Full wwPDB X-ray Structure Validation Report (i)

Aug 7, 2023 – 07:13 PM EDT

PDB ID	:	1QTY
Title	:	VASCULAR ENDOTHELIAL GROWTH FACTOR IN COMPLEX WITH DOMAIN 2 OF THE FLT-1 RECEPTOR
Authors	:	Wiesmann, C.; de Vos, A.M.
Deposited on	:	1999-06-29
Resolution	:	2.70 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

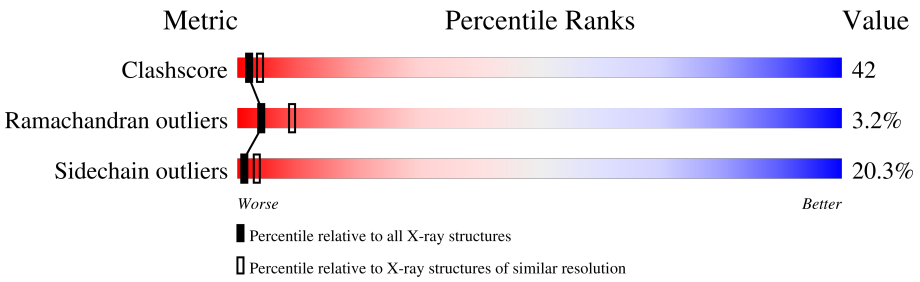
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	R	102	39% 42% 12% 7%
1	S	102	43% 42% 9% 6%
1	V	102	46% 35% 11% • 7%
1	W	102	41% 42% 10% 7%
2	T	101	36% 48% 10% 7%
2	U	101	35% 42% 16% • 7%
2	X	101	36% 45% 12% • 7%
2	Y	101	36% 43% 15% 7%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6121 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 VASCULAR ENDOTHELIAL GROWTH FACTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	V	95	770	483	129	145	13	0	0	0
1	W	95	770	483	129	145	13	0	0	0
1	R	95	770	483	129	145	13	0	0	0
1	S	96	779	489	131	146	13	0	0	0

- Molecule 2 is a protein called FMS-LIKE TYROSINE KINASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	X	94	758	487	130	137	4	0	0	0
2	Y	94	758	487	130	137	4	0	0	0
2	T	94	758	487	130	137	4	0	0	0
2	U	94	758	487	130	137	4	0	0	0

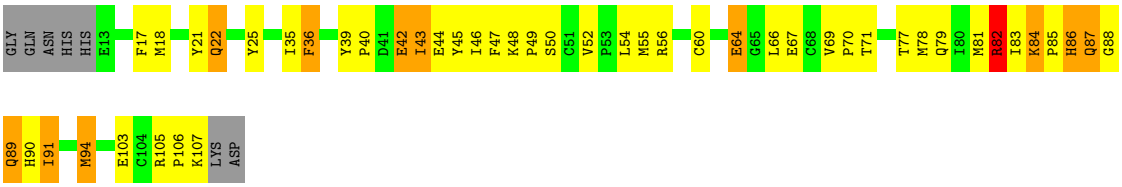
3 Residue-property plots (i)

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

Note EDS was not executed.

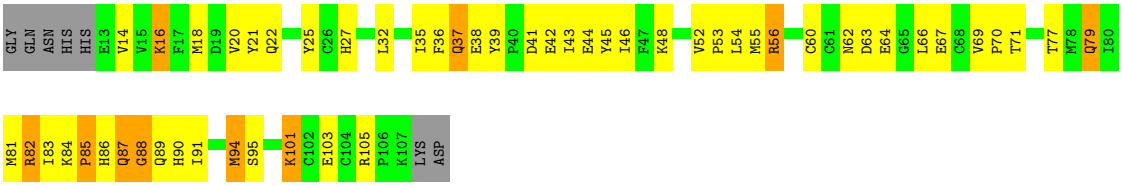
• Molecule 1: VASCULAR ENDOTHELIAL GROWTH FACTOR

Chain V: 46% 35% 11% • 7%



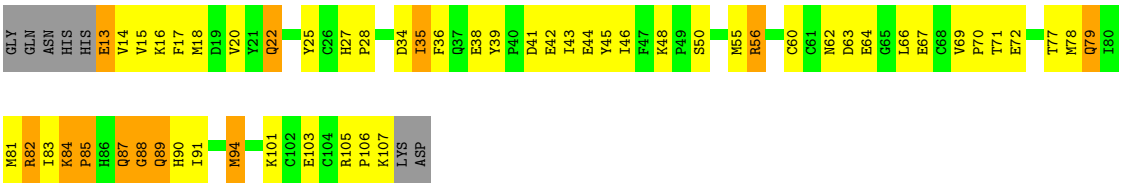
• Molecule 1: VASCULAR ENDOTHELIAL GROWTH FACTOR

Chain W: 41% 42% 10% 7%



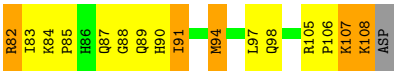
• Molecule 1: VASCULAR ENDOTHELIAL GROWTH FACTOR

Chain R: 39% 42% 12% 7%



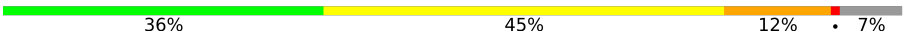
• Molecule 1: VASCULAR ENDOTHELIAL GROWTH FACTOR

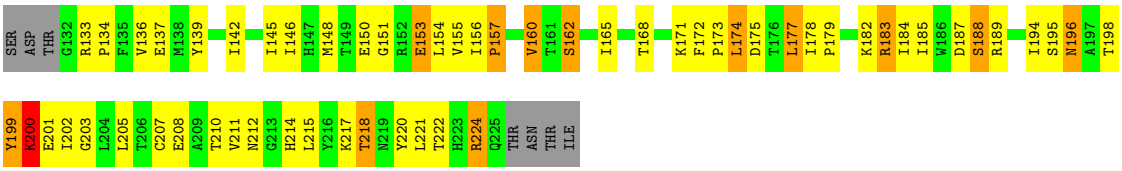
Chain S: 43% 42% 9% 6%



• Molecule 2: FMS-LIKE TYROSINE KINASE 1

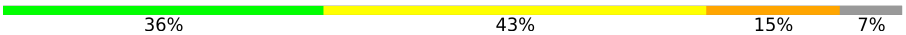
Chain X:

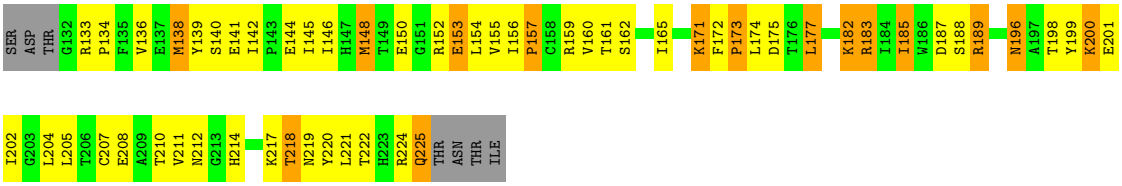




• Molecule 2: FMS-LIKE TYROSINE KINASE 1

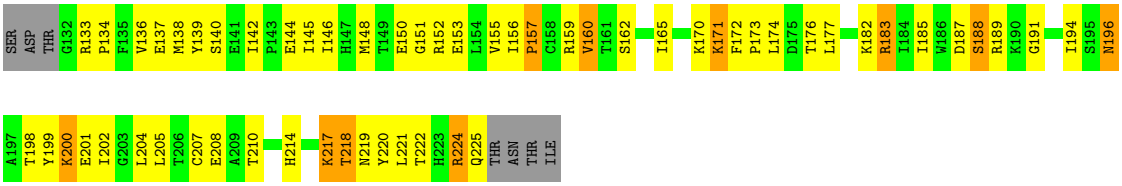
Chain Y:





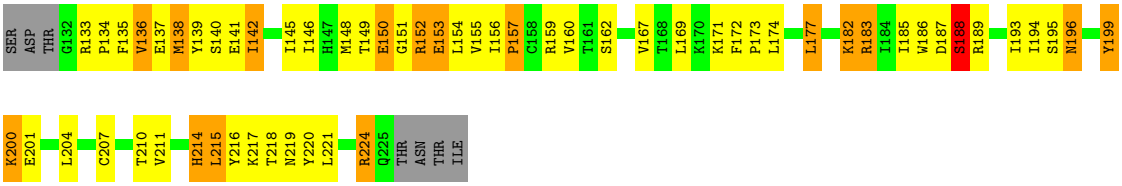
• Molecule 2: FMS-LIKE TYROSINE KINASE 1

Chain T:



• Molecule 2: FMS-LIKE TYROSINE KINASE 1

Chain U:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	124.31Å 67.01Å 120.84Å 90.00° 118.15° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	92.6 (20.00-2.70)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.233 , 0.284	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6121	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

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	R	0.54	0/788	0.74	0/1062
1	S	0.54	0/797	0.70	0/1073
1	V	0.58	1/788 (0.1%)	0.78	1/1062 (0.1%)
1	W	0.56	0/788	0.72	0/1062
2	T	0.54	0/775	0.77	0/1051
2	U	0.59	0/775	0.84	1/1051 (0.1%)
2	X	0.59	0/775	0.80	0/1051
2	Y	0.61	0/775	0.83	0/1051
All	All	0.57	1/6261 (0.0%)	0.77	2/8463 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	V	82	ARG	CZ-NH1	-5.23	1.26	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	V	82	ARG	NE-CZ-NH2	8.63	124.62	120.30
2	U	214	HIS	CB-CA-C	-5.87	98.66	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	770	0	732	66	0
1	S	779	0	745	60	0
1	V	770	0	732	63	0
1	W	770	0	732	51	0
2	T	758	0	775	62	0
2	U	758	0	775	102	0
2	X	758	0	775	82	0
2	Y	758	0	775	59	0
All	All	6121	0	6041	507	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 42.

All (507) 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)
2:U:133:ARG:HH22	2:U:139:TYR:CB	1.52	1.22
2:U:133:ARG:NH2	2:U:139:TYR:HB2	1.56	1.19
2:X:183:ARG:HG2	2:X:183:ARG:HH11	1.01	1.18
2:X:178:ILE:HD12	2:T:183:ARG:HD2	1.20	1.16
2:X:174:LEU:HD12	2:X:174:LEU:H	1.14	1.12
1:W:56:ARG:HG3	1:W:56:ARG:HH11	1.03	1.11
1:W:91:ILE:HG13	2:Y:142:ILE:HD12	1.29	1.11
2:T:139:TYR:H	2:T:218:THR:HG22	1.03	1.11
2:Y:183:ARG:HH11	2:Y:183:ARG:HG2	0.97	1.10
2:U:183:ARG:HG2	2:U:183:ARG:HH11	1.09	1.10
1:R:45:TYR:HD1	1:R:82:ARG:HB3	1.18	1.08
1:V:36:PHE:CZ	1:V:43:ILE:HG23	1.88	1.08
2:T:183:ARG:HH11	2:T:183:ARG:HG2	0.99	1.07
2:Y:138:MET:HG2	2:Y:218:THR:HG23	1.35	1.05
2:Y:139:TYR:H	2:Y:218:THR:HG22	1.19	1.04
1:V:45:TYR:HD1	1:V:82:ARG:HB3	1.22	1.02
1:S:18:MET:O	1:S:22:GLN:HG3	1.60	1.01
2:T:139:TYR:N	2:T:218:THR:HG22	1.77	1.00
2:T:138:MET:HA	2:T:218:THR:CG2	1.89	1.00
2:U:133:ARG:HH22	2:U:139:TYR:HB2	0.86	1.00
2:Y:138:MET:HA	2:Y:218:THR:CG2	1.93	0.98
1:R:45:TYR:CD1	1:R:82:ARG:HB3	1.98	0.97
2:X:199:TYR:CE1	2:X:200:LYS:HG2	1.99	0.97
1:S:56:ARG:HH11	1:S:56:ARG:CG	1.78	0.96
1:S:56:ARG:HH11	1:S:56:ARG:HG3	1.25	0.96
1:V:36:PHE:CE1	1:V:43:ILE:HD13	2.01	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:87:GLN:O	1:V:87:GLN:HG2	1.64	0.94
1:S:45:TYR:HD1	1:S:82:ARG:HB3	1.30	0.94
2:U:133:ARG:HH12	2:U:139:TYR:H	1.02	0.94
2:U:199:TYR:CE1	2:U:200:LYS:HG2	2.02	0.94
1:S:45:TYR:CD1	1:S:82:ARG:HB3	2.03	0.93
2:T:183:ARG:HG2	2:T:183:ARG:NH1	1.74	0.92
2:Y:157:PRO:HG2	2:Y:220:TYR:CE1	2.04	0.92
1:W:18:MET:O	1:W:22:GLN:HG3	1.70	0.91
2:X:183:ARG:HG2	2:X:183:ARG:NH1	1.74	0.91
2:U:136:VAL:HG21	2:U:159:ARG:HG3	1.52	0.90
2:U:183:ARG:HG2	2:U:183:ARG:NH1	1.82	0.90
2:X:182:LYS:O	2:X:185:ILE:HD11	1.70	0.90
2:Y:183:ARG:HG2	2:Y:183:ARG:NH1	1.68	0.90
1:W:56:ARG:HH11	1:W:56:ARG:CG	1.81	0.90
2:Y:139:TYR:N	2:Y:218:THR:HG22	1.87	0.90
1:V:44:GLU:HG2	1:V:45:TYR:HD2	1.35	0.89
1:R:91:ILE:HG13	2:T:142:ILE:HD12	1.52	0.89
2:T:138:MET:HA	2:T:218:THR:HG21	1.56	0.88
1:W:63:ASP:HB3	1:W:66:LEU:HD12	1.55	0.88
1:S:25:TYR:O	1:S:27:HIS:HD2	1.57	0.88
2:Y:225:GLN:C	2:Y:225:GLN:CD	2.32	0.88
1:W:55:MET:O	1:W:56:ARG:HD3	1.73	0.88
2:U:133:ARG:HH12	2:U:139:TYR:N	1.72	0.88
1:W:56:ARG:HG3	1:W:56:ARG:NH1	1.85	0.87
2:X:178:ILE:HD12	2:T:183:ARG:CD	2.05	0.87
1:V:36:PHE:HZ	1:V:43:ILE:HG23	1.33	0.86
2:Y:225:GLN:CD	2:Y:225:GLN:O	2.12	0.86
1:W:45:TYR:HD1	1:W:82:ARG:HB3	1.41	0.86
2:X:183:ARG:HH12	2:X:194:ILE:CG2	1.89	0.86
2:U:183:ARG:HH12	2:U:194:ILE:CG2	1.89	0.85
2:U:133:ARG:NH1	2:U:139:TYR:N	2.25	0.85
2:X:174:LEU:HD12	2:X:174:LEU:N	1.91	0.85
1:V:18:MET:O	1:V:22:GLN:HG3	1.76	0.84
1:S:40:PRO:O	1:S:43:ILE:HD11	1.79	0.83
2:T:183:ARG:HH11	2:T:183:ARG:CG	1.89	0.83
2:T:134:PRO:O	2:T:160:VAL:HG12	1.77	0.83
2:X:146:ILE:HD12	2:X:220:TYR:HB3	1.60	0.82
2:U:133:ARG:NH1	2:U:139:TYR:H	1.76	0.82
1:R:56:ARG:HG3	1:R:56:ARG:HH11	1.44	0.82
2:X:183:ARG:HH11	2:X:183:ARG:CG	1.88	0.81
2:U:155:VAL:O	2:U:157:PRO:HD3	1.80	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:196:ASN:N	2:Y:196:ASN:HD22	1.78	0.81
2:T:196:ASN:N	2:T:196:ASN:HD22	1.77	0.81
2:Y:138:MET:HA	2:Y:218:THR:HG21	1.59	0.81
2:U:196:ASN:N	2:U:196:ASN:HD22	1.79	0.80
2:X:199:TYR:CE1	2:X:200:LYS:HE3	2.16	0.80
1:R:55:MET:O	1:R:56:ARG:HD3	1.82	0.80
1:S:55:MET:O	1:S:56:ARG:HD3	1.81	0.79
2:Y:199:TYR:CE1	2:Y:200:LYS:HG2	2.16	0.79
2:U:133:ARG:NH1	2:U:138:MET:HA	1.97	0.79
2:Y:183:ARG:HH11	2:Y:183:ARG:CG	1.85	0.79
2:T:171:LYS:HE3	2:T:172:PHE:O	1.84	0.78
2:T:136:VAL:CG2	2:T:159:ARG:HG3	2.13	0.78
2:U:133:ARG:HH22	2:U:139:TYR:CA	1.97	0.78
2:U:155:VAL:HG22	2:U:193:ILE:HG23	1.64	0.78
1:V:87:GLN:O	1:V:87:GLN:CG	2.31	0.77
2:U:183:ARG:HH11	2:U:183:ARG:CG	1.96	0.77
1:R:84:LYS:HG2	1:R:87:GLN:HB3	1.65	0.77
1:V:44:GLU:HG2	1:V:45:TYR:CD2	2.20	0.77
1:W:25:TYR:O	1:W:27:HIS:HD2	1.68	0.77
1:V:83:ILE:HG23	1:V:89:GLN:CG	2.14	0.76
2:Y:225:GLN:O	2:Y:225:GLN:NE2	2.18	0.76
2:X:139:TYR:H	2:X:218:THR:CG2	1.99	0.75
2:X:173:PRO:HD2	2:X:174:LEU:CD1	2.17	0.75
1:V:55:MET:O	1:V:56:ARG:HD3	1.86	0.75
2:X:199:TYR:HE1	2:X:200:LYS:HE3	1.51	0.73
2:U:136:VAL:HG23	2:U:159:ARG:O	1.88	0.73
1:V:83:ILE:HG23	1:V:89:GLN:HG2	1.69	0.72
1:W:44:GLU:HG2	1:W:45:TYR:HD2	1.53	0.72
2:X:174:LEU:H	2:X:174:LEU:CD1	1.92	0.72
2:Y:155:VAL:O	2:Y:157:PRO:HD3	1.88	0.72
1:R:18:MET:O	1:R:22:GLN:HG3	1.90	0.72
2:X:139:TYR:H	2:X:218:THR:HG23	1.54	0.72
1:V:36:PHE:HZ	1:V:43:ILE:CG2	2.02	0.72
2:U:135:PHE:CZ	2:U:167:VAL:HG22	2.24	0.71
2:X:173:PRO:HD2	2:X:174:LEU:HD12	1.71	0.71
2:U:199:TYR:CE1	2:U:200:LYS:HE3	2.25	0.71
1:V:45:TYR:CD1	1:V:82:ARG:HB3	2.15	0.71
1:S:67:GLU:OE2	1:S:108:LYS:NZ	2.24	0.71
1:W:45:TYR:HD1	1:W:82:ARG:CB	2.03	0.71
2:U:136:VAL:CG2	2:U:159:ARG:HG3	2.19	0.71
2:T:136:VAL:HG21	2:T:159:ARG:HG3	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:91:ILE:HG13	2:X:142:ILE:HD12	1.74	0.69
1:V:44:GLU:HG3	1:V:84:LYS:NZ	2.08	0.69
2:Y:138:MET:HG2	2:Y:218:THR:CG2	2.17	0.69
2:U:150:GLU:HG3	2:U:224:ARG:NH1	2.08	0.68
1:S:107:LYS:C	1:S:108:LYS:HG3	2.12	0.68
2:U:199:TYR:CD1	2:U:200:LYS:HG2	2.28	0.68
1:R:63:ASP:HB3	1:R:66:LEU:HD12	1.75	0.68
1:R:44:GLU:HG2	1:R:45:TYR:HD2	1.58	0.68
2:Y:225:GLN:C	2:Y:225:GLN:OE1	2.32	0.68
1:V:35:ILE:HG13	1:V:50:SER:O	1.95	0.67
2:X:199:TYR:CD1	2:X:200:LYS:N	2.63	0.67
2:U:210:THR:HA	2:U:214:HIS:O	1.94	0.67
1:V:56:ARG:HG3	1:V:56:ARG:HH11	1.60	0.66
1:V:91:ILE:HG22	1:V:91:ILE:O	1.96	0.66
1:S:56:ARG:CG	1:S:56:ARG:NH1	2.47	0.66
1:R:88:GLY:C	1:R:89:GLN:HG3	2.16	0.66
2:X:172:PHE:CE2	2:X:173:PRO:HB3	2.31	0.66
2:U:139:TYR:CG	2:U:140:SER:N	2.63	0.66
1:V:36:PHE:HE1	1:V:43:ILE:HD13	1.60	0.66
1:V:81:MET:SD	2:X:145:ILE:HD11	2.35	0.66
1:R:16:LYS:O	1:R:20:VAL:HG23	1.95	0.66
2:X:173:PRO:HD2	2:X:174:LEU:H	1.61	0.66
1:S:83:ILE:HG23	1:S:89:GLN:HB3	1.79	0.65
2:X:174:LEU:HD13	2:X:175:ASP:CG	2.18	0.64
1:V:36:PHE:CZ	1:V:43:ILE:HA	2.32	0.64
1:R:83:ILE:O	1:R:85:PRO:HD3	1.97	0.64
1:W:16:LYS:O	1:W:20:VAL:HG23	1.98	0.64
1:S:38:GLU:O	1:S:40:PRO:HD3	1.97	0.64
2:U:133:ARG:NH1	2:U:138:MET:CA	2.60	0.64
2:X:182:LYS:O	2:X:185:ILE:CD1	2.44	0.63
1:W:91:ILE:HG13	2:Y:142:ILE:CD1	2.19	0.63
2:U:133:ARG:HD3	2:U:135:PHE:O	1.99	0.63
1:R:88:GLY:O	1:R:89:GLN:HG3	1.98	0.63
1:S:89:GLN:HG2	1:S:89:GLN:O	1.98	0.63
1:W:67:GLU:HG3	1:W:69:VAL:HG13	1.80	0.63
1:W:56:ARG:CG	1:W:56:ARG:NH1	2.47	0.63
1:R:35:ILE:HG13	1:R:50:SER:O	1.99	0.63
1:S:36:PHE:CZ	1:S:43:ILE:HA	2.34	0.63
1:V:45:TYR:HD1	1:V:82:ARG:CB	2.04	0.62
2:U:135:PHE:HZ	2:U:167:VAL:HG13	1.65	0.62
1:R:14:VAL:HG12	1:R:15:VAL:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:71:THR:CG2	1:W:103:GLU:HB2	2.31	0.61
2:Y:156:ILE:HD13	2:Y:156:ILE:N	2.15	0.61
2:T:138:MET:HA	2:T:218:THR:HG22	1.75	0.61
2:U:199:TYR:CD1	2:U:200:LYS:N	2.68	0.61
1:R:69:VAL:HB	1:R:70:PRO:HD2	1.81	0.61
2:T:134:PRO:O	2:T:160:VAL:HA	2.01	0.60
1:R:77:THR:HA	1:R:94:MET:O	2.01	0.60
2:T:138:MET:HG3	2:T:218:THR:HG23	1.83	0.60
2:X:199:TYR:CD1	2:X:200:LYS:HG2	2.36	0.60
2:U:224:ARG:O	2:U:224:ARG:HG3	1.98	0.60
2:T:139:TYR:H	2:T:218:THR:CG2	1.96	0.60
1:W:25:TYR:O	1:W:27:HIS:CD2	2.54	0.60
2:X:155:VAL:O	2:X:157:PRO:HD3	2.02	0.59
1:S:25:TYR:O	1:S:27:HIS:CD2	2.47	0.59
1:W:71:THR:HG21	1:W:103:GLU:HB2	1.84	0.59
1:V:83:ILE:HA	1:V:89:GLN:HB3	1.84	0.59
2:X:136:VAL:HB	2:X:137:GLU:OE2	2.04	0.58
2:U:134:PRO:HB3	2:U:211:VAL:HG21	1.85	0.58
1:R:14:VAL:HG22	1:S:77:THR:HG22	1.84	0.58
1:R:22:GLN:HB3	2:U:172:PHE:CZ	2.38	0.58
2:T:204:LEU:HD11	2:T:219:ASN:HB3	1.86	0.58
2:U:196:ASN:N	2:U:196:ASN:ND2	2.48	0.58
1:W:69:VAL:HB	1:W:70:PRO:HD2	1.84	0.58
1:R:56:ARG:HG3	1:R:56:ARG:NH1	2.16	0.58
2:X:195:SER:C	2:X:196:ASN:HD22	2.07	0.57
2:X:211:VAL:O	2:X:212:ASN:HB2	2.04	0.57
2:U:135:PHE:CZ	2:U:167:VAL:CG2	2.87	0.57
1:R:79:GLN:HG2	1:R:91:ILE:HG23	1.87	0.57
2:T:138:MET:CA	2:T:218:THR:CG2	2.75	0.57
2:X:134:PRO:HB3	2:X:165:ILE:HD13	1.87	0.57
1:W:79:GLN:HG2	1:W:91:ILE:CG2	2.34	0.57
1:V:36:PHE:HZ	1:V:43:ILE:HA	1.70	0.57
1:S:32:LEU:HD23	1:S:53:PRO:HA	1.87	0.57
2:T:208:GLU:HG2	2:T:217:LYS:HB3	1.87	0.57
2:X:183:ARG:HH12	2:X:194:ILE:HG22	1.67	0.57
2:U:199:TYR:HD1	2:U:200:LYS:N	2.02	0.57
1:S:35:ILE:HG13	1:S:50:SER:O	2.04	0.57
2:X:224:ARG:CG	2:X:224:ARG:O	2.53	0.57
1:W:77:THR:HA	1:W:94:MET:O	2.05	0.56
2:X:199:TYR:HD1	2:X:200:LYS:N	2.03	0.56
2:U:199:TYR:HE1	2:U:200:LYS:HE3	1.67	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:183:ARG:NH1	2:X:194:ILE:CG2	2.65	0.56
2:Y:138:MET:HE3	2:Y:217:LYS:O	2.05	0.56
2:U:135:PHE:CE1	2:U:167:VAL:HG21	2.41	0.56
2:U:182:LYS:O	2:U:185:ILE:CD1	2.54	0.56
1:R:83:ILE:HG23	1:R:89:GLN:HG2	1.87	0.56
2:Y:145:ILE:HG22	2:Y:146:ILE:N	2.20	0.56
2:U:137:GLU:O	2:U:138:MET:O	2.24	0.55
2:X:207:CYS:O	2:X:217:LYS:HA	2.06	0.55
1:R:79:GLN:HG2	1:R:91:ILE:CG2	2.36	0.55
2:T:196:ASN:N	2:T:196:ASN:ND2	2.49	0.55
1:V:44:GLU:HG3	1:V:84:LYS:HZ1	1.70	0.55
1:R:36:PHE:HE2	1:R:43:ILE:HG23	1.72	0.55
2:U:224:ARG:O	2:U:224:ARG:CG	2.53	0.55
2:T:207:CYS:O	2:T:217:LYS:HA	2.06	0.55
1:S:56:ARG:HG3	1:S:56:ARG:NH1	2.07	0.54
1:V:40:PRO:O	1:V:43:ILE:HD11	2.06	0.54
1:S:83:ILE:HG12	1:S:89:GLN:HB2	1.87	0.54
1:V:67:GLU:HB3	1:V:107:LYS:HG2	1.89	0.54
1:R:91:ILE:HG13	2:T:142:ILE:CD1	2.33	0.54
2:U:169:LEU:HD23	2:U:177:LEU:HB3	1.90	0.54
2:U:183:ARG:HH12	2:U:194:ILE:HG22	1.69	0.54
1:V:18:MET:O	1:V:22:GLN:CG	2.53	0.54
2:X:139:TYR:HB2	2:X:218:THR:HG22	1.90	0.54
2:U:183:ARG:NH1	2:U:194:ILE:CG2	2.65	0.54
2:X:202:ILE:HA	2:X:222:THR:OG1	2.08	0.54
1:R:14:VAL:HG22	1:S:77:THR:CG2	2.37	0.54
1:R:14:VAL:CG1	1:R:15:VAL:N	2.71	0.54
1:R:91:ILE:HG22	1:R:91:ILE:O	2.08	0.54
1:S:36:PHE:HZ	1:S:43:ILE:HA	1.72	0.54
2:X:174:LEU:HD13	2:X:175:ASP:OD2	2.07	0.54
1:R:48:LYS:O	1:S:17:PHE:HE1	1.91	0.53
2:U:133:ARG:NH2	2:U:139:TYR:CA	2.67	0.53
2:X:178:ILE:CD1	2:T:183:ARG:HD2	2.14	0.53
2:X:196:ASN:HD22	2:X:196:ASN:N	2.06	0.53
2:X:210:THR:HA	2:X:214:HIS:O	2.08	0.53
2:U:155:VAL:CG2	2:U:193:ILE:HG23	2.38	0.53
2:U:133:ARG:CZ	2:U:139:TYR:N	2.72	0.53
2:X:199:TYR:HE1	2:X:200:LYS:HG2	1.68	0.53
2:U:169:LEU:HD23	2:U:177:LEU:CB	2.38	0.53
2:U:153:GLU:HG3	2:U:154:LEU:N	2.23	0.53
2:Y:138:MET:CA	2:Y:218:THR:CG2	2.80	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:155:VAL:O	2:U:157:PRO:CD	2.55	0.53
2:U:211:VAL:HB	2:U:216:TYR:HE1	1.74	0.53
2:Y:138:MET:HA	2:Y:218:THR:HG22	1.85	0.53
2:Y:139:TYR:H	2:Y:218:THR:CG2	2.07	0.53
2:U:182:LYS:O	2:U:185:ILE:HD11	2.09	0.53
2:U:195:SER:C	2:U:196:ASN:HD22	2.12	0.53
2:Y:138:MET:CE	2:Y:217:LYS:O	2.57	0.53
1:V:69:VAL:HB	1:V:70:PRO:HD2	1.92	0.52
1:R:103:GLU:OE1	1:R:105:ARG:NH2	2.40	0.52
2:X:199:TYR:HA	2:X:202:ILE:CD1	2.39	0.52
2:U:139:TYR:CE2	2:U:141:GLU:N	2.77	0.52
2:U:149:THR:CG2	2:U:152:ARG:HG3	2.38	0.52
2:X:174:LEU:N	2:X:174:LEU:CD1	2.61	0.52
1:R:83:ILE:HG23	1:R:89:GLN:CG	2.39	0.52
1:R:84:LYS:HG2	1:R:87:GLN:CB	2.36	0.52
2:T:134:PRO:HB3	2:T:165:ILE:HD13	1.91	0.52
1:W:18:MET:O	1:W:22:GLN:CG	2.52	0.52
2:Y:196:ASN:N	2:Y:196:ASN:ND2	2.51	0.52
1:R:87:GLN:O	1:R:88:GLY:O	2.28	0.52
1:S:66:LEU:HA	1:S:105:ARG:O	2.10	0.52
2:X:172:PHE:CD2	2:X:173:PRO:HB3	2.45	0.52
1:V:64:GLU:O	1:V:107:LYS:HD2	2.09	0.52
1:R:62:ASN:OD1	1:S:49:PRO:HA	2.10	0.52
2:Y:172:PHE:CG	2:Y:173:PRO:HA	2.45	0.52
2:U:172:PHE:CG	2:U:173:PRO:HA	2.44	0.52
2:X:187:ASP:O	2:X:189:ARG:N	2.43	0.52
2:T:172:PHE:CE2	2:T:173:PRO:HB3	2.45	0.52
1:V:25:TYR:CE2	2:Y:173:PRO:HD3	2.44	0.52
1:W:63:ASP:CB	1:W:66:LEU:HD12	2.35	0.52
1:R:66:LEU:HA	1:R:105:ARG:O	2.09	0.52
1:S:44:GLU:HG2	1:S:45:TYR:CD2	2.45	0.52
2:U:139:TYR:CD2	2:U:140:SER:N	2.78	0.52
1:V:66:LEU:HA	1:V:105:ARG:O	2.10	0.51
2:X:179:PRO:HA	2:X:184:ILE:HB	1.92	0.51
2:T:138:MET:CA	2:T:218:THR:HG22	2.40	0.51
1:R:63:ASP:OD2	2:U:224:ARG:HG2	2.11	0.51
2:X:208:GLU:HG2	2:X:217:LYS:HB3	1.92	0.51
2:U:215:LEU:HD21	2:U:217:LYS:HE2	1.92	0.51
1:W:71:THR:OG1	1:W:101:LYS:HB3	2.11	0.51
1:R:17:PHE:HE1	1:S:48:LYS:O	1.94	0.51
1:S:64:GLU:O	1:S:107:LYS:HD2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:45:TYR:CD1	1:W:82:ARG:HB3	2.33	0.51
1:S:22:GLN:HE21	2:T:172:PHE:HE1	1.59	0.51
2:T:146:ILE:HD12	2:T:220:TYR:HB3	1.91	0.51
1:S:18:MET:CE	2:T:204:LEU:HD21	2.41	0.50
1:S:108:LYS:HE2	1:S:108:LYS:N	2.25	0.50
2:X:199:TYR:HA	2:X:202:ILE:HD12	1.92	0.50
1:V:56:ARG:HG3	1:V:56:ARG:NH1	2.23	0.50
1:V:83:ILE:HG12	1:V:89:GLN:HB3	1.94	0.50
1:W:45:TYR:CD1	1:W:82:ARG:CB	2.90	0.50
1:W:21:TYR:C	1:W:21:TYR:CD1	2.85	0.50
2:U:187:ASP:O	2:U:189:ARG:N	2.44	0.50
1:V:81:MET:HB2	1:V:91:ILE:CD1	2.41	0.50
2:T:171:LYS:HG2	2:T:205:LEU:CD2	2.41	0.50
2:U:133:ARG:HH11	2:U:138:MET:HA	1.72	0.50
1:R:106:PRO:HG3	2:U:199:TYR:CD2	2.46	0.50
1:R:78:MET:HB3	1:S:20:VAL:HG21	1.93	0.49
2:U:159:ARG:HD3	2:U:189:ARG:O	2.11	0.49
2:X:134:PRO:O	2:X:160:VAL:HA	2.11	0.49
2:X:151:GLY:O	2:X:196:ASN:HA	2.12	0.49
1:R:35:ILE:CG1	1:R:50:SER:O	2.60	0.49
2:X:173:PRO:CD	2:X:174:LEU:H	2.24	0.49
1:S:40:PRO:C	1:S:43:ILE:HD11	2.33	0.49
2:T:199:TYR:CE1	2:T:200:LYS:HG2	2.48	0.49
2:T:204:LEU:HD12	2:T:220:TYR:O	2.12	0.49
2:X:199:TYR:C	2:X:201:GLU:H	2.15	0.49
2:T:138:MET:HG3	2:T:218:THR:CG2	2.43	0.49
1:V:88:GLY:C	1:V:89:GLN:HG3	2.32	0.49
1:R:84:LYS:CG	1:R:87:GLN:HB3	2.41	0.49
1:S:91:ILE:HG22	1:S:91:ILE:O	2.12	0.49
2:U:183:ARG:HH12	2:U:194:ILE:HG23	1.76	0.48
1:S:91:ILE:HG13	2:U:142:ILE:HD12	1.95	0.48
2:Y:182:LYS:O	2:Y:185:ILE:HD12	2.13	0.48
1:R:84:LYS:HG2	1:R:87:GLN:OE1	2.14	0.48
2:T:199:TYR:CD1	2:T:200:LYS:N	2.82	0.48
2:T:210:THR:HA	2:T:214:HIS:O	2.14	0.48
1:W:22:GLN:HB3	2:X:172:PHE:CZ	2.48	0.48
2:Y:210:THR:HA	2:Y:214:HIS:O	2.14	0.48
2:U:135:PHE:CE1	2:U:167:VAL:CG2	2.97	0.48
1:V:71:THR:CG2	1:V:103:GLU:HB2	2.44	0.48
1:R:67:GLU:HG3	1:R:69:VAL:HG13	1.96	0.48
2:X:205:LEU:HD12	2:X:222:THR:HG23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:148:MET:HG2	2:Y:222:THR:HB	1.94	0.48
2:U:146:ILE:HD12	2:U:220:TYR:HB3	1.95	0.48
2:U:207:CYS:O	2:U:217:LYS:HA	2.14	0.48
2:U:133:ARG:NH2	2:U:139:TYR:N	2.62	0.47
2:U:211:VAL:HB	2:U:216:TYR:CE1	2.49	0.47
1:R:45:TYR:HD1	1:R:82:ARG:CB	2.07	0.47
1:S:69:VAL:HB	1:S:70:PRO:HD2	1.96	0.47
1:V:49:PRO:HA	1:W:62:ASN:OD1	2.14	0.47
2:X:174:LEU:CD1	2:X:175:ASP:OD2	2.62	0.47
2:Y:172:PHE:CD2	2:Y:173:PRO:HA	2.50	0.47
1:V:42:GLU:HA	1:V:44:GLU:OE1	2.15	0.47
1:S:44:GLU:O	1:S:84:LYS:HD2	2.14	0.47
2:T:225:GLN:HG3	2:T:225:GLN:O	2.13	0.47
2:U:154:LEU:HD23	2:U:194:ILE:HD13	1.97	0.47
1:W:66:LEU:HD21	2:X:199:TYR:HB2	1.96	0.47
1:R:13:GLU:C	1:R:14:VAL:HG23	2.35	0.47
2:T:133:ARG:HA	2:T:134:PRO:HD3	1.79	0.47
1:V:52:VAL:HG23	1:V:54:LEU:HG	1.96	0.47
1:V:105:ARG:HB3	1:V:106:PRO:CD	2.45	0.47
1:W:22:GLN:HE21	2:X:172:PHE:HE1	1.62	0.47
1:R:81:MET:SD	2:T:145:ILE:HD11	2.55	0.47
2:X:146:ILE:HD11	2:X:220:TYR:CD2	2.50	0.47
1:V:64:GLU:HA	1:V:64:GLU:OE1	2.13	0.47
1:W:44:GLU:HG2	1:W:45:TYR:CD2	2.42	0.47
1:W:66:LEU:HA	1:W:105:ARG:O	2.15	0.47
1:S:67:GLU:HB3	1:S:107:LYS:HG2	1.97	0.47
2:X:153:GLU:HG3	2:X:154:LEU:N	2.29	0.47
2:Y:183:ARG:NH1	2:Y:183:ARG:CG	2.51	0.47
2:U:137:GLU:CD	2:U:137:GLU:N	2.69	0.47
1:V:77:THR:HG22	1:W:14:VAL:HG13	1.95	0.46
1:R:38:GLU:O	1:R:39:TYR:CD2	2.68	0.46
2:X:168:THR:O	2:X:207:CYS:HA	2.15	0.46
2:X:196:ASN:N	2:X:196:ASN:ND2	2.63	0.46
2:Y:146:ILE:HD11	2:Y:220:TYR:CD1	2.50	0.46
1:W:67:GLU:HG3	1:W:69:VAL:CG1	2.45	0.46
2:U:136:VAL:HG12	2:U:137:GLU:OE2	2.15	0.46
1:R:67:GLU:HB3	1:R:107:LYS:HG2	1.97	0.46
2:T:151:GLY:O	2:T:196:ASN:HA	2.16	0.46
1:V:81:MET:HA	1:V:91:ILE:HD13	1.97	0.46
1:S:38:GLU:C	1:S:40:PRO:HD3	2.35	0.46
2:T:162:SER:HB2	2:T:165:ILE:HG13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:55:MET:C	1:S:56:ARG:HD3	2.35	0.46
1:R:44:GLU:HG2	1:R:45:TYR:CD2	2.46	0.46
2:X:187:ASP:C	2:X:187:ASP:OD1	2.53	0.46
2:Y:145:ILE:CG2	2:Y:146:ILE:N	2.79	0.46
1:S:84:LYS:O	1:S:85:PRO:C	2.54	0.46
2:X:172:PHE:CZ	2:X:173:PRO:HB3	2.51	0.46
1:R:27:HIS:HB2	1:R:28:PRO:CD	2.46	0.46
1:R:106:PRO:HG3	2:U:199:TYR:HD2	1.80	0.46
2:Y:199:TYR:CD1	2:Y:200:LYS:N	2.83	0.46
2:U:151:GLY:O	2:U:196:ASN:HA	2.16	0.46
2:U:204:LEU:HD11	2:U:219:ASN:HB3	1.97	0.46
1:S:43:ILE:H	1:S:43:ILE:HG12	1.51	0.46
1:S:97:LEU:HG	1:S:98:GLN:N	2.30	0.46
2:X:145:ILE:HG22	2:X:146:ILE:N	2.30	0.46
2:Y:134:PRO:HB3	2:Y:165:ILE:HD13	1.98	0.46
2:U:177:LEU:HD12	2:U:177:LEU:HA	1.66	0.46
2:Y:136:VAL:CG2	2:Y:159:ARG:HG3	2.46	0.45
2:Y:211:VAL:O	2:Y:212:ASN:HB2	2.15	0.45
2:T:156:ILE:O	2:T:191:GLY:HA3	2.16	0.45
2:T:183:ARG:HH12	2:T:194:ILE:CG2	2.28	0.45
1:S:91:ILE:HA	1:S:91:ILE:HD13	1.72	0.45
2:Y:155:VAL:O	2:Y:157:PRO:CD	2.62	0.45
2:U:136:VAL:CG1	2:U:137:GLU:OE2	2.64	0.45
1:V:81:MET:HB2	1:V:91:ILE:HD13	1.97	0.45
2:U:135:PHE:HZ	2:U:167:VAL:HG22	1.79	0.45
2:U:186:TRP:CZ2	2:U:188:SER:HA	2.52	0.45
2:X:156:ILE:N	2:X:156:ILE:HD13	2.31	0.45
2:U:183:ARG:NH1	2:U:194:ILE:HG23	2.31	0.45
2:U:199:TYR:CD1	2:U:199:TYR:C	2.89	0.45
1:V:71:THR:HG21	1:V:103:GLU:HB2	1.97	0.45
1:S:33:VAL:HG21	1:S:54:LEU:HD12	1.99	0.45
2:X:177:LEU:HA	2:X:177:LEU:HD12	1.65	0.45
2:X:199:TYR:CD1	2:X:199:TYR:C	2.89	0.45
2:T:139:TYR:CD1	2:T:144:GLU:HB2	2.52	0.45
1:W:91:ILE:CG1	2:Y:142:ILE:HD12	2.21	0.45
1:R:88:GLY:C	1:R:89:GLN:CG	2.84	0.45
2:U:135:PHE:HE1	2:U:167:VAL:HG21	1.81	0.45
1:W:86:HIS:O	1:W:87:GLN:HB2	2.16	0.45
2:Y:187:ASP:O	2:Y:189:ARG:N	2.50	0.45
2:T:198:THR:N	2:T:201:GLU:OE1	2.49	0.45
1:R:35:ILE:HG13	1:R:50:SER:C	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:45:TYR:CD1	1:R:82:ARG:CB	2.87	0.44
2:Y:199:TYR:OH	2:Y:200:LYS:HE3	2.18	0.44
2:U:135:PHE:HZ	2:U:167:VAL:CG1	2.30	0.44
1:R:14:VAL:HG13	1:S:77:THR:O	2.18	0.44
1:R:39:TYR:C	1:R:41:ASP:H	2.20	0.44
2:X:203:GLY:N	2:X:222:THR:OG1	2.45	0.44
1:W:36:PHE:O	1:W:37:GLN:C	2.54	0.44
2:T:182:LYS:O	2:T:185:ILE:HD12	2.17	0.44
1:V:48:LYS:HA	1:V:49:PRO:HA	1.75	0.44
1:S:44:GLU:HG2	1:S:45:TYR:HD2	1.82	0.44
1:R:44:GLU:CG	1:R:45:TYR:HD2	2.28	0.44
1:S:105:ARG:HB3	1:S:106:PRO:CD	2.48	0.44
2:X:172:PHE:HA	2:X:173:PRO:HA	1.68	0.44
2:X:183:ARG:NH2	2:X:201:GLU:OE2	2.50	0.44
2:Y:133:ARG:HA	2:Y:134:PRO:HD3	1.88	0.44
2:T:156:ILE:HA	2:T:157:PRO:HD2	1.63	0.44
2:Y:202:ILE:HA	2:Y:222:THR:OG1	2.18	0.44
1:W:79:GLN:HG2	1:W:91:ILE:HG23	1.99	0.43
2:Y:134:PRO:O	2:Y:161:THR:HG23	2.18	0.43
2:X:183:ARG:HH22	2:X:201:GLU:CD	2.21	0.43
2:U:154:LEU:HD21	2:U:156:ILE:HD11	2.00	0.43
2:Y:183:ARG:NH2	2:Y:201:GLU:OE2	2.51	0.43
2:U:134:PRO:HG3	2:U:211:VAL:CG2	2.48	0.43
2:U:150:GLU:HG3	2:U:224:ARG:HH11	1.83	0.43
2:U:182:LYS:O	2:U:185:ILE:HD12	2.18	0.43
2:X:133:ARG:HA	2:X:134:PRO:HD3	1.86	0.43
2:T:183:ARG:NH2	2:T:201:GLU:OE2	2.51	0.43
1:W:39:TYR:C	1:W:41:ASP:H	2.21	0.43
1:W:55:MET:C	1:W:56:ARG:HD3	2.37	0.43
1:W:87:GLN:O	1:W:88:GLY:O	2.36	0.43
2:X:173:PRO:CD	2:X:174:LEU:N	2.82	0.43
2:Y:134:PRO:CB	2:Y:165:ILE:HD13	2.49	0.43
1:R:103:GLU:OE1	1:R:105:ARG:NE	2.50	0.43
1:S:108:LYS:HE2	1:S:108:LYS:H	1.84	0.43
1:R:25:TYR:CE2	2:U:173:PRO:HD3	2.54	0.43
2:Y:172:PHE:CD2	2:Y:173:PRO:N	2.87	0.43
2:T:136:VAL:HG23	2:T:159:ARG:HG3	1.97	0.43
2:T:187:ASP:O	2:T:189:ARG:N	2.52	0.43
2:T:199:TYR:C	2:T:201:GLU:H	2.22	0.43
1:V:47:PHE:CE1	1:V:82:ARG:HG2	2.53	0.42
2:X:224:ARG:O	2:X:224:ARG:HG3	2.14	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:38:GLU:O	1:R:39:TYR:HD2	2.02	0.42
2:T:139:TYR:HD1	2:T:220:TYR:CE2	2.37	0.42
2:T:145:ILE:HG22	2:T:146:ILE:N	2.33	0.42
1:V:36:PHE:CZ	1:V:43:ILE:CG2	2.76	0.42
1:R:66:LEU:HD21	2:U:199:TYR:HB2	2.01	0.42
1:S:65:GLY:HA3	2:T:224:ARG:HH21	1.83	0.42
2:X:162:SER:HB2	2:X:165:ILE:HG13	2.02	0.42
2:Y:156:ILE:HA	2:Y:157:PRO:HD2	1.44	0.42
2:T:160:VAL:HG11	2:T:165:ILE:HG21	2.00	0.42
2:Y:153:GLU:HG3	2:Y:154:LEU:N	2.34	0.42
2:Y:207:CYS:O	2:Y:217:LYS:HA	2.19	0.42
1:W:38:GLU:OE2	1:W:38:GLU:HA	2.19	0.42
1:S:36:PHE:CE2	1:S:43:ILE:HG23	2.55	0.42
2:X:198:THR:N	2:X:201:GLU:OE1	2.52	0.42
2:Y:171:LYS:HG2	2:Y:205:LEU:CD2	2.50	0.42
1:V:85:PRO:O	1:V:86:HIS:HB2	2.19	0.42
2:T:134:PRO:O	2:T:160:VAL:CG1	2.60	0.42
2:U:134:PRO:HD3	2:U:216:TYR:CD1	2.54	0.42
2:U:172:PHE:CD1	2:U:173:PRO:HA	2.55	0.42
1:V:35:ILE:HG13	1:V:50:SER:C	2.40	0.42
1:W:85:PRO:O	1:W:86:HIS:C	2.58	0.42
2:U:133:ARG:NH1	2:U:138:MET:C	2.72	0.42
1:V:45:TYR:CD1	1:V:82:ARG:CB	2.92	0.42
1:W:83:ILE:O	1:W:85:PRO:HD3	2.20	0.42
1:R:71:THR:HG21	1:R:103:GLU:HB2	2.00	0.42
1:S:67:GLU:HG3	1:S:69:VAL:HG13	2.01	0.42
1:S:77:THR:HA	1:S:94:MET:O	2.20	0.42
2:U:133:ARG:HH22	2:U:139:TYR:N	2.18	0.42
2:U:199:TYR:C	2:U:201:GLU:H	2.22	0.42
2:U:156:ILE:HA	2:U:157:PRO:HD2	1.64	0.42
1:V:43:ILE:H	1:V:43:ILE:HG12	1.71	0.41
1:W:38:GLU:C	1:W:39:TYR:HD1	2.23	0.41
2:U:215:LEU:HD21	2:U:217:LYS:CE	2.50	0.41
1:V:35:ILE:O	1:V:35:ILE:HG22	2.20	0.41
1:V:39:TYR:CD2	1:V:94:MET:HE2	2.56	0.41
1:S:81:MET:HE3	1:S:81:MET:HB2	1.96	0.41
2:X:173:PRO:HD2	2:X:174:LEU:CG	2.50	0.41
1:V:17:PHE:HE1	1:W:48:LYS:O	2.03	0.41
1:V:44:GLU:HG3	1:V:84:LYS:CE	2.50	0.41
1:R:56:ARG:NH1	1:R:56:ARG:CG	2.83	0.41
1:S:56:ARG:NH1	1:S:56:ARG:HG2	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:182:LYS:O	2:T:185:ILE:CD1	2.68	0.41
1:V:67:GLU:HG3	1:V:69:VAL:HG13	2.02	0.41
1:V:77:THR:O	1:W:14:VAL:HG13	2.21	0.41
1:W:52:VAL:HG23	1:W:54:LEU:HG	2.02	0.41
1:S:48:LYS:HA	1:S:49:PRO:HA	1.85	0.41
2:U:140:SER:C	2:U:142:ILE:N	2.72	0.41
2:U:183:ARG:O	2:U:194:ILE:HA	2.19	0.41
2:U:145:ILE:HG22	2:U:146:ILE:N	2.36	0.41
1:R:84:LYS:HG2	1:R:87:GLN:CD	2.41	0.41
2:U:135:PHE:CZ	2:U:167:VAL:HG13	2.50	0.41
1:V:47:PHE:HE1	1:V:82:ARG:HG2	1.86	0.41
2:Y:208:GLU:HG2	2:Y:217:LYS:HB3	2.03	0.41
2:T:155:VAL:O	2:T:157:PRO:HD3	2.21	0.41
2:Y:139:TYR:CE1	2:Y:144:GLU:OE1	2.74	0.41
1:S:66:LEU:HD11	2:T:202:ILE:HD12	2.02	0.40
2:X:134:PRO:O	2:X:160:VAL:HG12	2.20	0.40
1:V:21:TYR:CD1	1:V:21:TYR:C	2.94	0.40
1:W:32:LEU:HD23	1:W:53:PRO:HA	2.04	0.40
2:X:154:LEU:HD23	2:X:194:ILE:HD13	2.03	0.40
2:T:202:ILE:HA	2:T:222:THR:OG1	2.21	0.40
1:R:91:ILE:HD13	1:R:91:ILE:HA	1.89	0.40
2:Y:177:LEU:HA	2:Y:177:LEU:HD12	1.76	0.40
1:W:39:TYR:OH	1:W:95:SER:O	2.30	0.40
1:S:52:VAL:HG23	1:S:54:LEU:HG	2.03	0.40
2:X:199:TYR:O	2:X:201:GLU:N	2.54	0.40
2:Y:204:LEU:HD11	2:Y:219:ASN:HB3	2.04	0.40
1:V:91:ILE:HD13	1:V:91:ILE:HA	1.77	0.40
1:R:106:PRO:CG	2:U:199:TYR:CD2	3.05	0.40
1:S:44:GLU:HG3	1:S:84:LYS:NZ	2.36	0.40
2:Y:182:LYS:O	2:Y:185:ILE:CD1	2.70	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	R	93/102 (91%)	83 (89%)	6 (6%)	4 (4%)	2	5
1	S	94/102 (92%)	85 (90%)	7 (7%)	2 (2%)	7	18
1	V	93/102 (91%)	85 (91%)	7 (8%)	1 (1%)	14	34
1	W	93/102 (91%)	82 (88%)	8 (9%)	3 (3%)	4	9
2	T	92/101 (91%)	82 (89%)	7 (8%)	3 (3%)	4	8
2	U	92/101 (91%)	76 (83%)	12 (13%)	4 (4%)	2	5
2	X	92/101 (91%)	81 (88%)	8 (9%)	3 (3%)	4	8
2	Y	92/101 (91%)	80 (87%)	8 (9%)	4 (4%)	2	5
All	All	741/812 (91%)	654 (88%)	63 (8%)	24 (3%)	4	9

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	W	88	GLY
2	U	138	MET
1	V	64	GLU
1	R	64	GLU
1	R	88	GLY
1	S	88	GLY
2	X	188	SER
2	X	200	LYS
2	Y	200	LYS
2	U	188	SER
1	W	64	GLU
2	Y	157	PRO
2	Y	188	SER
2	T	188	SER
2	T	200	LYS
2	U	157	PRO
1	R	87	GLN
2	Y	173	PRO
2	U	136	VAL
1	W	85	PRO
1	S	107	LYS
2	X	157	PRO
2	T	157	PRO
1	R	85	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	R	90/96 (94%)	74 (82%)	16 (18%)	2 4
1	S	91/96 (95%)	76 (84%)	15 (16%)	2 5
1	V	90/96 (94%)	74 (82%)	16 (18%)	2 4
1	W	90/96 (94%)	73 (81%)	17 (19%)	1 4
2	T	86/93 (92%)	67 (78%)	19 (22%)	1 2
2	U	86/93 (92%)	66 (77%)	20 (23%)	1 2
2	X	86/93 (92%)	69 (80%)	17 (20%)	1 3
2	Y	86/93 (92%)	63 (73%)	23 (27%)	0 1
All	All	705/756 (93%)	562 (80%)	143 (20%)	1 3

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	V	22	GLN
1	V	36	PHE
1	V	42	GLU
1	V	43	ILE
1	V	46	ILE
1	V	60	CYS
1	V	78	MET
1	V	79	GLN
1	V	82	ARG
1	V	84	LYS
1	V	86	HIS
1	V	87	GLN
1	V	89	GLN
1	V	90	HIS
1	V	91	ILE
1	V	94	MET
1	W	16	LYS
1	W	35	ILE
1	W	37	GLN

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Mol	Chain	Res	Type
1	W	42	GLU
1	W	43	ILE
1	W	46	ILE
1	W	56	ARG
1	W	60	CYS
1	W	79	GLN
1	W	81	MET
1	W	82	ARG
1	W	84	LYS
1	W	87	GLN
1	W	89	GLN
1	W	90	HIS
1	W	94	MET
1	W	101	LYS
1	R	13	GLU
1	R	22	GLN
1	R	34	ASP
1	R	35	ILE
1	R	42	GLU
1	R	46	ILE
1	R	56	ARG
1	R	60	CYS
1	R	72	GLU
1	R	79	GLN
1	R	82	ARG
1	R	84	LYS
1	R	89	GLN
1	R	90	HIS
1	R	94	MET
1	R	101	LYS
1	S	16	LYS
1	S	36	PHE
1	S	42	GLU
1	S	43	ILE
1	S	44	GLU
1	S	46	ILE
1	S	56	ARG
1	S	60	CYS
1	S	79	GLN
1	S	82	ARG
1	S	87	GLN
1	S	90	HIS

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Mol	Chain	Res	Type
1	S	91	ILE
1	S	94	MET
1	S	108	LYS
2	X	148	MET
2	X	150	GLU
2	X	153	GLU
2	X	160	VAL
2	X	162	SER
2	X	171	LYS
2	X	174	LEU
2	X	177	LEU
2	X	183	ARG
2	X	188	SER
2	X	196	ASN
2	X	199	TYR
2	X	200	LYS
2	X	215	LEU
2	X	218	THR
2	X	221	LEU
2	X	224	ARG
2	Y	138	MET
2	Y	140	SER
2	Y	141	GLU
2	Y	148	MET
2	Y	150	GLU
2	Y	152	ARG
2	Y	153	GLU
2	Y	160	VAL
2	Y	162	SER
2	Y	171	LYS
2	Y	174	LEU
2	Y	175	ASP
2	Y	177	LEU
2	Y	182	LYS
2	Y	183	ARG
2	Y	185	ILE
2	Y	189	ARG
2	Y	196	ASN
2	Y	198	THR
2	Y	218	THR
2	Y	221	LEU
2	Y	224	ARG

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Mol	Chain	Res	Type
2	Y	225	GLN
2	T	137	GLU
2	T	140	SER
2	T	148	MET
2	T	150	GLU
2	T	152	ARG
2	T	153	GLU
2	T	160	VAL
2	T	170	LYS
2	T	171	LYS
2	T	174	LEU
2	T	176	THR
2	T	177	LEU
2	T	183	ARG
2	T	188	SER
2	T	196	ASN
2	T	217	LYS
2	T	218	THR
2	T	221	LEU
2	T	224	ARG
2	U	142	ILE
2	U	148	MET
2	U	150	GLU
2	U	152	ARG
2	U	153	GLU
2	U	160	VAL
2	U	162	SER
2	U	171	LYS
2	U	174	LEU
2	U	177	LEU
2	U	182	LYS
2	U	183	ARG
2	U	188	SER
2	U	196	ASN
2	U	199	TYR
2	U	200	LYS
2	U	215	LEU
2	U	218	THR
2	U	221	LEU
2	U	224	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	W	27	HIS
1	W	98	GLN
1	R	98	GLN
1	S	27	HIS
2	X	196	ASN
2	Y	196	ASN
2	T	196	ASN
2	U	196	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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 (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.