1:1:146:ILE:HG21	2.37	0.59
1:1:173:GLY:HA3	2:2:188:LEU:O	2.03	0.59
1:1:156:PHE:CD2	3:3:25:LEU:HD12	2.38	0.59
2:2:78:ALA:HA	2:2:196:ILE:O	2.02	0.59
1:1:173:GLY:CA	2:2:188:LEU:O	2.50	0.59
2:2:36:TYR:HE2	2:2:130:PRO:CG	2.15	0.58
2:2:126:VAL:HG11	2:2:171:VAL:HG21	1.84	0.58
2:2:161:GLN:OE1	2:2:171:VAL:HA	2.03	0.58
3:3:14:PHE:O	3:3:15:MET:HB2	2.02	0.58
3:3:17:SER:O	3:3:19:PRO:HD3	2.03	0.58
3:3:100:TYR:CE1	3:3:167:MET:HB2	2.37	0.58
1:1:130:ILE:HD11	1:1:135:VAL:CG1	2.30	0.58
3:3:80:LEU:HD12	3:3:80:LEU:N	2.18	0.58
2:2:176:PRO:O	2:2:192:TRP:NE1	2.36	0.58
3:3:94:SER:HB3	3:3:169:VAL:HG13	1.85	0.58
1:1:84:LEU:O	1:1:155:GLY:HA2	2.04	0.58
2:2:223:ASN:H	2:2:223:ASN:ND2	2.01	0.58
1:1:40:VAL:O	1:1:41:GLU:HB2	2.03	0.58
2:2:35:CYS:O	2:2:36:TYR:HB2	2.03	0.58
2:2:160:HIS:HD1	2:2:160:HIS:H	1.52	0.58
2:2:98:VAL:HG12	2:2:98:VAL:O	2.04	0.57
1:1:170:PHE:O	2:2:131:GLU:HB3	2.04	0.57
2:2:151:THR:O	2:2:155:LEU:N	2.36	0.57
1:1:178:THR:O	1:1:180:GLU:N	2.36	0.57
2:2:153:GLN:NE2	3:3:55:SER:HB2	2.19	0.57
3:3:61:TYR:HB3	3:3:205:LEU:HD23	1.87	0.57
2:2:81:CYS:O	2:2:82:PRO:C	2.46	0.57
2:2:209:VAL:N	2:2:210:PRO:CD	2.68	0.57
1:1:206:GLY:O	1:1:207:CYS:SG	2.62	0.56
1:1:218:MET:HB3	3:3:40:PHE:CE1	2.39	0.56
1:1:165:ARG:O	3:3:34:ARG:HG2	2.05	0.56
2:2:36:TYR:HE2	2:2:130:PRO:HG3	1.71	0.56
3:3:122:VAL:O	3:3:143:HIS:HB2	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:218:ILE:O	2:2:219:ASP:HB2	2.06	0.56
3:3:99:GLN:HB2	3:3:217:ARG:HG3	1.87	0.56
2:2:75:HIS:HE2	3:3:59:LYS:HB3	1.71	0.56
2:2:119:ALA:O	2:2:205:PRO:HD3	2.06	0.56
2:2:126:VAL:HG13	2:2:161:GLN:O	2.06	0.56
2:2:202:LEU:HD11	2:2:209:VAL:HG21	1.88	0.55
3:3:86:HIS:ND1	3:3:87:GLY:N	2.54	0.55
1:1:19:LEU:HD12	3:3:160:TYR:HB3	1.89	0.55
1:1:88:PHE:CE1	1:1:205:GLY:C	2.85	0.55
3:3:179:VAL:HG12	3:3:181:GLY:H	1.71	0.55
1:1:88:PHE:HE1	1:1:205:GLY:C	2.14	0.55
1:1:165:ARG:HB2	3:3:33:PRO:O	2.07	0.55
1:1:244:ASN:OD1	3:3:172:ALA:HB1	2.06	0.55
3:3:53:PHE:CE1	3:3:205:LEU:HD13	2.41	0.55
1:1:49:THR:HG22	1:1:50:GLY:N	2.21	0.55
3:3:56:ILE:HG13	3:3:74:PHE:HE1	1.72	0.55
3:3:74:PHE:O	3:3:184:GLN:HA	2.07	0.55
3:3:121:LEU:HD22	3:3:186:TYR:HB2	1.89	0.55
1:1:80:SER:HB3	1:1:216:ALA:HA	1.88	0.55
2:2:84:PRO:HG3	2:2:108:TRP:HH2	1.72	0.55
2:2:84:PRO:HD3	2:2:108:TRP:HZ2	1.71	0.55
4:4:28:GLN:O	4:4:29:GLN:HG3	2.07	0.55
1:1:181:LYS:HA	2:2:137:GLU:HG3	1.89	0.55
2:2:36:TYR:CE2	2:2:130:PRO:HG2	2.42	0.55
1:1:239:PHE:HD2	3:3:226:GLN:NE2	2.05	0.54
2:2:27:GLN:CG	2:2:28:GLY:N	2.70	0.54
2:2:69:TRP:CH2	2:2:124:LEU:HG	2.42	0.54
1:1:48:LEU:HD21	1:1:103:TRP:CZ3	2.43	0.54
2:2:62:TYR:CE2	2:2:91:MET:HA	2.43	0.54
2:2:60:ARG:O	2:2:216:ALA:HB1	2.07	0.54
1:1:86:ILE:HD12	1:1:86:ILE:H	1.72	0.54
2:2:117:SER:OG	2:2:118:PHE:N	2.41	0.54
1:1:103:TRP:HB2	1:1:198:THR:HG22	1.89	0.54
2:2:22:THR:HG21	2:2:61:HIS:HB2	1.88	0.54
3:3:109:ILE:HB	3:3:205:LEU:HB2	1.88	0.54
3:3:15:MET:HB3	3:3:18:VAL:HG13	1.90	0.54
1:1:118:ALA:HB2	1:1:132:GLN:NE2	2.23	0.54
2:2:27:GLN:HG3	2:2:28:GLY:H	1.73	0.54
3:3:107:ASN:HA	3:3:154:PHE:O	2.08	0.53
2:2:69:TRP:HD1	2:2:70:PRO:N	2.07	0.53
1:1:115:THR:OG1	1:1:133:LEU:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:101:ARG:HA	3:3:160:TYR:HE1	1.73	0.53
3:3:48:LYS:HA	3:3:210:ALA:HB3	1.90	0.53
3:3:90:VAL:HG11	3:3:208:VAL:HG12	1.91	0.53
1:1:221:PRO:CA	3:3:40:PHE:HE2	2.21	0.53
1:1:157:SER:CB	3:3:24:PRO:HA	2.36	0.53
1:1:165:ARG:HD3	2:2:182:PRO:HG3	1.90	0.53
2:2:69:TRP:CZ3	2:2:124:LEU:CG	2.92	0.53
1:1:48:LEU:HD21	1:1:103:TRP:CE3	2.44	0.53
3:3:145:VAL:HG22	3:3:188:LEU:HD12	1.91	0.53
1:1:99:GLU:OE2	1:1:101:PHE:HE2	1.92	0.53
1:1:109:VAL:H	1:1:161:THR:HB	1.74	0.53
1:1:109:VAL:HG23	1:1:161:THR:OG1	2.09	0.53
1:1:186:TRP:O	1:1:187:LEU:HB3	2.09	0.53
2:2:73:GLN:HA	2:2:73:GLN:NE2	2.17	0.53
2:2:195:VAL:C	2:2:196:ILE:HG13	2.33	0.53
1:1:55:HIS:O	1:1:194:SER:CB	2.56	0.52
2:2:124:LEU:HD12	2:2:163:LEU:HD12	1.91	0.52
1:1:184:TYR:HE1	2:2:139:ALA:CB	2.23	0.52
1:1:219:TYR:OH	3:3:34:ARG:HD2	2.08	0.52
3:3:108:PHE:HA	3:3:205:LEU:O	2.09	0.52
3:3:42:ASN:HD22	3:3:44:ILE:N	2.08	0.52
1:1:37:PHE:HA	1:1:211:TYR:O	2.10	0.52
2:2:153:GLN:NE2	3:3:55:SER:N	2.58	0.52
2:2:178:ILE:HG22	2:2:191:PRO:CB	2.40	0.52
3:3:56:ILE:HD13	3:3:206:VAL:HG11	1.91	0.52
1:1:86:ILE:CD1	1:1:86:ILE:H	2.23	0.52
1:1:212:ARG:O	1:1:214:PRO:HD2	2.09	0.52
2:2:80:ILE:HG23	2:2:82:PRO:HD3	1.91	0.52
1:1:30:VAL:CG1	1:1:218:MET:HE3	2.34	0.52
1:1:48:LEU:O	1:1:131:GLN:NE2	2.43	0.52
1:1:50:GLY:O	1:1:131:GLN:NE2	2.43	0.52
2:2:152:TYR:CB	2:2:197:LEU:HD22	2.40	0.52
3:3:100:TYR:CZ	3:3:167:MET:HB2	2.45	0.52
1:1:76:THR:O	1:1:169:VAL:HG23	2.10	0.51
1:1:106:TRP:O	1:1:139:SER:HB2	2.11	0.51
2:2:186:LEU:O	2:2:186:LEU:HD23	2.11	0.51
3:3:60:PRO:O	3:3:61:TYR:HB3	2.11	0.51
4:4:25:PHE:CD2	4:4:26:TYR:CE1	2.98	0.51
2:2:152:TYR:CE1	3:3:60:PRO:HD3	2.45	0.51
3:3:31:VAL:HB	4:4:34:ILE:O	2.10	0.51
1:1:239:PHE:CD1	3:3:170:TYR:CD2	2.96	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:108:PRO:HA	1:1:161:THR:HG21	1.92	0.51
2:2:104:VAL:HG22	2:2:222:VAL:HG13	1.92	0.51
2:2:152:TYR:CD1	2:2:152:TYR:C	2.88	0.51
1:1:121:LEU:HD13	1:1:121:LEU:C	2.36	0.51
2:2:80:ILE:HD11	2:2:132:TYR:OH	2.11	0.51
3:3:169:VAL:HG12	3:3:169:VAL:O	2.09	0.51
2:2:163:LEU:HD21	2:2:169:SER:C	2.36	0.51
2:2:87:LYS:HG3	2:2:142:TRP:CD2	2.45	0.51
3:3:19:PRO:HG3	4:4:17:ASN:ND2	2.26	0.51
1:1:104:VAL:HG22	1:1:197:LEU:HD21	1.90	0.51
1:1:210:ARG:HD2	3:3:14:PHE:CZ	2.46	0.51
1:1:212:ARG:HG2	1:1:214:PRO:HD3	1.91	0.51
1:1:22:VAL:C	1:1:24:MET:H	2.18	0.50
1:1:149:SER:C	1:1:151:SER:H	2.18	0.50
2:2:16:THR:HA	2:2:24:ILE:O	2.11	0.50
2:2:153:GLN:HA	3:3:53:PHE:HB2	1.94	0.50
3:3:31:VAL:HG12	4:4:35:ASP:HA	1.92	0.50
1:1:113:THR:O	1:1:114:LYS:C	2.55	0.50
2:2:111:VAL:HG22	2:2:172:HIS:CD2	2.46	0.50
3:3:3:ILE:HG22	3:3:4:ARG:N	2.27	0.50
1:1:40:VAL:HG22	1:1:211:TYR:CE1	2.46	0.50
1:1:151:SER:C	1:1:153:ALA:H	2.19	0.50
3:3:75:GLN:HG3	3:3:184:GLN:HG2	1.93	0.50
1:1:48:LEU:HD23	1:1:198:THR:OG1	2.12	0.50
1:1:107:PHE:HE1	1:1:196:LEU:HB2	1.76	0.50
1:1:238:LYS:HA	3:3:171:SER:O	2.12	0.50
3:3:135:ARG:O	3:3:138:ALA:N	2.45	0.50
1:1:79:PHE:CZ	3:3:31:VAL:HG11	2.47	0.50
1:1:150:ARG:H	1:1:150:ARG:HE	1.60	0.50
2:2:140:LEU:HD22	2:2:190:ASN:OD1	2.12	0.50
2:2:124:LEU:HD12	2:2:163:LEU:CD1	2.40	0.50
3:3:97:PHE:CE1	3:3:216:LEU:HD23	2.47	0.50
2:2:21:VAL:H	2:2:60:ARG:HG2	1.75	0.49
2:2:158:PHE:O	2:2:159:PRO:C	2.55	0.49
1:1:109:VAL:HG22	1:1:191:HIS:CD2	2.46	0.49
2:2:84:PRO:HD2	2:2:186:LEU:HD22	1.95	0.49
1:1:181:LYS:O	1:1:182:ALA:HB2	2.11	0.49
2:2:180:PRO:HD2	2:2:189:HIS:HE1	1.76	0.49
3:3:102:GLY:HA3	3:3:214:PHE:HA	1.93	0.49
3:3:121:LEU:HD23	3:3:121:LEU:O	2.12	0.49
2:2:110:VAL:CG1	2:2:215:VAL:HA	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:135:THR:HB	2:2:139:ALA:CA	2.41	0.49
2:2:152:TYR:CE1	3:3:60:PRO:HG3	2.48	0.49
3:3:56:ILE:N	3:3:56:ILE:CD1	2.75	0.49
1:1:40:VAL:HG22	1:1:211:TYR:HE1	1.77	0.49
1:1:160:TYR:CE1	1:1:167:VAL:HG23	2.48	0.49
1:1:171:TYR:N	1:1:185:ASN:OD1	2.45	0.49
2:2:178:ILE:HG22	2:2:191:PRO:HB2	1.94	0.49
2:2:110:VAL:CG1	2:2:213:MET:HE3	2.42	0.49
3:3:101:ARG:HA	3:3:160:TYR:CE1	2.48	0.49
2:2:167:THR:O	2:2:168:ASN:HB3	2.13	0.48
1:1:13:THR:C	1:1:14:GLU:HG3	2.38	0.48
1:1:237:HIS:O	3:3:171:SER:HB2	2.13	0.48
1:1:170:PHE:CD1	1:1:222:ARG:CZ	2.87	0.48
2:2:32:THR:HG23	2:2:172:HIS:ND1	2.29	0.48
4:4:30:TYR:CD1	4:4:30:TYR:N	2.81	0.48
1:1:27:HIS:O	1:1:33:LEU:HD21	2.13	0.48
1:1:187:LEU:HD12	1:1:190:ALA:HB2	1.94	0.48
2:2:152:TYR:HE1	3:3:60:PRO:HB3	1.78	0.48
2:2:52:THR:O	2:2:221:MET:HA	2.13	0.48
2:2:125:CYS:HB2	2:2:199:LEU:HD11	1.94	0.48
3:3:101:ARG:HD2	3:3:165:ASP:O	2.14	0.48
1:1:82:LEU:HD23	1:1:84:LEU:HD11	1.94	0.48
3:3:80:LEU:HD12	3:3:80:LEU:H	1.77	0.48
3:3:130:ALA:O	3:3:131:ALA:HB3	2.13	0.48
1:1:79:PHE:CD1	1:1:79:PHE:C	2.92	0.48
2:2:200:SER:HA	3:3:61:TYR:CE2	2.48	0.48
3:3:56:ILE:CD1	3:3:206:VAL:HG11	2.43	0.48
1:1:176:ALA:C	1:1:178:THR:H	2.22	0.48
2:2:153:GLN:CD	3:3:55:SER:HB2	2.39	0.48
3:3:70:ASP:HA	3:3:135:ARG:HH12	1.79	0.48
1:1:4:VAL:HG22	3:3:151:ASN:O	2.14	0.48
2:2:140:LEU:HD22	2:2:190:ASN:CG	2.38	0.48
2:2:223:ASN:ND2	2:2:223:ASN:N	2.60	0.47
3:3:53:PHE:HB3	3:3:60:PRO:CB	2.44	0.47
2:2:95:HIS:C	2:2:95:HIS:CD2	2.93	0.47
1:1:101:PHE:O	1:1:199:SER:CB	2.62	0.47
2:2:121:SER:CB	2:2:203:THR:HG22	2.32	0.47
2:2:176:PRO:HD2	2:2:192:TRP:CZ2	2.49	0.47
1:1:113:THR:O	1:1:133:LEU:HD12	2.14	0.47
1:1:156:PHE:CG	3:3:25:LEU:HD12	2.49	0.47
2:2:84:PRO:HD3	2:2:108:TRP:CZ2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:84:GLU:N	3:3:84:GLU:OE1	2.48	0.47
1:1:224:ILE:HD11	3:3:89:TYR:CZ	2.49	0.47
1:1:237:HIS:HB2	3:3:81:SER:O	2.14	0.47
2:2:84:PRO:HG3	2:2:108:TRP:CH2	2.50	0.47
1:1:84:LEU:CD2	1:1:209:LEU:HD11	2.45	0.47
1:1:105:LYS:HE3	1:1:139:SER:OG	2.13	0.47
3:3:75:GLN:HA	3:3:183:LEU:O	2.14	0.47
3:3:160:TYR:HD2	3:3:161:SER:N	2.13	0.47
1:1:43:LEU:N	1:1:43:LEU:CD2	2.74	0.47
1:1:103:TRP:HB2	1:1:198:THR:HG23	1.96	0.47
2:2:84:PRO:HG2	2:2:88:LEU:HG	1.97	0.47
3:3:53:PHE:HB3	3:3:60:PRO:HB2	1.96	0.47
3:3:84:GLU:H	3:3:84:GLU:CD	2.21	0.47
1:1:120:GLN:HB2	1:1:129:ARG:HD3	1.96	0.47
3:3:73:LEU:HB3	3:3:185:VAL:O	2.14	0.47
3:3:157:ASN:O	3:3:159:PRO:HD3	2.14	0.47
3:3:220:VAL:HG12	3:3:221:ASP:O	2.15	0.47
1:1:37:PHE:CD1	1:1:212:ARG:HB2	2.49	0.47
1:1:46:SER:HB2	1:1:197:LEU:O	2.15	0.47
2:2:76:GLY:HA2	2:2:197:LEU:HD21	1.97	0.47
2:2:139:ALA:C	2:2:141:LYS:H	2.21	0.47
3:3:44:ILE:HG23	3:3:45:ASP:N	2.30	0.47
3:3:117:LYS:O	3:3:191:LEU:HD22	2.15	0.47
2:2:74:SER:O	2:2:75:HIS:C	2.58	0.46
1:1:187:LEU:HD22	1:1:188:PRO:N	2.30	0.46
2:2:212:THR:HG22	2:2:213:MET:N	2.30	0.46
3:3:62:PHE:CE1	3:3:204:VAL:HG11	2.50	0.46
1:1:101:PHE:CD1	1:1:143:VAL:HG11	2.44	0.46
3:3:108:PHE:O	3:3:153:ALA:HA	2.15	0.46
3:3:122:VAL:HG22	3:3:123:ALA:N	2.30	0.46
2:2:23:ILE:HD12	2:2:23:ILE:H	1.80	0.46
1:1:22:VAL:CG1	1:1:23:ASP:N	2.79	0.46
2:2:75:HIS:NE2	3:3:59:LYS:HB3	2.30	0.46
3:3:195:ASP:HB2	3:3:198:VAL:HG22	1.98	0.46
1:1:183:THR:HA	1:1:186:TRP:HB3	1.98	0.46
2:2:139:ALA:C	2:2:141:LYS:N	2.74	0.46
3:3:85:LEU:O	3:3:91:ALA:CB	2.64	0.46
3:3:120:PHE:HD1	3:3:146:TRP:CH2	2.34	0.46
1:1:82:LEU:CD2	1:1:84:LEU:HD11	2.46	0.45
1:1:184:TYR:CE1	2:2:139:ALA:HB2	2.51	0.45
2:2:22:THR:HG21	2:2:61:HIS:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:88:LEU:C	2:2:90:LYS:H	2.23	0.45
3:3:56:ILE:CG1	3:3:74:PHE:CE1	2.98	0.45
3:3:103:SER:HB3	3:3:159:PRO:C	2.40	0.45
2:2:81:CYS:O	2:2:83:LEU:N	2.49	0.45
2:2:152:TYR:HB2	2:2:197:LEU:HD22	1.98	0.45
2:2:211:VAL:HG12	2:2:212:THR:N	2.30	0.45
1:1:7:ASP:O	1:1:8:GLY:C	2.59	0.45
1:1:101:PHE:O	1:1:199:SER:OG	2.33	0.45
3:3:103:SER:HB3	3:3:159:PRO:CA	2.35	0.45
3:3:110:PHE:HB3	3:3:148:VAL:HG11	1.96	0.45
3:3:172:ALA:O	3:3:178:ASN:OD1	2.34	0.45
1:1:107:PHE:HB2	1:1:194:SER:OG	2.16	0.45
1:1:165:ARG:HG2	2:2:180:PRO:O	2.16	0.45
2:2:135:THR:HG23	2:2:145:LEU:HD11	1.99	0.45
2:2:75:HIS:HA	2:2:198:ILE:O	2.17	0.45
2:2:163:LEU:HG	2:2:171:VAL:HG23	1.99	0.45
1:1:219:TYR:HD1	3:3:39:ARG:HB2	1.79	0.45
2:2:49:ASP:HA	2:2:50:PRO:HD2	1.80	0.45
3:3:198:VAL:HG23	3:3:199:ASN:H	1.82	0.45
3:3:13:SER:OG	3:3:15:MET:CE	2.64	0.45
1:1:109:VAL:HG22	1:1:191:HIS:HD2	1.82	0.45
1:1:170:PHE:CD1	1:1:222:ARG:NH1	2.85	0.45
3:3:77:ASP:O	3:3:79:SER:N	2.50	0.45
2:2:160:HIS:HD1	2:2:160:HIS:N	2.14	0.45
2:2:39:PRO:HB3	2:2:176:PRO:HA	1.99	0.45
2:2:54:LEU:HD21	2:2:97:VAL:HG11	1.99	0.45
2:2:125:CYS:SG	2:2:160:HIS:HD2	2.40	0.45
2:2:156:SER:HA	2:2:160:HIS:CD2	2.52	0.45
1:1:83:GLU:C	1:1:84:LEU:HD12	2.41	0.44
3:3:7:SER:OG	3:3:11:SER:HB3	2.17	0.44
3:3:122:VAL:HA	3:3:185:VAL:HA	1.97	0.44
2:2:108:TRP:O	2:2:218:ILE:HD12	2.17	0.44
3:3:154:PHE:CG	3:3:155:SER:N	2.84	0.44
3:3:97:PHE:CD1	3:3:216:LEU:HD23	2.51	0.44
3:3:103:SER:HB2	3:3:159:PRO:HA	1.95	0.44
3:3:175:THR:OG1	3:3:178:ASN:ND2	2.51	0.44
1:1:146:ILE:HG22	1:1:146:ILE:O	2.17	0.44
2:2:78:ALA:HB1	2:2:195:VAL:HG12	1.99	0.44
2:2:153:GLN:NE2	3:3:55:SER:CB	2.80	0.44
2:2:157:VAL:HG23	3:3:50:THR:HG21	1.99	0.44
1:1:45:LEU:HB2	1:1:202:HIS:HA	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:201:ALA:O	1:1:202:HIS:CD2	2.71	0.44
1:1:199:SER:C	1:1:201:ALA:H	2.25	0.44
2:2:34:TYR:HA	2:2:174:VAL:O	2.18	0.44
2:2:84:PRO:HD2	2:2:186:LEU:CD2	2.48	0.44
2:2:152:TYR:OH	3:3:60:PRO:HD3	2.17	0.44
3:3:134:THR:OG1	3:3:137:GLU:HG3	2.17	0.44
4:4:16:GLY:O	4:4:18:SER:N	2.50	0.44
1:1:174:TRP:HB2	2:2:188:LEU:CD2	2.44	0.44
1:1:201:ALA:O	1:1:202:HIS:HD2	2.01	0.44
3:3:36:VAL:HA	3:3:37:PRO:HD3	1.53	0.44
2:2:36:TYR:CE2	2:2:130:PRO:CG	2.98	0.44
3:3:97:PHE:HB3	3:3:218:HIS:O	2.17	0.44
2:2:54:LEU:HB2	2:2:220:ALA:HB3	1.99	0.44
3:3:179:VAL:HG12	3:3:181:GLY:N	2.32	0.43
1:1:40:VAL:HB	1:1:68:TRP:CH2	2.53	0.43
1:1:62:SER:O	1:1:63:THR:CB	2.66	0.43
2:2:57:THR:HG22	2:2:58:LEU:H	1.82	0.43
2:2:69:TRP:CZ3	2:2:124:LEU:HD11	2.52	0.43
3:3:101:ARG:HG2	3:3:101:ARG:O	2.17	0.43
3:3:160:TYR:C	3:3:160:TYR:CD2	2.94	0.43
1:1:49:THR:HG22	1:1:50:GLY:H	1.82	0.43
1:1:55:HIS:O	1:1:194:SER:HB2	2.18	0.43
1:1:56:VAL:HG13	1:1:193:GLY:O	2.17	0.43
2:2:13:ARG:HD3	2:2:13:ARG:HA	1.72	0.43
1:1:181:LYS:O	1:1:182:ALA:CB	2.66	0.43
2:2:23:ILE:N	2:2:23:ILE:CD1	2.81	0.43
2:2:129:VAL:HA	2:2:130:PRO:HD3	1.78	0.43
3:3:217:ARG:HD3	3:3:218:HIS:CD2	2.54	0.43
1:1:52:PRO:HD3	1:1:115:THR:O	2.17	0.43
2:2:27:GLN:CD	2:2:27:GLN:C	2.87	0.43
1:1:26:VAL:HG12	1:1:27:HIS:N	2.32	0.43
1:1:106:TRP:CZ2	1:1:158:VAL:HG13	2.54	0.43
2:2:22:THR:O	2:2:22:THR:HG23	2.18	0.43
2:2:152:TYR:CE1	3:3:60:PRO:CG	3.01	0.43
3:3:86:HIS:ND1	3:3:86:HIS:C	2.77	0.43
2:2:57:THR:O	2:2:59:SER:N	2.52	0.43
4:4:18:SER:O	4:4:23:GLN:NE2	2.52	0.43
1:1:184:TYR:HE1	2:2:139:ALA:HB3	1.84	0.43
2:2:42:ARG:HA	2:2:43:PRO:HD2	1.64	0.43
3:3:43:PHE:O	3:3:44:ILE:C	2.60	0.43
3:3:121:LEU:C	3:3:121:LEU:CD2	2.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:119:LYS:O	3:3:120:PHE:CB	2.67	0.42
1:1:22:VAL:HG12	1:1:23:ASP:N	2.33	0.42
1:1:101:PHE:CD1	1:1:143:VAL:CG1	2.91	0.42
2:2:61:HIS:CG	2:2:216:ALA:HB2	2.54	0.42
2:2:83:LEU:HA	2:2:84:PRO:HA	1.60	0.42
2:2:216:ALA:HA	2:2:217:PRO:HD3	1.78	0.42
1:1:187:LEU:HD13	1:1:187:LEU:C	2.44	0.42
2:2:25:ASN:O	2:2:26:SER:HB3	2.18	0.42
2:2:69:TRP:HZ2	2:2:198:ILE:HG23	1.85	0.42
2:2:121:SER:O	2:2:202:LEU:HA	2.19	0.42
2:2:135:THR:O	2:2:137:GLU:N	2.53	0.42
2:2:150:TYR:O	2:2:151:THR:C	2.63	0.42
3:3:98:ALA:HB2	3:3:220:VAL:HG21	2.01	0.42
3:3:175:THR:HG1	3:3:178:ASN:CG	2.28	0.42
4:4:31:GLN:HE21	4:4:31:GLN:HA	1.85	0.42
1:1:128:VAL:HG13	1:1:128:VAL:O	2.19	0.42
2:2:77:HIS:HE1	2:2:144:GLU:HG2	1.84	0.42
2:2:152:TYR:HB3	2:2:197:LEU:HD22	2.00	0.42
1:1:172:ASN:HB2	2:2:132:TYR:O	2.19	0.42
2:2:135:THR:HB	2:2:139:ALA:CB	2.50	0.42
1:1:74:THR:O	1:1:74:THR:HG22	2.19	0.42
1:1:79:PHE:CE2	1:1:160:TYR:CD2	3.08	0.42
1:1:144:PHE:CD1	1:1:154:CYS:HB3	2.54	0.42
1:1:147:ALA:C	1:1:149:SER:H	2.28	0.42
2:2:31:GLY:O	2:2:172:HIS:HB3	2.20	0.42
4:4:29:GLN:HB2	4:4:30:TYR:HD1	1.84	0.42
1:1:48:LEU:HA	1:1:198:THR:OG1	2.20	0.42
1:1:49:THR:CG2	1:1:50:GLY:N	2.83	0.42
2:2:160:HIS:HB2	2:2:161:GLN:H	1.70	0.42
1:1:219:TYR:CE1	3:3:39:ARG:HD2	2.55	0.42
2:2:56:PRO:C	2:2:57:THR:O	2.59	0.42
3:3:119:LYS:HG2	3:3:147:ASP:CG	2.45	0.42
1:1:219:TYR:HA	3:3:39:ARG:HA	2.02	0.41
1:1:224:ILE:HD11	3:3:89:TYR:CE2	2.55	0.41
2:2:57:THR:O	2:2:58:LEU:CB	2.66	0.41
2:2:153:GLN:HE22	3:3:55:SER:CB	2.33	0.41
2:2:166:ARG:HD3	3:3:110:PHE:O	2.20	0.41
2:2:211:VAL:HG12	2:2:212:THR:H	1.85	0.41
3:3:79:SER:O	3:3:81:SER:N	2.51	0.41
2:2:33:THR:HG21	2:2:160:HIS:O	2.20	0.41
1:1:65:GLN:HG2	1:1:70:ARG:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:239:PHE:CD2	3:3:226:GLN:NE2	2.87	0.41
2:2:111:VAL:HG22	2:2:172:HIS:HD2	1.85	0.41
3:3:84:GLU:C	3:3:86:HIS:H	2.28	0.41
1:1:115:THR:HG23	1:1:133:LEU:N	2.25	0.41
2:2:22:THR:OG1	2:2:61:HIS:HB2	2.20	0.41
3:3:54:CYS:SG	3:3:208:VAL:HG21	2.61	0.41
4:4:21:ILE:O	4:4:21:ILE:HG22	2.20	0.41
2:2:24:ILE:HD11	2:2:61:HIS:ND1	2.35	0.41
2:2:190:ASN:HA	2:2:191:PRO:HD3	1.87	0.41
3:3:53:PHE:N	3:3:53:PHE:CD2	2.88	0.41
1:1:24:MET:O	1:1:25:HIS:HB2	2.21	0.41
1:1:48:LEU:O	1:1:131:GLN:HG2	2.20	0.41
1:1:140:PRO:HB3	3:3:25:LEU:HB3	2.03	0.41
2:2:69:TRP:CZ3	2:2:124:LEU:HD21	2.56	0.41
2:2:88:LEU:C	2:2:90:LYS:N	2.79	0.41
1:1:38:PHE:CD1	1:1:68:TRP:HB2	2.56	0.41
1:1:160:TYR:OH	1:1:167:VAL:HG23	2.21	0.41
2:2:28:GLY:O	2:2:168:ASN:HB2	2.21	0.41
2:2:68:GLU:O	2:2:69:TRP:C	2.63	0.41
2:2:178:ILE:HG22	2:2:191:PRO:HB3	2.02	0.41
3:3:113:ALA:HB2	3:3:199:ASN:CG	2.46	0.41
3:3:152:SER:O	3:3:153:ALA:HB2	2.21	0.41
1:1:41:GLU:O	1:1:42:THR:HB	2.19	0.40
1:1:175:GLY:N	1:1:183:THR:O	2.53	0.40
1:1:220:CYS:HA	1:1:221:PRO:HD2	1.82	0.40
2:2:153:GLN:HE22	3:3:55:SER:N	2.19	0.40
3:3:31:VAL:CB	4:4:34:ILE:O	2.69	0.40
3:3:47:ALA:HB2	3:3:89:TYR:CD1	2.56	0.40
3:3:168:ALA:C	3:3:170:TYR:H	2.29	0.40
1:1:38:PHE:CE1	1:1:68:TRP:HB2	2.56	0.40
1:1:55:HIS:O	1:1:194:SER:HA	2.21	0.40
2:2:20:GLY:CA	2:2:56:PRO:O	2.67	0.40
2:2:152:TYR:HB3	2:2:197:LEU:CD2	2.51	0.40
2:2:160:HIS:N	2:2:160:HIS:ND1	2.69	0.40
3:3:120:PHE:HD1	3:3:146:TRP:CZ2	2.38	0.40
4:4:32:ASN:HB3	4:4:33:SER:H	1.58	0.40
1:1:224:ILE:CD1	3:3:89:TYR:CE2	3.04	0.40
1:1:144:PHE:CD2	1:1:144:PHE:C	2.99	0.40
1:1:168:PRO:HB3	2:2:180:PRO:HB3	2.03	0.40
1:1:184:TYR:HE1	2:2:139:ALA:HB2	1.86	0.40
2:2:15:GLU:CB	2:2:29:SER:HB2	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:103:LEU:HD12	2:2:223:ASN:HB2	2.02	0.40
2:2:149:ALA:O	2:2:152:TYR:CD2	2.74	0.40
3:3:64:VAL:HG13	3:3:120:PHE:HE2	1.86	0.40
1:1:82:LEU:HG	1:1:83:GLU:H	1.86	0.40
1:1:87:GLN:O	1:1:88:PHE:CB	2.62	0.40
1:1:87:GLN:HA	1:1:153:ALA:HB2	2.02	0.40
1:1:174:TRP:CD1	1:1:184:TYR:HA	2.56	0.40
1:1:176:ALA:C	1:1:178:THR:N	2.79	0.40
2:2:64:PHE:CD1	2:2:64:PHE:N	2.90	0.40
2:2:139:ALA:O	2:2:140:LEU:HB2	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	244/246 (99%)	145 (59%)	59 (24%)	40 (16%)	0	3
2	2	217/230 (94%)	145 (67%)	49 (23%)	23 (11%)	0	7
3	3	224/226 (99%)	156 (70%)	45 (20%)	23 (10%)	0	7
4	4	20/80 (25%)	9 (45%)	7 (35%)	4 (20%)	0	1
All	All	705/782 (90%)	455 (64%)	160 (23%)	90 (13%)	0	4

All (90) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	10	PRO
1	1	18	ALA
1	1	22	VAL
1	1	26	VAL
1	1	63	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	1	67	ALA
1	1	127	SER
1	1	135	VAL
1	1	162	SER
1	1	179	LYS
1	1	182	ALA
1	1	226	PRO
1	1	243	ILE
2	2	27	GLN
2	2	92	GLY
2	2	136	HIS
2	2	201	GLU
2	2	208	THR
2	2	209	VAL
2	2	224	GLY
3	3	20	ASP
3	3	21	ASN
3	3	27	PRO
3	3	78	VAL
3	3	80	LEU
3	3	120	PHE
3	3	153	ALA
3	3	191	LEU
4	4	17	ASN
1	1	21	PRO
1	1	42	THR
1	1	71	LEU
1	1	88	PHE
1	1	99	GLU
1	1	100	GLY
1	1	114	LYS
1	1	118	ALA
1	1	140	PRO
1	1	150	ARG
1	1	151	SER
1	1	207	CYS
2	2	28	GLY
2	2	43	PRO
2	2	70	PRO
2	2	134	HIS
2	2	135	THR
3	3	14	PHE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	3	15	MET
3	3	113	ALA
3	3	128	HIS
3	3	129	SER
3	3	150	LEU
3	3	152	SER
4	4	31	GLN
1	1	94	PRO
1	1	152	GLN
1	1	184	TYR
1	1	187	LEU
1	1	213	PHE
1	1	231	PRO
2	2	26	SER
2	2	89	LYS
2	2	102	HIS
2	2	159	PRO
3	3	60	PRO
3	3	174	ALA
3	3	223	PRO
4	4	29	GLN
1	1	9	GLU
1	1	65	GLN
2	2	58	LEU
2	2	86	ASP
2	2	149	ALA
3	3	11	SER
3	3	200	SER
3	3	218	HIS
1	1	8	GLY
1	1	14	GLU
1	1	19	LEU
1	1	112	PRO
2	2	82	PRO
2	2	182	PRO
3	3	61	TYR
3	3	131	ALA
1	1	188	PRO
1	1	221	PRO
2	2	196	ILE
4	4	21	ILE
1	1	30	VAL

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Mol	Chain	Res	Type
2	2	84	PRO

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	1	208/208 (100%)	169 (81%)	39 (19%)	<b>1</b> <b>11</b>
2	2	193/204 (95%)	148 (77%)	45 (23%)	<b>1</b> <b>5</b>
3	3	190/190 (100%)	142 (75%)	48 (25%)	<b>0</b> <b>4</b>
4	4	18/65 (28%)	15 (83%)	3 (17%)	<b>2</b> <b>13</b>
All	All	609/667 (91%)	474 (78%)	135 (22%)	<b>1</b> <b>6</b>

All (135) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	1	VAL
1	1	10	PRO
1	1	14	GLU
1	1	19	LEU
1	1	20	SER
1	1	21	PRO
1	1	23	ASP
1	1	28	THR
1	1	36	ARG
1	1	39	ASP
1	1	40	VAL
1	1	43	LEU
1	1	45	LEU
1	1	46	SER
1	1	54	THR
1	1	59	PRO
1	1	71	LEU
1	1	86	ILE
1	1	87	GLN
1	1	90	PHE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	1	92	THR
1	1	119	TRP
1	1	130	ILE
1	1	132	GLN
1	1	138	MET
1	1	144	PHE
1	1	150	ARG
1	1	163	MET
1	1	177	PRO
1	1	178	THR
1	1	187	LEU
1	1	195	ILE
1	1	196	LEU
1	1	202	HIS
1	1	207	CYS
1	1	209	LEU
1	1	226	PRO
1	1	241	THR
1	1	245	LYS
2	2	13	ARG
2	2	18	VAL
2	2	22	THR
2	2	27	GLN
2	2	29	SER
2	2	45	SER
2	2	56	PRO
2	2	58	LEU
2	2	71	HIS
2	2	73	GLN
2	2	75	HIS
2	2	80	ILE
2	2	84	PRO
2	2	88	LEU
2	2	93	SER
2	2	103	LEU
2	2	104	VAL
2	2	110	VAL
2	2	112	VAL
2	2	126	VAL
2	2	134	HIS
2	2	135	THR
2	2	150	TYR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	2	159	PRO
2	2	160	HIS
2	2	162	LEU
2	2	166	ARG
2	2	167	THR
2	2	174	VAL
2	2	176	PRO
2	2	178	ILE
2	2	184	THR
2	2	186	LEU
2	2	188	LEU
2	2	193	THR
2	2	194	ILE
2	2	195	VAL
2	2	197	LEU
2	2	200	SER
2	2	202	LEU
2	2	203	THR
2	2	210	PRO
2	2	214	SER
2	2	222	VAL
2	2	223	ASN
3	3	8	VAL
3	3	15	MET
3	3	16	SER
3	3	18	VAL
3	3	31	VAL
3	3	35	GLN
3	3	36	VAL
3	3	41	THR
3	3	42	ASN
3	3	46	VAL
3	3	50	THR
3	3	51	TYR
3	3	54	CYS
3	3	56	ILE
3	3	59	LYS
3	3	63	GLU
3	3	65	THR
3	3	67	THR
3	3	76	MET
3	3	78	VAL

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Mol	Chain	Res	Type
3	3	84	GLU
3	3	86	HIS
3	3	90	VAL
3	3	93	LEU
3	3	95	SER
3	3	103	SER
3	3	107	ASN
3	3	109	ILE
3	3	119	LYS
3	3	120	PHE
3	3	121	LEU
3	3	133	LYS
3	3	134	THR
3	3	139	MET
3	3	142	ILE
3	3	146	TRP
3	3	148	VAL
3	3	150	LEU
3	3	158	VAL
3	3	162	SER
3	3	175	THR
3	3	188	LEU
3	3	189	THR
3	3	195	ASP
3	3	204	VAL
3	3	206	VAL
3	3	217	ARG
3	3	222	LEU
4	4	17	ASN
4	4	30	TYR
4	4	33	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	27	HIS
1	1	47	ASN
1	1	73	ASN
1	1	87	GLN
1	1	132	GLN
1	1	191	HIS
1	1	202	HIS

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Mol	Chain	Res	Type
2	2	71	HIS
2	2	73	GLN
2	2	95	HIS
2	2	101	HIS
2	2	134	HIS
2	2	136	HIS
2	2	160	HIS
2	2	189	HIS
2	2	223	ASN
3	3	35	GLN
3	3	42	ASN
3	3	49	GLN
3	3	218	HIS
3	3	226	GLN
4	4	17	ASN
4	4	23	GLN
4	4	24	ASN
4	4	31	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<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	1	246/246 (100%)	-1.12	0 100 100	2, 4, 42, 72	0
2	2	219/230 (95%)	-1.08	0 100 100	2, 4, 47, 93	0
3	3	226/226 (100%)	-1.12	0 100 100	2, 3, 23, 56	0
4	4	22/80 (27%)	-1.06	0 100 100	13, 36, 45, 55	0
All	All	713/782 (91%)	-1.11	0 100 100	2, 4, 41, 93	0

There are no RSRZ outliers to report.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.