Full wwPDB X-ray Structure Validation Report (i)

Jun 13, 2024 – 11:56 AM EDT

PDB ID	:	1OQD
Title	:	Crystal structure of sTALL-1 and BCMA
Authors	:	Zhang, G.
Deposited on	:	2003-03-07
Resolution	:	2.60 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 (1)) were used in the production of this report:

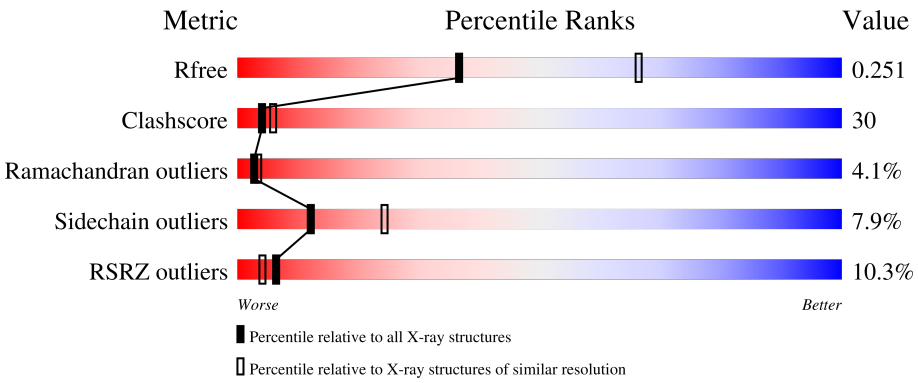
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.60 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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% 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	144	.% 56% 39% 5%
1	B	144	.% 58% 38% 5%
1	C	144	.% 58% 35% 6%
1	D	144	57% 38% 6%
1	E	144	56% 39% 5%

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Mol	Chain	Length	Quality of chain
1	F	144	53% 40% 6%
1	G	144	56% 38% 6%
1	H	144	% 58% 35% 7%
1	I	144	% 56% 38% 6%
1	J	144	% 62% 33% 5%
2	K	39	62% 33% 44% 15% 8%
2	L	39	56% 33% 49% 18%
2	M	39	62% 36% 46% 15% •
2	N	39	44% 18% 18% 15% • 46%
2	O	39	54% 46% 38% 13% •
2	P	39	49% 36% 46% 15% •
2	Q	39	54% 33% 49% 18%
2	R	39	62% 28% 56% 13% •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13704 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 Tumor necrosis factor ligand superfamily member 13B, soluble form.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	144	1143	736	184	218	5	0	0	0
1	B	144	1143	736	184	218	5	0	0	0
1	C	144	1143	736	184	218	5	0	0	0
1	D	144	1143	736	184	218	5	0	0	0
1	E	144	1143	736	184	218	5	0	0	0
1	F	144	1143	736	184	218	5	0	0	0
1	G	144	1143	736	184	218	5	0	0	0
1	H	144	1143	736	184	218	5	0	0	0
1	I	144	1143	736	184	218	5	0	0	0
1	J	144	1143	736	184	218	5	0	0	0

- Molecule 2 is a protein called Tumor necrosis factor receptor superfamily member 17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	K	39	301	182	53	60	6	0	0	0
2	L	39	301	182	53	60	6	0	0	0
2	M	39	301	182	53	60	6	0	0	0
2	N	21	167	103	29	31	4	0	0	0

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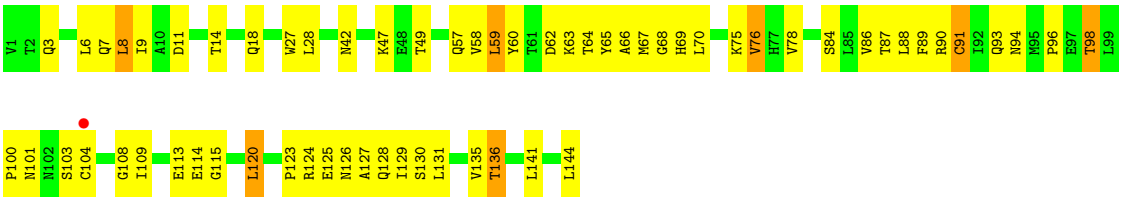
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	O	39	301	182	53	60	6	0	0	0
			Total	C	N	O	S			
2	P	39	301	182	53	60	6	0	0	0
			Total	C	N	O	S			
2	Q	39	301	182	53	60	6	0	0	0
			Total	C	N	O	S			
2	R	39	301	182	53	60	6	0	0	0

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 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.

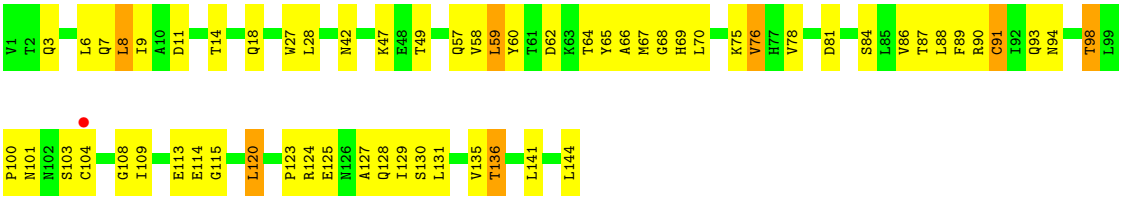
• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

Chain A:



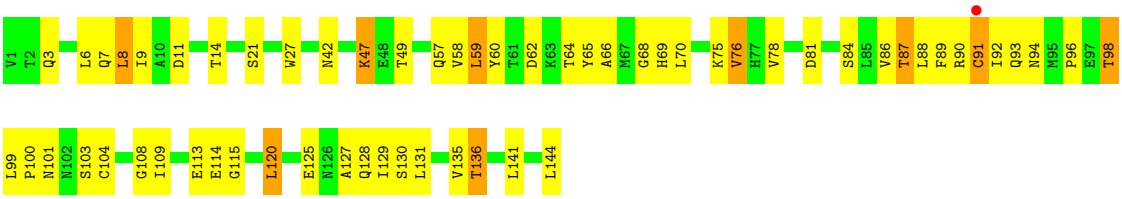
• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

Chain B:



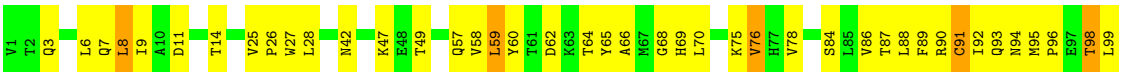
• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

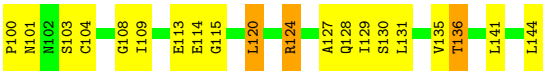
Chain C:



• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

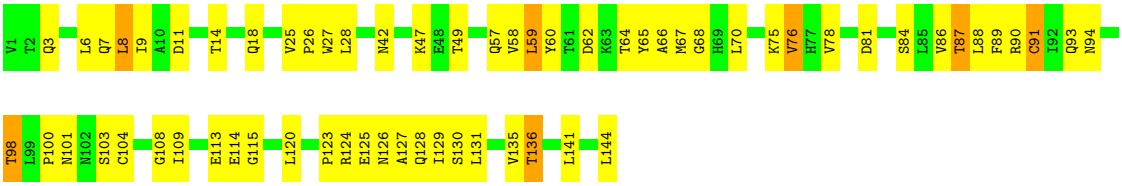
Chain D:





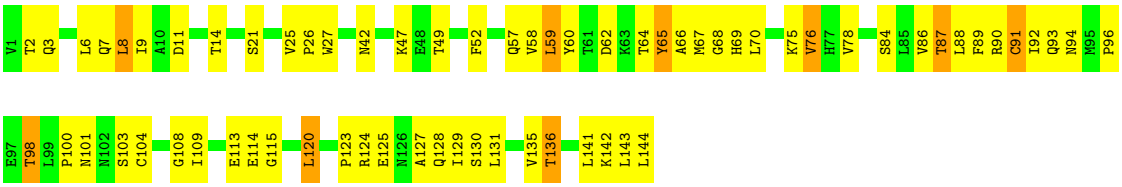
• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

Chain E:



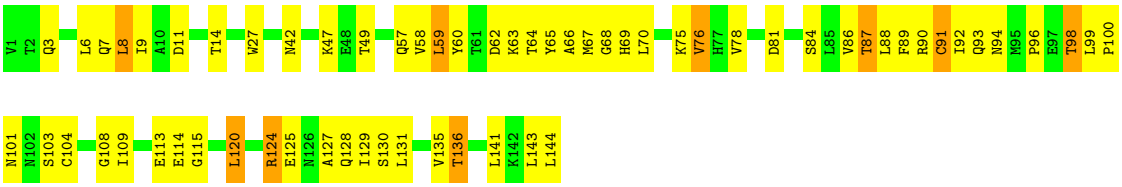
• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

Chain F:



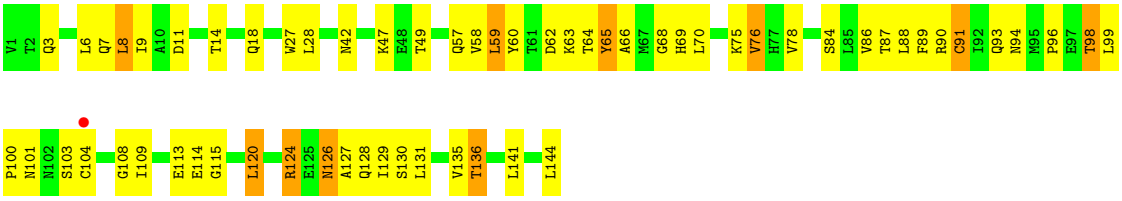
• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

Chain G:



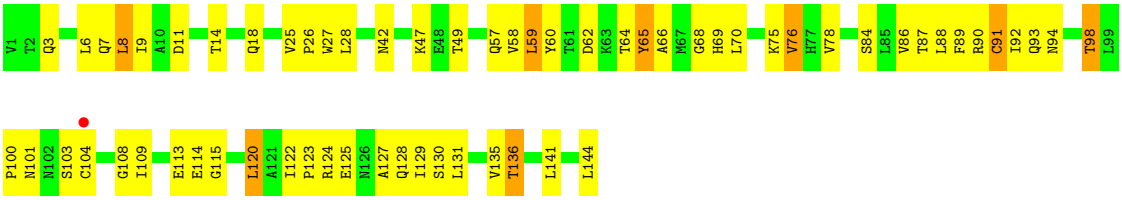
• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

Chain H:



• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

Chain I:

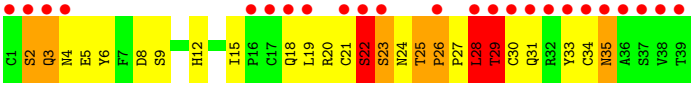


• Molecule 1: Tumor necrosis factor ligand superfamily member 13B, soluble form

Chain J:

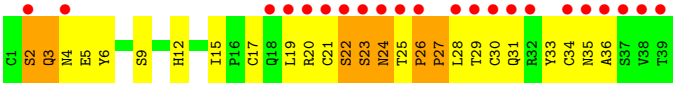
• Molecule 2: Tumor necrosis factor receptor superfamily member 17

Chain K:



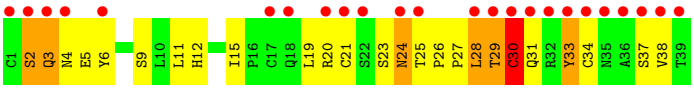
• Molecule 2: Tumor necrosis factor receptor superfamily member 17

Chain L:



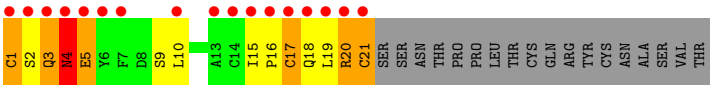
• Molecule 2: Tumor necrosis factor receptor superfamily member 17

Chain M:



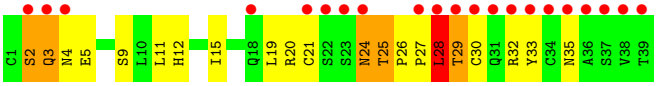
• Molecule 2: Tumor necrosis factor receptor superfamily member 17

Chain N:



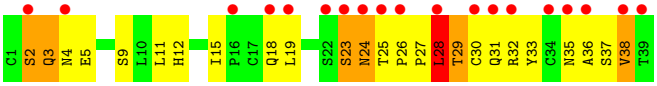
• Molecule 2: Tumor necrosis factor receptor superfamily member 17

Chain O:



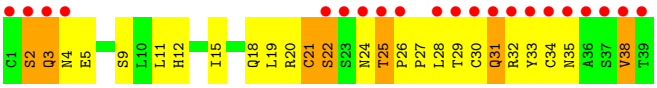
• Molecule 2: Tumor necrosis factor receptor superfamily member 17

Chain P:



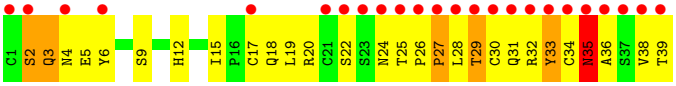
• Molecule 2: Tumor necrosis factor receptor superfamily member 17

Chain Q:



• Molecule 2: Tumor necrosis factor receptor superfamily member 17

Chain R:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α, β, γ	232.85Å 232.85Å 212.48Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.87 – 2.60 46.26 – 2.60	Depositor EDS
% Data completeness (in resolution range)	75.5 (19.87-2.60) 81.9 (46.26-2.60)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	0.90 (at 2.61Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.240 , 0.260 0.232 , 0.251	Depositor DCC
R_{free} test set	1715 reflections (2.01%)	wwPDB-VP
Wilson B-factor (Å^2)	40.4	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 51.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	13704	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.07% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	A	0.43	0/1165	0.71	1/1574 (0.1%)
1	B	0.43	0/1165	0.71	1/1574 (0.1%)
1	C	0.44	0/1165	0.71	1/1574 (0.1%)
1	D	0.45	0/1165	0.72	1/1574 (0.1%)
1	E	0.44	0/1165	0.71	1/1574 (0.1%)
1	F	0.43	0/1165	0.71	1/1574 (0.1%)
1	G	0.45	0/1165	0.72	1/1574 (0.1%)
1	H	0.44	0/1165	0.73	1/1574 (0.1%)
1	I	0.43	0/1165	0.71	1/1574 (0.1%)
1	J	0.43	0/1165	0.71	1/1574 (0.1%)
2	K	0.74	0/307	0.77	0/417
2	L	0.66	0/307	0.74	0/417
2	M	0.76	0/307	0.77	0/417
2	N	0.92	0/170	0.89	0/229
2	O	0.68	0/307	0.67	0/417
2	P	0.62	0/307	0.70	0/417
2	Q	0.73	0/307	0.65	0/417
2	R	1.28	2/307 (0.7%)	0.94	1/417 (0.2%)
All	All	0.52	2/13969 (0.0%)	0.72	11/18888 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	35	ASN	C-N	-16.79	0.95	1.34
2	R	34	CYS	C-N	6.91	1.50	1.34

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	R	35	ASN	O-C-N	-6.46	112.36	122.70
1	D	91	CYS	CA-CB-SG	5.90	124.62	114.00
1	H	91	CYS	CA-CB-SG	5.83	124.50	114.00
1	G	91	CYS	CA-CB-SG	5.83	124.50	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	91	CYS	CA-CB-SG	5.81	124.46	114.00
1	F	91	CYS	CA-CB-SG	5.63	124.14	114.00
1	B	91	CYS	CA-CB-SG	5.63	124.13	114.00
1	A	91	CYS	CA-CB-SG	5.55	123.99	114.00
1	E	91	CYS	CA-CB-SG	5.53	123.96	114.00
1	C	91	CYS	CA-CB-SG	5.51	123.92	114.00
1	J	91	CYS	CA-CB-SG	5.33	123.59	114.00

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	A	1143	0	1148	68	0
1	B	1143	0	1148	69	0
1	C	1143	0	1148	69	0
1	D	1143	0	1148	79	0
1	E	1143	0	1148	85	0
1	F	1143	0	1148	80	0
1	G	1143	0	1148	73	0
1	H	1143	0	1148	68	0
1	I	1143	0	1148	68	0
1	J	1143	0	1148	49	0
2	K	301	0	279	35	0
2	L	301	0	279	32	0
2	M	301	0	279	46	0
2	N	167	0	156	22	0
2	O	301	0	279	29	0
2	P	301	0	279	39	0
2	Q	301	0	279	31	0
2	R	301	0	278	27	0
All	All	13704	0	13588	819	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 30.

All (819) 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:M:28:LEU:HD23	2:M:29:THR:HG22	1.26	1.16
2:N:5:GLU:HG2	2:N:16:PRO:HA	1.32	1.10
2:R:4:ASN:HB3	2:R:33:TYR:HD1	1.19	1.08
1:F:49:THR:HG22	1:F:114:GLU:H	1.19	1.07
1:E:49:THR:HG22	1:E:114:GLU:H	1.20	1.05
1:J:49:THR:HG22	1:J:114:GLU:H	1.21	1.05
1:H:49:THR:HG22	1:H:114:GLU:H	1.21	1.05
1:A:49:THR:HG22	1:A:114:GLU:H	1.20	1.04
1:C:49:THR:HG22	1:C:114:GLU:H	1.20	1.03
1:D:49:THR:HG22	1:D:114:GLU:H	1.21	1.03
1:G:49:THR:HG22	1:G:114:GLU:H	1.20	1.02
1:B:49:THR:HG22	1:B:114:GLU:H	1.20	1.01
1:I:49:THR:HG22	1:I:114:GLU:H	1.19	1.00
2:L:4:ASN:HD22	2:L:33:TYR:HD1	1.05	1.00
2:M:4:ASN:HD22	2:M:33:TYR:HD1	1.09	0.99
1:G:144:LEU:H	1:H:3:GLN:HE21	1.11	0.97
2:L:21:CYS:HA	2:L:26:PRO:HG2	1.44	0.97
2:O:4:ASN:HD22	2:O:33:TYR:HD1	0.98	0.96
1:D:3:GLN:HE21	1:F:144:LEU:H	0.98	0.96
2:Q:4:ASN:HD22	2:Q:33:TYR:HD1	1.05	0.96
1:A:3:GLN:HE21	1:C:144:LEU:H	1.12	0.94
2:O:32:ARG:HA	2:O:35:ASN:HD22	1.31	0.94
1:H:144:LEU:H	1:I:3:GLN:HE21	1.10	0.93
1:E:62:ASP:HB2	1:E:128:GLN:HB2	1.51	0.93
2:M:20:ARG:HB3	2:M:27:PRO:HD3	1.52	0.92
1:E:144:LEU:H	1:F:3:GLN:HE21	1.11	0.92
2:P:4:ASN:HD22	2:P:33:TYR:HD1	1.17	0.91
2:R:4:ASN:HB3	2:R:33:TYR:CD1	2.05	0.91
1:A:62:ASP:HB2	1:A:128:GLN:HB2	1.53	0.90
1:D:94:ASN:HD21	1:E:101:ASN:H	1.09	0.90
1:J:62:ASP:HB2	1:J:128:GLN:HB2	1.54	0.90
1:B:144:LEU:H	1:C:3:GLN:HE21	1.16	0.90
1:C:62:ASP:HB2	1:C:128:GLN:HB2	1.53	0.90
1:A:94:ASN:HD21	1:B:101:ASN:H	1.17	0.88
1:B:62:ASP:HB2	1:B:128:GLN:HB2	1.55	0.88
1:D:144:LEU:H	1:E:3:GLN:HE21	1.15	0.88
1:H:62:ASP:HB2	1:H:128:GLN:HB2	1.56	0.88
2:M:20:ARG:CZ	2:M:27:PRO:HG3	2.03	0.88
1:H:94:ASN:HD21	1:I:101:ASN:H	1.16	0.88
1:F:62:ASP:HB2	1:F:128:GLN:HB2	1.56	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3:GLN:HE21	1:I:144:LEU:H	1.23	0.87
1:D:62:ASP:HB2	1:D:128:GLN:HB2	1.57	0.86
1:G:62:ASP:HB2	1:G:128:GLN:HB2	1.57	0.86
1:A:109:ILE:H	1:B:7:GLN:HE22	1.23	0.86
1:B:27:TRP:H	1:B:42:ASN:HD21	1.23	0.86
1:E:109:ILE:H	1:F:7:GLN:HE22	1.24	0.86
1:A:144:LEU:H	1:B:3:GLN:HE21	1.21	0.85
1:G:7:GLN:HE22	1:I:109:ILE:H	1.24	0.84
1:H:109:ILE:H	1:I:7:GLN:HE22	1.25	0.84
1:D:27:TRP:H	1:D:42:ASN:HD21	1.25	0.84
1:G:27:TRP:H	1:G:42:ASN:HD21	1.24	0.84
1:A:27:TRP:H	1:A:42:ASN:HD21	1.25	0.84
1:I:27:TRP:H	1:I:42:ASN:HD21	1.24	0.84
1:D:7:GLN:HE22	1:F:109:ILE:H	1.22	0.83
1:F:130:SER:O	1:F:136:THR:HG21	1.79	0.82
2:O:28:LEU:HD13	2:O:28:LEU:H	1.42	0.82
1:B:109:ILE:H	1:C:7:GLN:HE22	1.25	0.82
1:F:27:TRP:H	1:F:42:ASN:HD21	1.24	0.82
1:C:130:SER:O	1:C:136:THR:HG21	1.80	0.82
1:E:94:ASN:HD21	1:F:101:ASN:H	1.26	0.82
1:D:3:GLN:NE2	1:F:144:LEU:H	1.78	0.81
1:C:27:TRP:H	1:C:42:ASN:HD21	1.24	0.81
1:E:27:TRP:H	1:E:42:ASN:HD21	1.26	0.81
1:H:27:TRP:H	1:H:42:ASN:HD21	1.25	0.81
1:I:62:ASP:HB2	1:I:128:GLN:HB2	1.61	0.81
1:J:27:TRP:H	1:J:42:ASN:HD21	1.26	0.80
1:I:130:SER:O	1:I:136:THR:HG21	1.81	0.80
1:E:124:ARG:HH21	2:N:10:LEU:CD2	1.94	0.80
2:K:28:LEU:HG	2:K:29:THR:H	1.46	0.80
2:M:28:LEU:CD2	2:M:29:THR:HG22	2.10	0.80
2:N:5:GLU:HG2	2:N:16:PRO:CA	2.10	0.80
1:A:130:SER:O	1:A:136:THR:HG21	1.82	0.79
1:F:49:THR:HG22	1:F:114:GLU:N	1.97	0.79
1:A:49:THR:HG22	1:A:114:GLU:N	1.98	0.79
1:G:109:ILE:H	1:H:7:GLN:HE22	1.31	0.79
1:E:81:ASP:OD2	1:J:87:THR:HG23	1.80	0.79
2:M:4:ASN:ND2	2:M:33:TYR:HD1	1.81	0.79
1:D:130:SER:O	1:D:136:THR:HG21	1.83	0.78
1:B:94:ASN:HD21	1:C:101:ASN:H	1.31	0.78
2:K:4:ASN:HD22	2:K:33:TYR:HD1	1.32	0.78
2:P:28:LEU:HD13	2:P:28:LEU:H	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:49:THR:HG22	1:E:114:GLU:N	1.98	0.77
1:B:49:THR:HG22	1:B:114:GLU:N	1.99	0.77
1:E:130:SER:O	1:E:136:THR:HG21	1.84	0.77
1:G:94:ASN:HD21	1:H:101:ASN:H	1.33	0.77
1:G:49:THR:HG22	1:G:114:GLU:N	1.99	0.77
1:J:49:THR:HG22	1:J:114:GLU:N	1.99	0.77
1:G:135:VAL:HG23	1:G:136:THR:HG22	1.67	0.77
1:J:130:SER:O	1:J:136:THR:HG21	1.84	0.77
1:G:130:SER:O	1:G:136:THR:HG21	1.83	0.77
1:H:130:SER:O	1:H:136:THR:HG21	1.85	0.77
1:B:135:VAL:HG23	1:B:136:THR:HG22	1.67	0.76
1:C:49:THR:HG22	1:C:114:GLU:N	1.99	0.76
1:D:109:ILE:H	1:E:7:GLN:HE22	1.31	0.76
1:G:101:ASN:H	1:I:94:ASN:HD21	1.32	0.76
1:B:130:SER:O	1:B:136:THR:HG21	1.85	0.76
1:A:7:GLN:HE22	1:C:109:ILE:H	1.32	0.76
1:C:135:VAL:HG23	1:C:136:THR:HG22	1.68	0.75
2:M:28:LEU:HD23	2:M:29:THR:CG2	2.14	0.75
1:A:101:ASN:H	1:C:94:ASN:HD21	1.35	0.75
1:I:49:THR:HG22	1:I:114:GLU:N	1.98	0.75
1:A:135:VAL:HG23	1:A:136:THR:HG22	1.68	0.75
1:H:49:THR:HG22	1:H:114:GLU:N	2.00	0.74
1:F:135:VAL:HG23	1:F:136:THR:HG22	1.67	0.74
1:E:124:ARG:HH21	2:N:10:LEU:HD22	1.49	0.74
1:D:135:VAL:HG23	1:D:136:THR:HG22	1.67	0.74
2:N:5:GLU:HA	2:N:17:CYS:H	1.52	0.74
1:E:135:VAL:HG23	1:E:136:THR:HG22	1.68	0.73
2:Q:27:PRO:O	2:Q:30:CYS:HB2	1.87	0.73
1:J:62:ASP:CB	1:J:128:GLN:HB2	2.18	0.73
2:O:32:ARG:HA	2:O:35:ASN:ND2	2.03	0.73
1:D:101:ASN:H	1:F:94:ASN:HD21	1.34	0.73
1:H:135:VAL:HG23	1:H:136:THR:HG22	1.70	0.73
1:D:94:ASN:ND2	1:E:101:ASN:H	1.85	0.73
2:L:4:ASN:ND2	2:L:33:TYR:HD1	1.83	0.73
2:L:20:ARG:C	2:L:26:PRO:HG3	2.09	0.73
1:I:135:VAL:HG23	1:I:136:THR:HG22	1.68	0.73
2:Q:2:SER:C	2:Q:3:GLN:HE21	1.92	0.73
2:P:28:LEU:O	2:P:30:CYS:N	2.22	0.72
2:P:2:SER:C	2:P:3:GLN:HE21	1.93	0.72
1:J:135:VAL:HG23	1:J:136:THR:HG22	1.69	0.72
2:K:6:TYR:HB3	2:K:30:CYS:SG	2.29	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:THR:HG22	1:D:114:GLU:N	2.00	0.71
1:B:62:ASP:CB	1:B:128:GLN:HB2	2.21	0.71
2:K:2:SER:H	2:K:3:GLN:NE2	1.89	0.71
1:J:60:TYR:CD2	1:J:129:ILE:HD11	2.26	0.71
1:C:62:ASP:CB	1:C:128:GLN:HB2	2.21	0.71
2:O:2:SER:C	2:O:3:GLN:HE21	1.94	0.70
1:A:123:PRO:O	1:A:124:ARG:HD3	1.90	0.70
2:O:2:SER:H	2:O:3:GLN:NE2	1.90	0.70
2:M:2:SER:H	2:M:3:GLN:NE2	1.90	0.70
2:L:2:SER:C	2:L:3:GLN:HE21	1.94	0.70
2:M:28:LEU:O	2:M:30:CYS:N	2.25	0.70
2:R:2:SER:H	2:R:3:GLN:NE2	1.90	0.70
2:Q:2:SER:H	2:Q:3:GLN:NE2	1.89	0.70
2:L:2:SER:H	2:L:3:GLN:NE2	1.89	0.70
2:R:2:SER:C	2:R:3:GLN:HE21	1.94	0.69
1:A:62:ASP:CB	1:A:128:GLN:HB2	2.22	0.69
2:K:2:SER:C	2:K:3:GLN:HE21	1.96	0.69
1:D:3:GLN:HE21	1:F:144:LEU:N	1.82	0.69
1:H:94:ASN:ND2	1:I:101:ASN:H	1.90	0.69
1:E:62:ASP:CB	1:E:128:GLN:HB2	2.23	0.69
2:P:2:SER:H	2:P:3:GLN:NE2	1.91	0.69
1:F:60:TYR:CD2	1:F:129:ILE:HD11	2.28	0.69
2:Q:25:THR:O	2:Q:27:PRO:HD3	1.93	0.69
2:O:4:ASN:ND2	2:O:33:TYR:HD1	1.83	0.68
2:M:2:SER:C	2:M:3:GLN:HE21	1.96	0.68
1:G:64:THR:O	1:G:66:ALA:N	2.25	0.68
2:K:28:LEU:CG	2:K:29:THR:H	2.07	0.68
2:M:20:ARG:O	2:M:26:PRO:HG3	1.94	0.67
1:F:62:ASP:CB	1:F:128:GLN:HB2	2.23	0.67
1:B:18:GLN:NE2	1:B:125:GLU:O	2.26	0.67
1:B:70:LEU:HD23	1:B:90:ARG:HB2	1.77	0.67
1:D:62:ASP:CB	1:D:128:GLN:HB2	2.24	0.67
2:Q:3:GLN:HG2	2:Q:5:GLU:HG3	1.76	0.67
2:L:31:GLN:O	2:L:35:ASN:HB2	1.94	0.67
1:D:70:LEU:HD23	1:D:90:ARG:HB2	1.76	0.67
1:H:70:LEU:HD23	1:H:90:ARG:HB2	1.76	0.67
1:G:125:GLU:OE1	2:P:27:PRO:HB3	1.95	0.67
1:G:93:GLN:HE22	1:I:93:GLN:HE22	1.43	0.66
1:B:123:PRO:O	1:B:124:ARG:HD2	1.94	0.66
1:C:60:TYR:CD2	1:C:129:ILE:HD11	2.30	0.66
1:A:94:ASN:ND2	1:B:101:ASN:H	1.91	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:TYR:CD2	1:B:129:ILE:HD11	2.31	0.66
2:P:3:GLN:HG2	2:P:5:GLU:HG3	1.78	0.66
1:B:64:THR:O	1:B:66:ALA:N	2.27	0.66
1:G:62:ASP:CB	1:G:128:GLN:HB2	2.25	0.66
2:N:16:PRO:O	2:N:18:GLN:N	2.29	0.66
1:F:64:THR:O	1:F:66:ALA:N	2.27	0.66
1:A:64:THR:O	1:A:66:ALA:N	2.25	0.65
1:G:60:TYR:CD2	1:G:129:ILE:HD11	2.30	0.65
1:I:70:LEU:HD23	1:I:90:ARG:HB2	1.78	0.65
2:L:15:ILE:CG2	2:L:19:LEU:HD12	2.26	0.65
2:O:3:GLN:HG2	2:O:5:GLU:HG3	1.79	0.65
1:H:62:ASP:CB	1:H:128:GLN:HB2	2.25	0.65
2:K:3:GLN:HG2	2:K:5:GLU:HG3	1.78	0.65
2:K:28:LEU:HG	2:K:29:THR:N	2.10	0.65
1:F:70:LEU:HD23	1:F:90:ARG:HB2	1.78	0.65
1:E:93:GLN:HE22	1:F:93:GLN:HE22	1.45	0.65
2:R:15:ILE:CG2	2:R:19:LEU:HD12	2.26	0.65
1:A:70:LEU:HD23	1:A:90:ARG:HB2	1.77	0.65
1:A:98:THR:O	1:A:100:PRO:HD3	1.97	0.65
1:G:70:LEU:HD23	1:G:90:ARG:HB2	1.78	0.65
2:P:15:ILE:CG2	2:P:19:LEU:HD12	2.27	0.65
1:D:64:THR:O	1:D:64:THR:HG22	1.97	0.65
2:O:15:ILE:CG2	2:O:19:LEU:HD12	2.27	0.65
1:D:98:THR:O	1:D:100:PRO:HD3	1.97	0.64
2:M:15:ILE:CG2	2:M:19:LEU:HD12	2.26	0.64
1:G:98:THR:O	1:G:100:PRO:HD3	1.96	0.64
1:C:70:LEU:HD23	1:C:90:ARG:HB2	1.79	0.64
1:F:76:VAL:HG21	1:F:114:GLU:O	1.98	0.64
1:G:64:THR:O	1:G:64:THR:HG22	1.97	0.64
2:R:2:SER:O	2:R:3:GLN:HG2	1.97	0.64
1:H:76:VAL:HG21	1:H:114:GLU:O	1.97	0.64
1:I:98:THR:O	1:I:100:PRO:HD3	1.97	0.64
2:Q:15:ILE:CG2	2:Q:19:LEU:HD12	2.27	0.64
1:F:98:THR:O	1:F:100:PRO:HD3	1.98	0.64
1:B:76:VAL:HG21	1:B:114:GLU:O	1.97	0.64
1:I:64:THR:O	1:I:66:ALA:N	2.26	0.64
1:J:98:THR:O	1:J:100:PRO:HD3	1.98	0.64
1:I:76:VAL:HG21	1:I:114:GLU:O	1.98	0.64
1:E:70:LEU:HD23	1:E:90:ARG:HB2	1.79	0.64
2:K:18:GLN:HG2	2:K:33:TYR:HE2	1.63	0.64
1:E:98:THR:O	1:E:100:PRO:HD3	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:64:THR:O	1:I:64:THR:HG22	1.98	0.64
1:A:93:GLN:HE22	1:B:93:GLN:HE22	1.46	0.63
2:L:3:GLN:HG2	2:L:5:GLU:HG3	1.79	0.63
1:J:76:VAL:HG21	1:J:114:GLU:O	1.98	0.63
2:K:15:ILE:CG2	2:K:19:LEU:HD12	2.28	0.63
2:M:2:SER:O	2:M:3:GLN:HG2	1.98	0.63
2:Q:2:SER:O	2:Q:3:GLN:HG2	1.98	0.63
2:L:2:SER:O	2:L:3:GLN:HG2	1.98	0.63
2:M:3:GLN:HG2	2:M:5:GLU:HG3	1.81	0.63
1:A:76:VAL:HG21	1:A:114:GLU:O	1.98	0.63
1:J:70:LEU:HD23	1:J:90:ARG:HB2	1.79	0.63
2:Q:20:ARG:O	2:Q:22:SER:N	2.32	0.63
2:R:36:ALA:O	2:R:39:THR:HB	1.99	0.63
1:C:98:THR:O	1:C:100:PRO:HD3	1.98	0.63
1:F:123:PRO:O	1:F:124:ARG:HD3	1.98	0.63
1:H:64:THR:O	1:H:66:ALA:N	2.26	0.63
2:R:3:GLN:HG2	2:R:5:GLU:HG3	1.79	0.63
1:E:64:THR:HG22	1:E:64:THR:O	1.98	0.63
1:F:64:THR:O	1:F:64:THR:HG22	1.98	0.63
1:B:98:THR:O	1:B:100:PRO:HD3	1.98	0.63
1:C:76:VAL:HG21	1:C:114:GLU:O	1.98	0.63
1:I:62:ASP:CB	1:I:128:GLN:HB2	2.28	0.63
1:G:76:VAL:HG21	1:G:114:GLU:O	1.99	0.62
2:P:2:SER:O	2:P:3:GLN:HG2	1.99	0.62
2:K:2:SER:O	2:K:3:GLN:HG2	2.00	0.62
1:A:3:GLN:NE2	1:C:144:LEU:H	1.92	0.62
1:D:76:VAL:HG21	1:D:114:GLU:O	2.00	0.62
1:I:60:TYR:CD2	1:I:129:ILE:HD11	2.33	0.62
1:H:144:LEU:H	1:I:3:GLN:NE2	1.92	0.62
1:A:64:THR:O	1:A:64:THR:HG22	1.99	0.62
1:D:109:ILE:HD11	1:E:141:LEU:HD12	1.82	0.62
1:J:64:THR:HG22	1:J:64:THR:O	1.99	0.62
1:C:64:THR:O	1:C:66:ALA:N	2.26	0.61
1:D:60:TYR:CD2	1:D:129:ILE:HD11	2.35	0.61
1:E:76:VAL:HG21	1:E:114:GLU:O	2.00	0.61
1:H:98:THR:O	1:H:100:PRO:HD3	2.00	0.61
2:O:2:SER:O	2:O:3:GLN:HG2	2.00	0.61
1:B:64:THR:O	1:B:64:THR:HG22	1.99	0.61
1:C:64:THR:O	1:C:64:THR:HG22	1.99	0.61
2:L:28:LEU:HG	2:L:29:THR:OG1	1.99	0.61
1:A:125:GLU:CD	2:K:27:PRO:HB3	2.20	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:30:CYS:O	2:M:33:TYR:HB3	2.00	0.61
1:B:93:GLN:HE22	1:C:93:GLN:HE22	1.48	0.61
1:J:64:THR:O	1:J:66:ALA:N	2.27	0.61
2:K:22:SER:O	2:K:23:SER:HB3	2.01	0.61
1:D:93:GLN:HE22	1:E:93:GLN:HE22	1.47	0.61
2:P:29:THR:HG23	2:P:29:THR:O	2.01	0.61
1:E:87:THR:HG23	1:J:81:ASP:OD2	2.00	0.61
1:E:60:TYR:CD2	1:E:129:ILE:HD11	2.36	0.61
1:E:64:THR:O	1:E:66:ALA:N	2.28	0.60
1:E:81:ASP:CG	1:J:87:THR:HG23	2.21	0.60
2:P:4:ASN:ND2	2:P:33:TYR:HD1	1.94	0.60
2:Q:4:ASN:ND2	2:Q:33:TYR:HD1	1.87	0.60
1:A:60:TYR:CD2	1:A:129:ILE:HD11	2.37	0.60
1:D:64:THR:O	1:D:66:ALA:N	2.26	0.60
1:H:64:THR:O	1:H:64:THR:HG22	2.00	0.60
2:Q:32:ARG:H	2:Q:32:ARG:HD3	1.67	0.60
1:A:125:GLU:HG2	2:K:27:PRO:HA	1.84	0.60
1:C:87:THR:HG23	1:G:81:ASP:OD2	2.02	0.60
2:M:6:TYR:HB3	2:M:30:CYS:SG	2.42	0.60
1:H:144:LEU:N	1:I:3:GLN:HE21	1.93	0.60
1:D:6:LEU:HD21	1:D:8:LEU:HD13	1.84	0.59
2:O:28:LEU:CD2	2:O:29:THR:HG22	2.32	0.59
1:B:6:LEU:HD21	1:B:8:LEU:HD13	1.84	0.59
1:C:6:LEU:HD21	1:C:8:LEU:HD13	1.83	0.59
1:G:144:LEU:HD12	1:H:144:LEU:CD1	2.33	0.59
1:G:135:VAL:HG12	1:I:90:ARG:HG2	1.85	0.59
1:F:21:SER:HB2	1:F:125:GLU:OE2	2.03	0.59
1:A:11:ASP:OD2	1:A:14:THR:HG23	2.03	0.59
1:D:96:PRO:HG2	1:F:94:ASN:ND2	2.18	0.59
2:M:38:VAL:HG12	2:M:38:VAL:O	2.04	0.58
2:P:35:ASN:O	2:P:38:VAL:HG23	2.03	0.58
1:A:6:LEU:HD21	1:A:8:LEU:HD13	1.84	0.58
1:I:6:LEU:HD21	1:I:8:LEU:HD13	1.84	0.58
1:E:6:LEU:HD21	1:E:8:LEU:HD13	1.85	0.58
1:C:57:GLN:O	1:C:136:THR:HA	2.03	0.58
2:Q:32:ARG:H	2:Q:32:ARG:CD	2.17	0.58
1:G:6:LEU:HD21	1:G:8:LEU:HD13	1.86	0.58
2:K:2:SER:H	2:K:3:GLN:HE21	1.51	0.58
1:D:64:THR:CG2	1:D:124:ARG:HH21	2.17	0.58
1:E:129:ILE:HG22	1:E:131:LEU:CD1	2.33	0.58
2:M:23:SER:O	2:M:26:PRO:HD3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:94:ASN:ND2	1:F:101:ASN:H	1.99	0.58
1:F:6:LEU:HD21	1:F:8:LEU:HD13	1.85	0.57
1:G:67:MET:SD	1:G:124:ARG:HD3	2.44	0.57
2:L:21:CYS:HA	2:L:26:PRO:CG	2.27	0.57
1:G:135:VAL:CG1	1:I:90:ARG:HG2	2.34	0.57
2:L:30:CYS:O	2:L:34:CYS:N	2.29	0.57
1:G:63:LYS:HD2	2:P:23:SER:OG	2.04	0.57
1:A:129:ILE:HG22	1:A:131:LEU:CD1	2.34	0.57
1:I:11:ASP:OD2	1:I:14:THR:HG23	2.04	0.57
1:H:6:LEU:HD21	1:H:8:LEU:HD13	1.87	0.57
2:Q:2:SER:H	2:Q:3:GLN:HE21	1.52	0.57
1:F:11:ASP:OD2	1:F:14:THR:HG23	2.05	0.57
2:O:2:SER:H	2:O:3:GLN:HE21	1.52	0.57
1:J:129:ILE:HG22	1:J:131:LEU:CD1	2.34	0.56
2:K:34:CYS:O	2:K:35:ASN:CG	2.43	0.56
2:N:3:GLN:O	2:N:5:GLU:N	2.37	0.56
2:P:4:ASN:HB3	2:P:33:TYR:CD1	2.40	0.56
1:E:87:THR:HG23	1:J:81:ASP:CG	2.25	0.56
1:J:6:LEU:HD21	1:J:8:LEU:HD13	1.86	0.56
2:N:19:LEU:C	2:N:21:CYS:H	2.07	0.56
2:R:18:GLN:HG2	2:R:33:TYR:CE2	2.40	0.56
1:D:57:GLN:O	1:D:136:THR:HA	2.05	0.56
1:F:129:ILE:HG22	1:F:131:LEU:CD1	2.35	0.56
2:L:21:CYS:CA	2:L:26:PRO:HG2	2.29	0.56
2:L:24:ASN:O	2:L:25:THR:C	2.43	0.56
1:G:125:GLU:HG3	2:P:27:PRO:HG3	1.87	0.56
1:H:93:GLN:HE22	1:I:93:GLN:HE22	1.53	0.56
1:H:129:ILE:HG22	1:H:131:LEU:CD1	2.36	0.56
2:O:28:LEU:HD23	2:O:29:THR:HG22	1.87	0.56
1:A:109:ILE:HD11	1:B:141:LEU:HD12	1.88	0.56
1:E:124:ARG:HH11	2:N:20:ARG:NH2	2.03	0.56
1:A:18:GLN:NE2	1:A:125:GLU:O	2.39	0.56
2:P:31:GLN:C	2:P:33:TYR:N	2.59	0.56
1:B:129:ILE:HG22	1:B:131:LEU:CD1	2.35	0.56
2:K:18:GLN:HG2	2:K:33:TYR:CE2	2.41	0.56
2:P:2:SER:H	2:P:3:GLN:HE21	1.54	0.55
1:B:70:LEU:CD2	1:B:90:ARG:HB2	2.36	0.55
1:D:129:ILE:HG22	1:D:131:LEU:CD1	2.36	0.55
1:G:144:LEU:HD12	1:H:144:LEU:HD11	1.88	0.55
2:M:2:SER:H	2:M:3:GLN:HE21	1.53	0.55
2:P:31:GLN:HB3	2:P:35:ASN:HD21	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:11:ASP:OD2	1:H:14:THR:HG23	2.06	0.55
1:H:57:GLN:O	1:H:136:THR:HA	2.07	0.55
1:A:57:GLN:O	1:A:136:THR:HA	2.06	0.55
1:E:57:GLN:O	1:E:136:THR:HA	2.05	0.55
1:J:63:LYS:HG3	2:R:24:ASN:OD1	2.06	0.55
1:C:11:ASP:OD2	1:C:14:THR:HG23	2.07	0.55
1:I:129:ILE:HG22	1:I:131:LEU:CD1	2.36	0.55
2:L:2:SER:H	2:L:3:GLN:HE21	1.52	0.55
1:J:11:ASP:OD2	1:J:14:THR:HG23	2.06	0.55
1:A:70:LEU:CD2	1:A:90:ARG:HB2	2.37	0.55
1:D:70:LEU:CD2	1:D:90:ARG:HB2	2.37	0.55
1:C:129:ILE:HG22	1:C:131:LEU:CD1	2.36	0.55
1:H:70:LEU:CD2	1:H:90:ARG:HB2	2.36	0.55
1:J:58:VAL:HA	1:J:136:THR:HB	1.89	0.55
2:R:2:SER:H	2:R:3:GLN:HE21	1.53	0.55
1:G:129:ILE:HG22	1:G:131:LEU:CD1	2.36	0.54
1:J:70:LEU:CD2	1:J:90:ARG:HB2	2.37	0.54
1:B:11:ASP:OD2	1:B:14:THR:HG23	2.08	0.54
2:L:33:TYR:C	2:L:35:ASN:H	2.09	0.54
2:M:21:CYS:HA	2:M:26:PRO:CG	2.37	0.54
1:D:11:ASP:OD2	1:D:14:THR:HG23	2.08	0.54
1:E:70:LEU:CD2	1:E:90:ARG:HB2	2.37	0.54
1:G:11:ASP:OD2	1:G:14:THR:HG23	2.06	0.54
1:D:93:GLN:HE22	1:F:93:GLN:HE22	1.55	0.54
1:G:70:LEU:CD2	1:G:90:ARG:HB2	2.38	0.54
1:E:11:ASP:OD2	1:E:14:THR:HG23	2.08	0.54
1:D:64:THR:CG2	1:D:124:ARG:NH2	2.70	0.54
1:B:109:ILE:HD11	1:C:141:LEU:HD12	1.89	0.54
1:D:64:THR:HG23	1:D:124:ARG:HH21	1.73	0.54
1:E:90:ARG:HG2	1:F:135:VAL:HG12	1.90	0.53
2:O:28:LEU:O	2:O:30:CYS:N	2.41	0.53
1:D:58:VAL:HA	1:D:136:THR:HB	1.90	0.53
1:I:70:LEU:CD2	1:I:90:ARG:HB2	2.38	0.53
2:P:28:LEU:HD23	2:P:29:THR:HB	1.89	0.53
2:P:31:GLN:HB3	2:P:35:ASN:ND2	2.22	0.53
2:Q:32:ARG:O	2:Q:35:ASN:HB2	2.07	0.53
2:M:33:TYR:CD2	2:M:34:CYS:N	2.77	0.53
1:C:70:LEU:CD2	1:C:90:ARG:HB2	2.38	0.53
1:G:57:GLN:O	1:G:136:THR:HA	2.08	0.53
1:G:109:ILE:HD11	1:H:141:LEU:HD12	1.91	0.53
2:K:22:SER:O	2:K:23:SER:CB	2.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:19:LEU:O	2:N:21:CYS:N	2.42	0.53
2:R:28:LEU:O	2:R:30:CYS:N	2.41	0.53
1:H:60:TYR:CD2	1:H:129:ILE:HD11	2.43	0.53
1:C:58:VAL:HA	1:C:136:THR:HB	1.90	0.53
1:G:144:LEU:H	1:H:3:GLN:NE2	1.94	0.53
1:I:18:GLN:NE2	1:I:125:GLU:O	2.40	0.53
2:M:28:LEU:O	2:M:30:CYS:HB2	2.08	0.53
1:A:76:VAL:HG22	1:A:115:GLY:C	2.29	0.53
1:A:96:PRO:HG2	1:C:94:ASN:ND2	2.24	0.53
2:L:22:SER:O	2:L:23:SER:HB3	2.09	0.53
2:P:33:TYR:O	2:P:36:ALA:N	2.41	0.53
2:M:28:LEU:O	2:M:29:THR:C	2.47	0.53
1:C:93:GLN:HG2	1:C:104:CYS:HB2	1.91	0.53
1:D:96:PRO:HG2	1:F:94:ASN:CG	2.28	0.53
1:F:70:LEU:CD2	1:F:90:ARG:HB2	2.39	0.52
1:I:93:GLN:HG2	1:I:104:CYS:HB2	1.92	0.52
1:A:58:VAL:HA	1:A:136:THR:HB	1.91	0.52
1:B:58:VAL:HA	1:B:136:THR:HB	1.91	0.52
1:D:94:ASN:HD21	1:E:101:ASN:N	1.92	0.52
1:J:60:TYR:CE2	1:J:129:ILE:HD11	2.45	0.52
1:F:127:ALA:HB1	1:F:129:ILE:HD13	1.91	0.52
1:H:58:VAL:HA	1:H:136:THR:HB	1.92	0.52
1:H:76:VAL:HG22	1:H:115:GLY:C	2.29	0.52
1:G:76:VAL:HG22	1:G:115:GLY:C	2.30	0.52
1:H:93:GLN:HG2	1:H:104:CYS:HB2	1.92	0.52
2:Q:18:GLN:HG2	2:Q:33:TYR:CE2	2.44	0.52
1:A:125:GLU:OE1	2:K:27:PRO:HB3	2.09	0.52
1:D:76:VAL:HG22	1:D:115:GLY:C	2.30	0.52
1:C:6:LEU:CD2	1:C:8:LEU:HD13	2.40	0.52
1:F:93:GLN:HG2	1:F:104:CYS:HB2	1.91	0.52
2:R:28:LEU:O	2:R:29:THR:C	2.48	0.52
1:E:127:ALA:HB1	1:E:129:ILE:HD13	1.91	0.52
1:F:67:MET:SD	1:F:124:ARG:HG3	2.49	0.52
1:I:127:ALA:HB1	1:I:129:ILE:HD13	1.91	0.52
2:M:28:LEU:CG	2:M:29:THR:H	2.23	0.52
1:D:101:ASN:H	1:F:94:ASN:ND2	2.04	0.52
1:F:76:VAL:HG22	1:F:115:GLY:C	2.30	0.52
1:J:93:GLN:HG2	1:J:104:CYS:HB2	1.91	0.52
2:R:32:ARG:O	2:R:35:ASN:N	2.43	0.52
1:B:93:GLN:HG2	1:B:104:CYS:HB2	1.91	0.51
2:P:31:GLN:O	2:P:33:TYR:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:7:GLN:NE2	1:F:109:ILE:H	2.01	0.51
1:H:90:ARG:HG2	1:I:135:VAL:CG1	2.39	0.51
2:M:20:ARG:NH2	2:M:27:PRO:HG3	2.25	0.51
2:M:34:CYS:HA	2:M:37:SER:OG	2.10	0.51
1:B:57:GLN:O	1:B:136:THR:HA	2.10	0.51
1:E:109:ILE:HD11	1:F:141:LEU:HD12	1.91	0.51
1:G:58:VAL:HA	1:G:136:THR:HB	1.90	0.51
1:J:127:ALA:HB1	1:J:129:ILE:HD13	1.92	0.51
2:K:20:ARG:C	2:K:26:PRO:HG3	2.30	0.51
1:B:127:ALA:HB1	1:B:129:ILE:HD13	1.92	0.51
1:G:93:GLN:HG2	1:G:104:CYS:HB2	1.91	0.51
1:H:94:ASN:HD21	1:I:101:ASN:N	1.98	0.51
2:P:18:GLN:HG2	2:P:33:TYR:CE2	2.46	0.51
1:A:6:LEU:CD2	1:A:8:LEU:HD13	2.39	0.51
1:C:21:SER:HB2	1:C:125:GLU:OE2	2.10	0.51
1:D:6:LEU:CD2	1:D:8:LEU:HD13	2.41	0.51
1:G:96:PRO:HG2	1:I:94:ASN:CG	2.31	0.51
1:C:60:TYR:CE2	1:C:129:ILE:HD11	2.46	0.51
1:I:6:LEU:CD2	1:I:8:LEU:HD13	2.40	0.51
1:B:67:MET:SD	1:B:124:ARG:HG2	2.50	0.51
1:E:93:GLN:HG2	1:E:104:CYS:HB2	1.92	0.51
1:F:6:LEU:CD2	1:F:8:LEU:HD13	2.40	0.51
1:G:60:TYR:CE2	1:G:129:ILE:HD11	2.46	0.51
1:E:76:VAL:HG22	1:E:115:GLY:C	2.31	0.51
1:D:93:GLN:HG2	1:D:104:CYS:HB2	1.92	0.51
1:F:57:GLN:O	1:F:136:THR:HA	2.10	0.51
1:F:58:VAL:HA	1:F:136:THR:HB	1.93	0.51
1:J:67:MET:SD	1:J:124:ARG:HG2	2.50	0.51
1:E:6:LEU:CD2	1:E:8:LEU:HD13	2.41	0.50
1:J:57:GLN:O	1:J:136:THR:HA	2.11	0.50
1:J:76:VAL:HG22	1:J:115:GLY:C	2.31	0.50
2:L:30:CYS:O	2:L:33:TYR:N	2.45	0.50
1:A:93:GLN:HG2	1:A:104:CYS:HB2	1.93	0.50
1:A:127:ALA:HB1	1:A:129:ILE:HD13	1.93	0.50
1:C:127:ALA:HB1	1:C:129:ILE:HD13	1.93	0.50
1:E:109:ILE:H	1:F:7:GLN:NE2	2.02	0.50
2:K:28:LEU:CG	2:K:29:THR:N	2.71	0.50
1:C:76:VAL:HG22	1:C:115:GLY:C	2.31	0.50
1:E:60:TYR:CE2	1:E:129:ILE:HD11	2.46	0.50
1:E:90:ARG:HG2	1:F:135:VAL:CG1	2.41	0.50
2:P:33:TYR:O	2:P:36:ALA:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LEU:CD2	1:B:8:LEU:HD13	2.41	0.50
1:B:76:VAL:HG22	1:B:115:GLY:C	2.32	0.50
1:G:93:GLN:HE22	1:H:93:GLN:HE22	1.60	0.50
1:H:90:ARG:HG2	1:I:135:VAL:HG12	1.93	0.50
1:I:76:VAL:HG22	1:I:115:GLY:C	2.30	0.50
2:M:4:ASN:HB3	2:M:33:TYR:CD1	2.46	0.50
1:D:141:LEU:HD11	1:F:143:LEU:HD22	1.94	0.50
1:E:18:GLN:NE2	1:E:126:ASN:HA	2.26	0.50
1:J:59:LEU:HB3	1:J:130:SER:HB3	1.94	0.50
2:Q:28:LEU:O	2:Q:29:THR:HB	2.12	0.50
1:C:128:GLN:O	1:C:129:ILE:HD12	2.12	0.49
2:M:33:TYR:CD2	2:M:33:TYR:C	2.86	0.49
1:G:127:ALA:HB1	1:G:129:ILE:HD13	1.93	0.49
1:I:92:ILE:HD13	2:Q:11:LEU:HD23	1.94	0.49
2:O:4:ASN:ND2	2:O:33:TYR:CD1	2.65	0.49
1:D:127:ALA:HB1	1:D:129:ILE:HD13	1.94	0.49
2:M:24:ASN:C	2:M:26:PRO:HD3	2.33	0.49
1:B:90:ARG:HG2	1:C:135:VAL:HG12	1.93	0.49
1:D:92:ILE:HD12	1:E:59:LEU:HD11	1.95	0.49
1:H:109:ILE:HD11	1:I:141:LEU:HD12	1.94	0.49
2:M:25:THR:O	2:M:25:THR:HG22	2.11	0.49
1:E:89:PHE:CZ	1:E:108:GLY:HA3	2.47	0.49
1:F:128:GLN:O	1:F:129:ILE:HD12	2.12	0.49
1:J:6:LEU:CD2	1:J:8:LEU:HD13	2.42	0.49
2:Q:20:ARG:C	2:Q:22:SER:N	2.65	0.49
2:K:28:LEU:N	2:K:28:LEU:HD23	2.28	0.48
2:Q:29:THR:HG22	2:Q:29:THR:O	2.12	0.48
1:B:144:LEU:H	1:C:3:GLN:NE2	1.97	0.48
2:N:19:LEU:C	2:N:21:CYS:N	2.66	0.48
2:R:6:TYR:HB3	2:R:30:CYS:SG	2.52	0.48
2:R:31:GLN:O	2:R:32:ARG:C	2.52	0.48
1:F:60:TYR:CE2	1:F:129:ILE:HD11	2.49	0.48
1:F:78:VAL:HG21	1:F:84:SER:HB3	1.95	0.48
1:J:60:TYR:HD2	1:J:129:ILE:HD11	1.77	0.48
1:G:6:LEU:CD2	1:G:8:LEU:HD13	2.43	0.48
2:O:28:LEU:H	2:O:28:LEU:CD1	2.17	0.48
2:Q:18:GLN:HG2	2:Q:33:TYR:HE2	1.79	0.48
1:E:123:PRO:HB3	2:N:9:SER:HB2	1.96	0.48
1:I:57:GLN:O	1:I:136:THR:HA	2.14	0.48
1:A:59:LEU:HB3	1:A:130:SER:HB3	1.96	0.48
1:D:109:ILE:H	1:E:7:GLN:NE2	2.07	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:VAL:HA	1:E:136:THR:HB	1.94	0.48
1:G:101:ASN:H	1:I:94:ASN:ND2	2.04	0.48
1:B:94:ASN:CG	1:C:96:PRO:HG2	2.34	0.48
1:H:6:LEU:CD2	1:H:8:LEU:HD13	2.44	0.48
1:H:109:ILE:H	1:I:7:GLN:NE2	2.04	0.48
1:J:62:ASP:CA	1:J:128:GLN:HB2	2.43	0.48
2:K:24:ASN:O	2:K:25:THR:C	2.53	0.48
1:A:78:VAL:HG21	1:A:84:SER:HB3	1.96	0.48
1:B:49:THR:HB	1:B:113:GLU:HA	1.96	0.48
1:C:81:ASP:CG	1:G:87:THR:HG23	2.35	0.48
1:I:49:THR:HB	1:I:113:GLU:HA	1.96	0.48
2:K:4:ASN:ND2	2:K:33:TYR:HD1	2.06	0.47
2:K:21:CYS:HA	2:K:26:PRO:HG2	1.95	0.47
1:B:89:PHE:CZ	1:B:108:GLY:HA3	2.50	0.47
1:C:75:LYS:HE3	1:C:86:VAL:HG21	1.96	0.47
2:M:28:LEU:HG	2:M:29:THR:H	1.79	0.47
1:A:128:GLN:O	1:A:129:ILE:HD12	2.14	0.47
1:G:49:THR:HB	1:G:113:GLU:HA	1.95	0.47
1:A:109:ILE:H	1:B:7:GLN:NE2	2.01	0.47
1:C:81:ASP:OD2	1:G:87:THR:HG23	2.15	0.47
1:H:127:ALA:HB1	1:H:129:ILE:HD13	1.95	0.47
2:O:24:ASN:O	2:O:25:THR:C	2.53	0.47
1:B:94:ASN:ND2	1:C:96:PRO:HG2	2.30	0.47
1:C:6:LEU:HD21	1:C:8:LEU:CD1	2.44	0.47
1:E:129:ILE:HG22	1:E:131:LEU:HD12	1.96	0.47
1:H:18:GLN:NE2	1:H:126:ASN:HA	2.29	0.47
1:J:129:ILE:HG22	1:J:131:LEU:HD12	1.96	0.47
2:M:20:ARG:CB	2:M:27:PRO:HD3	2.36	0.47
2:N:4:ASN:O	2:N:17:CYS:SG	2.73	0.47
1:A:68:GLY:HA3	1:A:91:CYS:O	2.15	0.47
1:C:87:THR:HG23	1:G:81:ASP:CG	2.35	0.47
1:I:141:LEU:C	1:I:141:LEU:HD23	2.35	0.47
2:N:3:GLN:C	2:N:5:GLU:H	2.17	0.47
1:A:67:MET:SD	1:A:124:ARG:HG3	2.55	0.47
1:E:78:VAL:HG21	1:E:84:SER:HB3	1.96	0.47
1:G:75:LYS:HE3	1:G:86:VAL:HG21	1.97	0.47
1:J:89:PHE:CZ	1:J:108:GLY:HA3	2.49	0.47
2:P:31:GLN:C	2:P:33:TYR:H	2.17	0.47
1:E:49:THR:HB	1:E:113:GLU:HA	1.97	0.47
1:F:49:THR:HB	1:F:113:GLU:HA	1.95	0.47
1:G:96:PRO:HG2	1:I:94:ASN:ND2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:75:LYS:HE3	1:H:86:VAL:HG21	1.97	0.47
1:I:58:VAL:HA	1:I:136:THR:HB	1.96	0.47
2:R:25:THR:HA	2:R:26:PRO:HD3	1.74	0.47
1:B:6:LEU:HD21	1:B:8:LEU:CD1	2.45	0.47
1:B:68:GLY:HA3	1:B:91:CYS:O	2.15	0.47
1:F:6:LEU:HD21	1:F:8:LEU:CD1	2.45	0.47
1:H:49:THR:HB	1:H:113:GLU:HA	1.97	0.47
1:A:6:LEU:HD21	1:A:8:LEU:CD1	2.44	0.46
1:G:7:GLN:NE2	1:I:109:ILE:H	2.03	0.46
1:I:6:LEU:HD21	1:I:8:LEU:CD1	2.45	0.46
1:I:89:PHE:CZ	1:I:108:GLY:HA3	2.50	0.46
2:M:27:PRO:O	2:M:28:LEU:O	2.34	0.46
1:B:59:LEU:HB3	1:B:130:SER:HB3	1.97	0.46
1:B:75:LYS:HE3	1:B:86:VAL:HG21	1.98	0.46
1:C:49:THR:HB	1:C:113:GLU:HA	1.96	0.46
1:D:78:VAL:HG21	1:D:84:SER:HB3	1.97	0.46
1:G:59:LEU:HB3	1:G:130:SER:HB3	1.97	0.46
2:M:26:PRO:HA	2:M:27:PRO:HD3	1.65	0.46
2:O:32:ARG:O	2:O:35:ASN:N	2.49	0.46
2:Q:21:CYS:O	2:Q:22:SER:O	2.33	0.46
1:A:129:ILE:HG22	1:A:131:LEU:HD12	1.97	0.46
1:B:129:ILE:HG22	1:B:131:LEU:HD12	1.96	0.46
1:C:59:LEU:HB3	1:C:130:SER:HB3	1.97	0.46
1:D:144:LEU:H	1:E:3:GLN:NE2	1.97	0.46
1:G:78:VAL:HG21	1:G:84:SER:HB3	1.96	0.46
2:L:33:TYR:C	2:L:35:ASN:N	2.69	0.46
1:G:94:ASN:ND2	1:H:101:ASN:H	2.08	0.46
2:P:24:ASN:O	2:P:26:PRO:CD	2.63	0.46
1:B:90:ARG:HG2	1:C:135:VAL:CG1	2.45	0.46
1:D:60:TYR:CE2	1:D:129:ILE:HD11	2.51	0.46
2:L:31:GLN:HA	2:L:34:CYS:HB2	1.98	0.46
2:M:28:LEU:HD23	2:M:29:THR:N	2.30	0.46
1:D:6:LEU:HD21	1:D:8:LEU:CD1	2.45	0.46
1:D:49:THR:HB	1:D:113:GLU:HA	1.96	0.46
1:D:75:LYS:HE3	1:D:86:VAL:HG21	1.96	0.46
1:E:81:ASP:OD2	1:J:87:THR:CG2	2.59	0.46
1:F:75:LYS:HE3	1:F:86:VAL:HG21	1.98	0.46
1:H:78:VAL:HG21	1:H:84:SER:HB3	1.96	0.46
1:A:93:GLN:HE22	1:C:93:GLN:HE22	1.61	0.46
1:A:94:ASN:HD21	1:B:101:ASN:N	1.99	0.46
1:D:89:PHE:CZ	1:D:108:GLY:HA3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:144:LEU:HD12	1:E:144:LEU:CD1	2.46	0.46
1:E:6:LEU:HD21	1:E:8:LEU:CD1	2.46	0.46
1:G:94:ASN:ND2	1:H:96:PRO:HG2	2.31	0.46
1:G:128:GLN:O	1:G:129:ILE:HD12	2.16	0.46
2:K:21:CYS:O	2:K:23:SER:N	2.48	0.46
2:N:1:CYS:HB2	2:N:2:SER:H	1.56	0.46
1:A:49:THR:HB	1:A:113:GLU:HA	1.98	0.46
1:B:94:ASN:ND2	1:C:101:ASN:H	2.05	0.46
1:D:64:THR:HG23	1:D:124:ARG:NH2	2.30	0.46
1:D:141:LEU:C	1:D:141:LEU:HD23	2.36	0.46
1:F:60:TYR:HD2	1:F:129:ILE:HD11	1.77	0.46
1:H:68:GLY:HA3	1:H:91:CYS:O	2.16	0.46
1:J:49:THR:HB	1:J:113:GLU:HA	1.98	0.46
1:J:78:VAL:HG21	1:J:84:SER:HB3	1.97	0.46
1:J:18:GLN:NE2	1:J:125:GLU:O	2.48	0.46
1:J:75:LYS:HE3	1:J:86:VAL:HG21	1.97	0.46
1:B:128:GLN:O	1:B:129:ILE:HD12	2.15	0.45
1:C:129:ILE:HG22	1:C:131:LEU:HD12	1.97	0.45
1:I:60:TYR:CE2	1:I:129:ILE:HD11	2.51	0.45
1:J:128:GLN:O	1:J:129:ILE:HD12	2.17	0.45
2:R:26:PRO:HA	2:R:27:PRO:HD3	1.55	0.45
1:B:109:ILE:H	1:C:7:GLN:NE2	2.03	0.45
1:H:59:LEU:HB2	1:H:135:VAL:HB	1.97	0.45
1:J:68:GLY:HA3	1:J:91:CYS:O	2.16	0.45
2:R:15:ILE:HG23	2:R:19:LEU:HD12	1.98	0.45
1:C:78:VAL:HG21	1:C:84:SER:HB3	1.97	0.45
1:D:68:GLY:HA3	1:D:91:CYS:O	2.15	0.45
1:E:68:GLY:HA3	1:E:91:CYS:O	2.16	0.45
1:A:89:PHE:CZ	1:A:108:GLY:HA3	2.52	0.45
1:B:60:TYR:CE2	1:B:129:ILE:HD11	2.51	0.45
1:B:62:ASP:CA	1:B:128:GLN:HB2	2.47	0.45
1:C:68:GLY:HA3	1:C:91:CYS:O	2.16	0.45
1:H:89:PHE:CZ	1:H:108:GLY:HA3	2.51	0.45
2:P:28:LEU:H	2:P:28:LEU:CD1	2.25	0.45
1:G:141:LEU:HD23	1:G:141:LEU:C	2.36	0.45
1:G:68:GLY:HA3	1:G:91:CYS:O	2.16	0.45
1:I:78:VAL:HG21	1:I:84:SER:HB3	1.98	0.45
1:I:129:ILE:HG22	1:I:131:LEU:HD12	1.98	0.45
2:K:26:PRO:HB3	2:K:27:PRO:HD2	1.98	0.45
2:M:15:ILE:HG23	2:M:19:LEU:HD12	1.97	0.45
2:P:36:ALA:C	2:P:38:VAL:N	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:TYR:CE2	1:A:129:ILE:HD11	2.51	0.45
1:D:128:GLN:O	1:D:129:ILE:HD12	2.15	0.45
1:G:89:PHE:CZ	1:G:108:GLY:HA3	2.52	0.45
1:H:129:ILE:HG22	1:H:131:LEU:HD12	1.98	0.45
2:M:20:ARG:HG3	2:M:27:PRO:HG2	1.97	0.45
1:E:128:GLN:O	1:E:129:ILE:HD12	2.17	0.45
2:N:5:GLU:OE2	2:N:16:PRO:HG3	2.16	0.45
2:Q:15:ILE:HG23	2:Q:19:LEU:HD12	1.98	0.45
1:C:89:PHE:CZ	1:C:108:GLY:HA3	2.52	0.45
1:F:141:LEU:C	1:F:141:LEU:HD23	2.37	0.45
2:P:28:LEU:O	2:P:29:THR:C	2.56	0.45
1:A:18:GLN:NE2	1:A:126:ASN:HA	2.32	0.45
1:D:6:LEU:C	1:D:6:LEU:HD23	2.37	0.45
1:F:129:ILE:HG22	1:F:131:LEU:HD12	1.98	0.45
1:H:128:GLN:O	1:H:129:ILE:HD12	2.17	0.45
1:J:6:LEU:HD21	1:J:8:LEU:CD1	2.47	0.45
2:O:15:ILE:HG23	2:O:19:LEU:HD12	1.99	0.45
1:A:58:VAL:O	1:A:103:SER:HA	2.17	0.44
1:A:141:LEU:C	1:A:141:LEU:HD23	2.38	0.44
1:D:58:VAL:O	1:D:103:SER:HA	2.17	0.44
1:F:68:GLY:HA3	1:F:91:CYS:O	2.17	0.44
1:H:60:TYR:CE2	1:H:129:ILE:HD11	2.52	0.44
1:J:58:VAL:O	1:J:103:SER:HA	2.17	0.44
2:L:15:ILE:HG23	2:L:19:LEU:HD12	1.98	0.44
2:M:20:ARG:HB3	2:M:27:PRO:CD	2.36	0.44
1:B:78:VAL:HG21	1:B:84:SER:HB3	1.98	0.44
1:E:75:LYS:HE3	1:E:86:VAL:HG21	1.98	0.44
1:E:94:ASN:CG	1:F:96:PRO:HG2	2.37	0.44
2:O:21:CYS:HA	2:O:26:PRO:HG2	2.00	0.44
1:B:58:VAL:O	1:B:103:SER:HA	2.17	0.44
1:D:59:LEU:HB2	1:D:135:VAL:HB	2.00	0.44
1:F:59:LEU:HB3	1:F:130:SER:HB3	1.98	0.44
1:F:89:PHE:CZ	1:F:108:GLY:HA3	2.52	0.44
1:I:75:LYS:HE3	1:I:86:VAL:HG21	1.99	0.44
2:O:26:PRO:HA	2:O:27:PRO:HD3	1.60	0.44
2:P:15:ILE:HG23	2:P:19:LEU:HD12	1.98	0.44
1:B:141:LEU:HD23	1:B:141:LEU:C	2.37	0.44
1:F:58:VAL:O	1:F:103:SER:HA	2.17	0.44
1:G:129:ILE:HG22	1:G:131:LEU:HD12	2.00	0.44
2:P:28:LEU:HD23	2:P:29:THR:N	2.32	0.44
2:R:4:ASN:CB	2:R:33:TYR:HD1	2.08	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:141:LEU:C	1:C:141:LEU:HD23	2.37	0.44
1:H:58:VAL:O	1:H:103:SER:HA	2.18	0.44
1:I:58:VAL:O	1:I:103:SER:HA	2.17	0.44
2:L:17:CYS:SG	2:L:29:THR:O	2.76	0.44
2:R:27:PRO:HD2	2:R:30:CYS:CB	2.48	0.44
1:C:99:LEU:HD11	2:L:19:LEU:CD1	2.47	0.44
1:D:144:LEU:CD1	1:F:144:LEU:HD12	2.48	0.44
2:L:20:ARG:O	2:L:26:PRO:HG3	2.18	0.44
2:R:2:SER:N	2:R:3:GLN:HE21	2.16	0.44
1:C:58:VAL:O	1:C:103:SER:HA	2.18	0.44
1:E:144:LEU:H	1:F:3:GLN:NE2	1.94	0.44
1:H:141:LEU:C	1:H:141:LEU:HD23	2.38	0.44
1:I:68:GLY:HA3	1:I:91:CYS:O	2.17	0.44
1:J:141:LEU:HD23	1:J:141:LEU:C	2.39	0.44
1:A:96:PRO:HG2	1:C:94:ASN:CG	2.38	0.43
1:A:101:ASN:H	1:C:94:ASN:ND2	2.08	0.43
1:E:58:VAL:O	1:E:103:SER:HA	2.17	0.43
1:E:144:LEU:N	1:F:3:GLN:HE21	1.94	0.43
1:G:6:LEU:C	1:G:6:LEU:HD23	2.38	0.43
1:I:125:GLU:HG2	2:Q:20:ARG:NH2	2.33	0.43
2:M:25:THR:N	2:M:26:PRO:HD3	2.32	0.43
1:I:128:GLN:O	1:I:129:ILE:HD12	2.18	0.43
2:K:9:SER:O	2:K:12:HIS:CD2	2.71	0.43
2:R:28:LEU:O	2:R:30:CYS:HB2	2.18	0.43
1:D:144:LEU:N	1:E:3:GLN:HE21	1.97	0.43
1:E:141:LEU:HD23	1:E:141:LEU:C	2.38	0.43
1:F:25:VAL:HA	1:F:26:PRO:HD3	1.86	0.43
1:I:59:LEU:HB3	1:I:130:SER:HB3	1.99	0.43
2:N:4:ASN:O	2:N:17:CYS:HB2	2.19	0.43
1:H:69:HIS:CD2	1:H:120:LEU:HD21	2.53	0.43
2:O:20:ARG:HA	2:O:24:ASN:HD21	1.82	0.43
1:B:60:TYR:HD2	1:B:129:ILE:HD11	1.79	0.43
1:C:60:TYR:HD2	1:C:129:ILE:HD11	1.82	0.43
1:E:6:LEU:C	1:E:6:LEU:HD23	2.39	0.43
2:K:2:SER:N	2:K:3:GLN:HE21	2.15	0.43
2:Q:2:SER:N	2:Q:3:GLN:HE21	2.15	0.43
1:E:144:LEU:OXT	1:F:2:THR:HG22	2.18	0.43
1:G:75:LYS:HE3	1:G:86:VAL:CG2	2.49	0.43
2:M:21:CYS:HA	2:M:26:PRO:HG2	2.01	0.43
1:A:90:ARG:HG2	1:B:135:VAL:CG1	2.49	0.43
1:C:6:LEU:HD23	1:C:6:LEU:C	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:6:LEU:HD21	1:G:8:LEU:CD1	2.48	0.43
1:I:6:LEU:C	1:I:6:LEU:HD23	2.39	0.43
1:J:89:PHE:CE2	1:J:108:GLY:HA3	2.54	0.43
2:M:9:SER:O	2:M:12:HIS:CD2	2.71	0.43
2:P:36:ALA:O	2:P:38:VAL:N	2.51	0.43
1:D:59:LEU:HB3	1:D:130:SER:HB3	2.01	0.43
1:D:129:ILE:HG22	1:D:131:LEU:HD12	2.00	0.43
1:E:89:PHE:CE2	1:E:108:GLY:HA3	2.54	0.43
1:F:75:LYS:HE3	1:F:86:VAL:CG2	2.49	0.43
1:J:75:LYS:HE3	1:J:86:VAL:CG2	2.49	0.43
1:A:75:LYS:HE3	1:A:86:VAL:HG21	1.99	0.42
1:F:62:ASP:CA	1:F:128:GLN:HB2	2.49	0.42
1:J:6:LEU:C	1:J:6:LEU:HD23	2.39	0.42
1:E:93:GLN:HE22	1:F:93:GLN:NE2	2.15	0.42
1:G:99:LEU:HD11	2:Q:19:LEU:CD1	2.49	0.42
2:L:26:PRO:HA	2:L:27:PRO:HD3	1.75	0.42
2:Q:9:SER:O	2:Q:12:HIS:CD2	2.72	0.42
2:R:17:CYS:SG	2:R:29:THR:O	2.77	0.42
1:A:63:LYS:HE2	1:A:63:LYS:HB3	1.87	0.42
1:H:6:LEU:HD23	1:H:6:LEU:C	2.40	0.42
2:M:2:SER:N	2:M:3:GLN:HE21	2.16	0.42
1:B:75:LYS:HE3	1:B:86:VAL:CG2	2.49	0.42
1:D:75:LYS:HE3	1:D:86:VAL:CG2	2.49	0.42
1:D:99:LEU:HD11	2:O:19:LEU:CD1	2.50	0.42
1:D:141:LEU:HD12	1:F:109:ILE:HD11	2.01	0.42
1:E:67:MET:C	2:N:10:LEU:HD21	2.40	0.42
1:F:92:ILE:HD13	2:O:11:LEU:HD23	2.02	0.42
1:H:6:LEU:HD21	1:H:8:LEU:CD1	2.48	0.42
2:P:9:SER:O	2:P:12:HIS:CD2	2.73	0.42
1:D:90:ARG:HG2	1:E:135:VAL:CG1	2.50	0.42
2:O:4:ASN:HB3	2:O:33:TYR:CD1	2.54	0.42
1:B:89:PHE:CE2	1:B:108:GLY:HA3	2.55	0.42
1:E:124:ARG:NH2	2:N:10:LEU:HB2	2.34	0.42
1:F:52:PHE:CE2	1:F:142:LYS:HB2	2.55	0.42
1:I:11:ASP:HB2	1:I:28:LEU:HB2	2.02	0.42
2:Q:4:ASN:HB3	2:Q:33:TYR:CD1	2.55	0.42
1:B:81:ASP:OD2	1:F:87:THR:HG23	2.20	0.42
1:C:75:LYS:HE3	1:C:86:VAL:CG2	2.50	0.42
2:Q:4:ASN:ND2	2:Q:33:TYR:CD1	2.73	0.42
1:D:135:VAL:HG12	1:F:90:ARG:HG2	2.02	0.42
1:E:94:ASN:ND2	1:F:96:PRO:HG2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:59:LEU:HB3	1:H:130:SER:HB3	2.01	0.42
1:I:89:PHE:CE2	1:I:108:GLY:HA3	2.55	0.42
2:K:15:ILE:HG23	2:K:19:LEU:HD12	1.99	0.42
2:Q:31:GLN:O	2:Q:34:CYS:N	2.53	0.42
1:A:141:LEU:HD12	1:C:109:ILE:HD11	2.01	0.42
1:B:69:HIS:CD2	1:B:120:LEU:HD21	2.55	0.42
1:C:69:HIS:CD2	1:C:120:LEU:HD21	2.55	0.42
1:I:75:LYS:HE3	1:I:86:VAL:CG2	2.50	0.42
2:P:28:LEU:CD2	2:P:29:THR:N	2.82	0.42
1:D:93:GLN:HE22	1:E:93:GLN:NE2	2.13	0.42
1:E:59:LEU:HB3	1:E:130:SER:HB3	2.01	0.42
2:M:31:GLN:O	2:M:34:CYS:HB2	2.20	0.42
2:O:9:SER:O	2:O:12:HIS:CD2	2.73	0.42
1:A:124:ARG:HH12	2:K:8:ASP:CG	2.21	0.41
1:F:6:LEU:HD23	1:F:6:LEU:C	2.41	0.41
2:K:26:PRO:HG2	2:K:34:CYS:SG	2.60	0.41
2:L:22:SER:O	2:L:23:SER:CB	2.67	0.41
1:E:144:LEU:HD12	1:F:144:LEU:CD1	2.49	0.41
1:G:69:HIS:CD2	1:G:120:LEU:HD21	2.56	0.41
1:H:75:LYS:HE3	1:H:86:VAL:CG2	2.49	0.41
2:L:33:TYR:O	2:L:36:ALA:HB3	2.19	0.41
1:D:64:THR:O	1:D:64:THR:CG2	2.65	0.41
1:G:143:LEU:HD22	1:H:141:LEU:HD11	2.02	0.41
2:P:26:PRO:HA	2:P:27:PRO:HD3	1.81	0.41
2:R:29:THR:O	2:R:29:THR:HG23	2.19	0.41
2:R:9:SER:O	2:R:12:HIS:CD2	2.73	0.41
1:D:141:LEU:HD11	1:F:143:LEU:CD2	2.51	0.41
1:F:124:ARG:HB2	1:F:127:ALA:HB2	2.02	0.41
1:G:62:ASP:CA	1:G:128:GLN:HB2	2.50	0.41
2:L:9:SER:O	2:L:12:HIS:CD2	2.73	0.41
1:B:11:ASP:HB2	1:B:28:LEU:HB2	2.03	0.41
1:G:58:VAL:O	1:G:103:SER:HA	2.20	0.41
1:I:69:HIS:CD2	1:I:120:LEU:HD21	2.56	0.41
1:J:25:VAL:HA	1:J:26:PRO:HD3	1.86	0.41
2:L:2:SER:N	2:L:3:GLN:HE21	2.16	0.41
2:O:2:SER:N	2:O:3:GLN:HE21	2.16	0.41
1:A:6:LEU:HD23	1:A:6:LEU:C	2.41	0.41
1:E:75:LYS:HE3	1:E:86:VAL:CG2	2.50	0.41
1:A:11:ASP:HB2	1:A:28:LEU:HB2	2.03	0.41
1:A:69:HIS:CD2	1:A:120:LEU:HD21	2.55	0.41
1:C:92:ILE:HD13	2:M:11:LEU:CD2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:69:HIS:CD2	1:D:120:LEU:HD21	2.56	0.41
1:G:92:ILE:HD13	2:P:11:LEU:HD23	2.02	0.41
1:G:93:GLN:NE2	1:I:93:GLN:HE22	2.14	0.41
1:H:63:LYS:HE2	1:H:63:LYS:HB3	1.87	0.41
2:K:28:LEU:N	2:K:28:LEU:CD2	2.84	0.41
2:L:6:TYR:CE2	2:L:15:ILE:HB	2.56	0.41
2:L:29:THR:O	2:L:29:THR:HG22	2.21	0.41
2:M:28:LEU:HD23	2:M:29:THR:H	1.85	0.41
2:M:30:CYS:O	2:M:34:CYS:SG	2.79	0.41
2:N:15:ILE:CG2	2:N:19:LEU:HD12	2.50	0.41
2:P:24:ASN:O	2:P:26:PRO:HD3	2.21	0.41
2:Q:24:ASN:O	2:Q:25:THR:C	2.60	0.41
1:A:75:LYS:HE3	1:A:86:VAL:CG2	2.51	0.41
1:B:6:LEU:C	1:B:6:LEU:HD23	2.41	0.41
1:E:25:VAL:HA	1:E:26:PRO:HD3	1.86	0.41
1:E:123:PRO:CB	2:N:9:SER:HB2	2.52	0.41
1:G:144:LEU:N	1:H:3:GLN:HE21	1.95	0.41
1:A:93:GLN:HE22	1:B:93:GLN:NE2	2.13	0.40
1:C:47:LYS:HB3	1:C:47:LYS:NZ	2.37	0.40
1:D:109:ILE:CD1	1:E:141:LEU:HD12	2.49	0.40
1:H:99:LEU:HD11	2:P:19:LEU:CD1	2.50	0.40
2:K:27:PRO:HG2	2:K:30:CYS:HB2	2.02	0.40
1:G:125:GLU:HG3	2:P:27:PRO:CG	2.51	0.40
1:E:11:ASP:HB2	1:E:28:LEU:HB2	2.03	0.40
1:H:11:ASP:HB2	1:H:28:LEU:HB2	2.03	0.40
1:H:64:THR:HG21	1:H:124:ARG:CZ	2.52	0.40
2:O:32:ARG:O	2:O:35:ASN:HB2	2.22	0.40
1:D:95:MET:HA	1:D:96:PRO:HD3	1.92	0.40
1:D:103:SER:OG	1:F:91:CYS:HB2	2.22	0.40
1:F:69:HIS:CD2	1:F:120:LEU:HD21	2.55	0.40
2:K:4:ASN:ND2	2:K:33:TYR:CD1	2.80	0.40
1:A:90:ARG:HG2	1:B:135:VAL:HG12	2.03	0.40
1:C:62:ASP:CA	1:C:128:GLN:HB2	2.52	0.40
1:D:11:ASP:HB2	1:D:28:LEU:HB2	2.03	0.40
1:D:25:VAL:HA	1:D:26:PRO:HD3	1.86	0.40
1:E:124:ARG:NH2	2:N:10:LEU:HD22	2.26	0.40
1:I:25:VAL:HA	1:I:26:PRO:HD3	1.86	0.40
1:I:122:ILE:HA	1:I:123:PRO:HD3	1.90	0.40
2:O:24:ASN:O	2:O:26:PRO:N	2.54	0.40
2:Q:20:ARG:O	2:Q:21:CYS:C	2.59	0.40
2:R:20:ARG:O	2:R:24:ASN: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	A	142/144 (99%)	133 (94%)	7 (5%)	2 (1%)	11	22
1	B	142/144 (99%)	134 (94%)	6 (4%)	2 (1%)	11	22
1	C	142/144 (99%)	134 (94%)	6 (4%)	2 (1%)	11	22
1	D	142/144 (99%)	134 (94%)	6 (4%)	2 (1%)	11	22
1	E	142/144 (99%)	133 (94%)	7 (5%)	2 (1%)	11	22
1	F	142/144 (99%)	134 (94%)	6 (4%)	2 (1%)	11	22
1	G	142/144 (99%)	133 (94%)	7 (5%)	2 (1%)	11	22
1	H	142/144 (99%)	136 (96%)	4 (3%)	2 (1%)	11	22
1	I	142/144 (99%)	133 (94%)	7 (5%)	2 (1%)	11	22
1	J	142/144 (99%)	134 (94%)	6 (4%)	2 (1%)	11	22
2	K	37/39 (95%)	19 (51%)	9 (24%)	9 (24%)	0	0
2	L	37/39 (95%)	20 (54%)	12 (32%)	5 (14%)	0	0
2	M	37/39 (95%)	24 (65%)	8 (22%)	5 (14%)	0	0
2	N	19/39 (49%)	12 (63%)	2 (10%)	5 (26%)	0	0
2	O	37/39 (95%)	23 (62%)	9 (24%)	5 (14%)	0	0
2	P	37/39 (95%)	19 (51%)	10 (27%)	8 (22%)	0	0
2	Q	37/39 (95%)	23 (62%)	7 (19%)	7 (19%)	0	0
2	R	37/39 (95%)	25 (68%)	7 (19%)	5 (14%)	0	0
All	All	1698/1752 (97%)	1503 (88%)	126 (7%)	69 (4%)	3	3

All (69) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	TYR

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Mol	Chain	Res	Type
1	B	65	TYR
1	C	65	TYR
1	D	65	TYR
1	D	98	THR
1	E	65	TYR
1	G	65	TYR
1	H	65	TYR
1	I	65	TYR
1	J	65	TYR
2	K	23	SER
2	K	35	ASN
2	L	23	SER
2	L	27	PRO
2	M	28	LEU
2	M	29	THR
2	M	30	CYS
2	N	4	ASN
2	N	5	GLU
2	N	17	CYS
2	O	29	THR
2	P	29	THR
2	P	38	VAL
2	Q	22	SER
2	R	22	SER
2	R	29	THR
1	A	98	THR
1	B	98	THR
1	C	98	THR
1	E	98	THR
1	F	65	TYR
1	F	98	THR
1	G	98	THR
1	H	98	THR
1	I	98	THR
1	J	98	THR
2	K	22	SER
2	K	29	THR
2	M	24	ASN
2	N	20	ARG
2	P	23	SER
2	Q	21	CYS
2	R	27	PRO

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Mol	Chain	Res	Type
2	K	2	SER
2	K	26	PRO
2	L	2	SER
2	L	22	SER
2	M	2	SER
2	N	3	GLN
2	O	2	SER
2	O	24	ASN
2	O	28	LEU
2	P	2	SER
2	P	32	ARG
2	P	37	SER
2	Q	2	SER
2	Q	31	GLN
2	R	2	SER
2	K	28	LEU
2	P	28	LEU
2	Q	38	VAL
2	K	31	GLN
2	O	25	THR
2	R	35	ASN
2	P	25	THR
2	Q	25	THR
2	Q	26	PRO
2	K	25	THR
2	L	26	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	126/126 (100%)	117 (93%)	9 (7%)	14	29
1	B	126/126 (100%)	117 (93%)	9 (7%)	14	29
1	C	126/126 (100%)	117 (93%)	9 (7%)	14	29
1	D	126/126 (100%)	116 (92%)	10 (8%)	12	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	126/126 (100%)	116 (92%)	10 (8%)	12	24
1	F	126/126 (100%)	116 (92%)	10 (8%)	12	24
1	G	126/126 (100%)	116 (92%)	10 (8%)	12	24
1	H	126/126 (100%)	114 (90%)	12 (10%)	8	16
1	I	126/126 (100%)	115 (91%)	11 (9%)	10	20
1	J	126/126 (100%)	117 (93%)	9 (7%)	14	29
2	K	37/37 (100%)	33 (89%)	4 (11%)	6	12
2	L	37/37 (100%)	35 (95%)	2 (5%)	22	44
2	M	37/37 (100%)	34 (92%)	3 (8%)	11	23
2	N	20/37 (54%)	17 (85%)	3 (15%)	3	5
2	O	37/37 (100%)	35 (95%)	2 (5%)	22	44
2	P	37/37 (100%)	34 (92%)	3 (8%)	11	23
2	Q	37/37 (100%)	35 (95%)	2 (5%)	22	44
2	R	37/37 (100%)	33 (89%)	4 (11%)	6	12
All	All	1539/1556 (99%)	1417 (92%)	122 (8%)	12	24

All (122) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LEU
1	A	9	ILE
1	A	47	LYS
1	A	59	LEU
1	A	76	VAL
1	A	87	THR
1	A	88	LEU
1	A	120	LEU
1	A	136	THR
1	B	8	LEU
1	B	9	ILE
1	B	47	LYS
1	B	59	LEU
1	B	76	VAL
1	B	87	THR
1	B	88	LEU
1	B	120	LEU
1	B	136	THR

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Mol	Chain	Res	Type
1	C	8	LEU
1	C	9	ILE
1	C	47	LYS
1	C	59	LEU
1	C	76	VAL
1	C	87	THR
1	C	88	LEU
1	C	120	LEU
1	C	136	THR
1	D	8	LEU
1	D	9	ILE
1	D	47	LYS
1	D	59	LEU
1	D	76	VAL
1	D	87	THR
1	D	88	LEU
1	D	120	LEU
1	D	124	ARG
1	D	136	THR
1	E	8	LEU
1	E	9	ILE
1	E	47	LYS
1	E	59	LEU
1	E	76	VAL
1	E	87	THR
1	E	88	LEU
1	E	120	LEU
1	E	125	GLU
1	E	136	THR
1	F	8	LEU
1	F	9	ILE
1	F	47	LYS
1	F	59	LEU
1	F	65	TYR
1	F	76	VAL
1	F	87	THR
1	F	88	LEU
1	F	120	LEU
1	F	136	THR
1	G	8	LEU
1	G	9	ILE
1	G	47	LYS

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Mol	Chain	Res	Type
1	G	59	LEU
1	G	76	VAL
1	G	87	THR
1	G	88	LEU
1	G	120	LEU
1	G	124	ARG
1	G	136	THR
1	H	8	LEU
1	H	9	ILE
1	H	47	LYS
1	H	59	LEU
1	H	65	TYR
1	H	76	VAL
1	H	87	THR
1	H	88	LEU
1	H	120	LEU
1	H	124	ARG
1	H	126	ASN
1	H	136	THR
1	I	8	LEU
1	I	9	ILE
1	I	47	LYS
1	I	59	LEU
1	I	65	TYR
1	I	76	VAL
1	I	87	THR
1	I	88	LEU
1	I	120	LEU
1	I	124	ARG
1	I	136	THR
1	J	8	LEU
1	J	9	ILE
1	J	47	LYS
1	J	59	LEU
1	J	76	VAL
1	J	87	THR
1	J	88	LEU
1	J	120	LEU
1	J	136	THR
2	K	3	GLN
2	K	22	SER
2	K	28	LEU

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Mol	Chain	Res	Type
2	K	29	THR
2	L	3	GLN
2	L	24	ASN
2	M	3	GLN
2	M	30	CYS
2	M	33	TYR
2	N	1	CYS
2	N	4	ASN
2	N	21	CYS
2	O	3	GLN
2	O	28	LEU
2	P	3	GLN
2	P	24	ASN
2	P	28	LEU
2	Q	3	GLN
2	Q	38	VAL
2	R	3	GLN
2	R	33	TYR
2	R	35	ASN
2	R	38	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (90) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	GLN
1	A	7	GLN
1	A	42	ASN
1	A	93	GLN
1	A	94	ASN
1	A	119	GLN
1	B	3	GLN
1	B	7	GLN
1	B	42	ASN
1	B	77	HIS
1	B	93	GLN
1	B	94	ASN
1	B	119	GLN
1	C	3	GLN
1	C	7	GLN
1	C	18	GLN
1	C	42	ASN
1	C	77	HIS

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Mol	Chain	Res	Type
1	C	93	GLN
1	C	94	ASN
1	C	119	GLN
1	D	3	GLN
1	D	7	GLN
1	D	18	GLN
1	D	42	ASN
1	D	93	GLN
1	D	94	ASN
1	D	119	GLN
1	E	3	GLN
1	E	7	GLN
1	E	18	GLN
1	E	42	ASN
1	E	93	GLN
1	E	94	ASN
1	E	119	GLN
1	F	3	GLN
1	F	7	GLN
1	F	18	GLN
1	F	42	ASN
1	F	77	HIS
1	F	93	GLN
1	F	94	ASN
1	F	119	GLN
1	G	3	GLN
1	G	7	GLN
1	G	42	ASN
1	G	77	HIS
1	G	93	GLN
1	G	94	ASN
1	G	119	GLN
1	H	3	GLN
1	H	7	GLN
1	H	18	GLN
1	H	42	ASN
1	H	93	GLN
1	H	94	ASN
1	H	119	GLN
1	I	3	GLN
1	I	7	GLN
1	I	42	ASN

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Mol	Chain	Res	Type
1	I	93	GLN
1	I	94	ASN
1	I	119	GLN
1	J	7	GLN
1	J	42	ASN
1	J	77	HIS
1	J	119	GLN
2	K	3	GLN
2	K	12	HIS
2	K	18	GLN
2	L	3	GLN
2	L	12	HIS
2	L	18	GLN
2	M	3	GLN
2	M	12	HIS
2	O	3	GLN
2	O	12	HIS
2	O	24	ASN
2	O	35	ASN
2	P	3	GLN
2	P	12	HIS
2	P	18	GLN
2	P	35	ASN
2	Q	3	GLN
2	Q	12	HIS
2	Q	31	GLN
2	Q	35	ASN
2	R	3	GLN
2	R	12	HIS
2	R	18	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	35:ASN	C	36:ALA	N	0.95

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, 95th 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^2)	Q<0.9
1	A	144/144 (100%)	-0.24	1 (0%)	87	86	24, 39, 65, 79	0
1	B	144/144 (100%)	-0.31	1 (0%)	87	86	23, 39, 62, 79	0
1	C	144/144 (100%)	-0.31	1 (0%)	87	86	24, 37, 63, 78	0
1	D	144/144 (100%)	-0.51	0	100	100	20, 33, 54, 68	0
1	E	144/144 (100%)	-0.47	0	100	100	23, 35, 57, 76	0
1	F	144/144 (100%)	-0.47	0	100	100	20, 35, 58, 70	0
1	G	144/144 (100%)	-0.28	0	100	100	18, 33, 52, 62	0
1	H	144/144 (100%)	-0.42	1 (0%)	87	86	21, 31, 46, 63	0
1	I	144/144 (100%)	-0.35	1 (0%)	87	86	21, 33, 53, 71	0
1	J	144/144 (100%)	-0.51	1 (0%)	87	86	21, 36, 60, 71	0
2	K	39/39 (100%)	2.72	24 (61%)	0	0	74, 125, 149, 157	0
2	L	39/39 (100%)	2.35	22 (56%)	0	0	65, 124, 137, 142	0
2	M	39/39 (100%)	3.00	24 (61%)	0	0	63, 129, 148, 150	0
2	N	21/39 (53%)	3.62	17 (80%)	0	0	103, 126, 143, 147	0
2	O	39/39 (100%)	2.30	21 (53%)	0	0	49, 113, 134, 140	0
2	P	39/39 (100%)	2.32	19 (48%)	0	0	44, 111, 141, 147	0
2	Q	39/39 (100%)	2.67	21 (53%)	0	0	40, 119, 155, 156	0
2	R	39/39 (100%)	2.71	24 (61%)	0	0	50, 115, 160, 167	0
All	All	1734/1752 (98%)	0.13	178 (10%)	6	4	18, 38, 132, 167	0

All (178) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	N	20	ARG	9.6
2	Q	39	THR	9.1
2	Q	38	VAL	9.0

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Mol	Chain	Res	Type	RSRZ
2	M	24	ASN	8.6
2	K	39	THR	7.8
2	R	39	THR	7.7
2	K	36	ALA	7.4
2	R	36	ALA	7.1
2	Q	37	SER	7.1
2	K	38	VAL	7.0
2	M	32	ARG	6.9
2	R	37	SER	6.9
2	O	23	SER	6.6
2	N	21	CYS	6.5
2	M	30	CYS	6.5
2	P	23	SER	6.2
2	P	39	THR	6.2
2	P	25	THR	6.0
2	M	39	THR	6.0
2	M	22	SER	5.9
2	Q	28	LEU	5.9
2	M	34	CYS	5.7
2	O	33	TYR	5.7
2	P	2	SER	5.5
2	L	35	ASN	5.5
2	R	22	SER	5.5
2	O	39	THR	5.5
2	Q	35	ASN	5.3
2	P	38	VAL	5.3
2	K	37	SER	5.3
2	R	35	ASN	5.1
2	O	32	ARG	5.1
2	L	32	ARG	5.0
2	N	4	ASN	5.0
2	N	19	LEU	4.9
2	O	36	ALA	4.9
2	Q	36	ALA	4.9
2	Q	31	GLN	4.9
2	Q	32	ARG	4.8
2	L	36	ALA	4.8
2	M	4	ASN	4.7
2	K	32	ARG	4.7
2	N	6	TYR	4.6
2	N	15	ILE	4.6
2	O	34	CYS	4.6

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Mol	Chain	Res	Type	RSRZ
2	R	24	ASN	4.6
2	R	25	THR	4.5
2	K	34	CYS	4.5
2	R	38	VAL	4.5
2	P	30	CYS	4.4
2	M	37	SER	4.4
2	O	38	VAL	4.4
2	N	18	GLN	4.4
2	R	23	SER	4.3
2	M	1	CYS	4.3
2	N	17	CYS	4.3
2	Q	22	SER	4.3
2	N	16	PRO	4.2
2	L	30	CYS	4.2
2	M	29	THR	4.2
2	P	31	GLN	4.2
2	L	22	SER	4.1
2	L	39	THR	4.1
2	P	35	ASN	4.1
2	K	22	SER	4.1
2	L	29	THR	4.0
2	N	5	GLU	4.0
2	M	28	LEU	4.0
2	M	6	TYR	4.0
2	Q	24	ASN	3.9
2	K	2	SER	3.9
2	K	35	ASN	3.9
2	N	3	GLN	3.9
2	K	28	LEU	3.9
2	R	32	ARG	3.8
2	L	31	GLN	3.8
2	M	25	THR	3.8
2	M	36	ALA	3.8
2	M	35	ASN	3.7
2	K	21	CYS	3.7
2	N	2	SER	3.7
2	K	29	THR	3.6
2	M	20	ARG	3.6
2	P	24	ASN	3.6
2	P	34	CYS	3.6
2	M	31	GLN	3.6
2	O	30	CYS	3.5

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Mol	Chain	Res	Type	RSRZ
2	Q	26	PRO	3.5
2	R	6	TYR	3.5
2	O	21	CYS	3.4
2	M	2	SER	3.4
2	L	23	SER	3.4
2	O	31	GLN	3.4
2	O	37	SER	3.4
2	P	32	ARG	3.4
2	R	21	CYS	3.4
2	Q	29	THR	3.4
2	L	38	VAL	3.4
2	Q	30	CYS	3.3
2	R	27	PRO	3.3
2	K	1	CYS	3.3
2	L	28	LEU	3.3
2	L	25	THR	3.3
2	Q	2	SER	3.3
2	K	23	SER	3.3
2	K	4	ASN	3.3
2	R	29	THR	3.3
2	R	30	CYS	3.3
2	M	21	CYS	3.3
2	R	28	LEU	3.2
2	R	2	SER	3.2
2	O	4	ASN	3.2
2	L	4	ASN	3.2
2	M	18	GLN	3.2
2	K	30	CYS	3.1
2	K	31	GLN	3.1
2	O	28	LEU	3.1
2	L	34	CYS	3.1
2	M	33	TYR	3.1
2	R	33	TYR	3.1
2	L	18	GLN	3.1
2	L	24	ASN	3.1
2	O	27	PRO	3.1
2	Q	23	SER	3.1
2	P	4	ASN	3.0
2	K	19	LEU	3.0
2	K	33	TYR	3.0
2	O	24	ASN	2.9
2	R	34	CYS	2.9

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Mol	Chain	Res	Type	RSRZ
2	P	28	LEU	2.9
2	R	31	GLN	2.9
2	L	37	SER	2.8
2	P	19	LEU	2.8
2	L	21	CYS	2.8
2	L	26	PRO	2.8
2	R	26	PRO	2.8
2	P	22	SER	2.7
2	K	16	PRO	2.7
2	O	22	SER	2.7
2	Q	25	THR	2.7
2	L	20	ARG	2.7
2	P	26	PRO	2.7
2	R	17	CYS	2.7
2	Q	34	CYS	2.7
2	L	2	SER	2.6
2	P	36	ALA	2.6
2	O	2	SER	2.6
2	L	19	LEU	2.6
2	N	1	CYS	2.5
2	R	4	ASN	2.5
2	O	35	ASN	2.5
2	N	7	PHE	2.5
2	Q	3	GLN	2.4
2	M	3	GLN	2.4
2	P	16	PRO	2.4
1	B	104	CYS	2.4
2	K	17	CYS	2.4
2	O	3	GLN	2.4
2	K	18	GLN	2.3
2	O	18	GLN	2.3
2	N	10	LEU	2.3
2	R	1	CYS	2.3
2	O	29	THR	2.3
1	C	91	CYS	2.3
1	A	104	CYS	2.2
2	M	17	CYS	2.2
1	J	20	GLY	2.2
2	M	38	VAL	2.2
2	Q	4	ASN	2.2
2	P	18	GLN	2.1
2	N	14	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	Q	33	TYR	2.1
2	K	3	GLN	2.1
2	N	13	ALA	2.1
2	Q	1	CYS	2.0
2	K	26	PRO	2.0
1	H	104	CYS	2.0
1	I	104	CYS	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.