



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:37 AM GMT

PDB ID : 2DOI
Title : The X-ray crystallographic structure of the angiogenesis inhibitor, angiostatin, bound to a peptide from the group A streptococcus protein PAM
Authors : Cnudde, S.E.; Prorok, M.; Castellino, F.J.; Geiger, J.H.
Deposited on : 2006-04-29
Resolution : 3.10 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

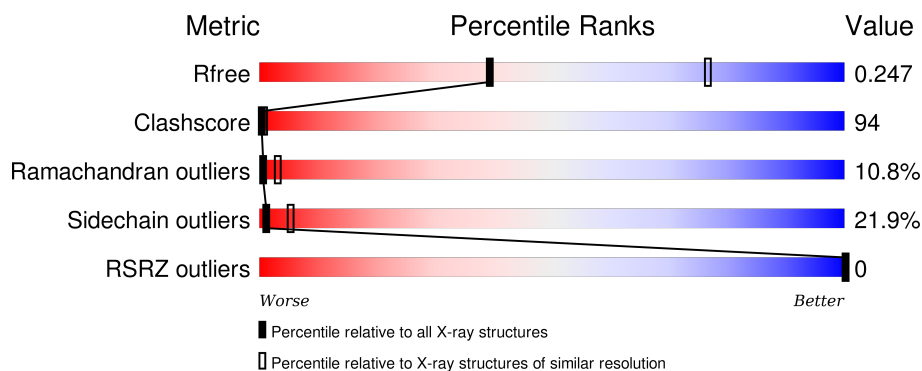
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	234	
1	X	234	
2	B	30	
2	C	30	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3064 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 Angiostatin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	168	Total	C	N	O	S	0	0	0
			1347	824	242	264	17			
1	A	164	Total	C	N	O	S	0	0	0
			1313	803	235	259	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	289	GLU	ASN	ENGINEERED	UNP P00747
A	289	GLU	ASN	ENGINEERED	UNP P00747

- Molecule 2 is a protein called Plasminogen-binding group A streptococcal M-like protein PAM.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	24	Total	C	N	O	0	0	0
			202	122	39	41			
2	B	24	Total	C	N	O	0	0	0
			202	122	39	41			

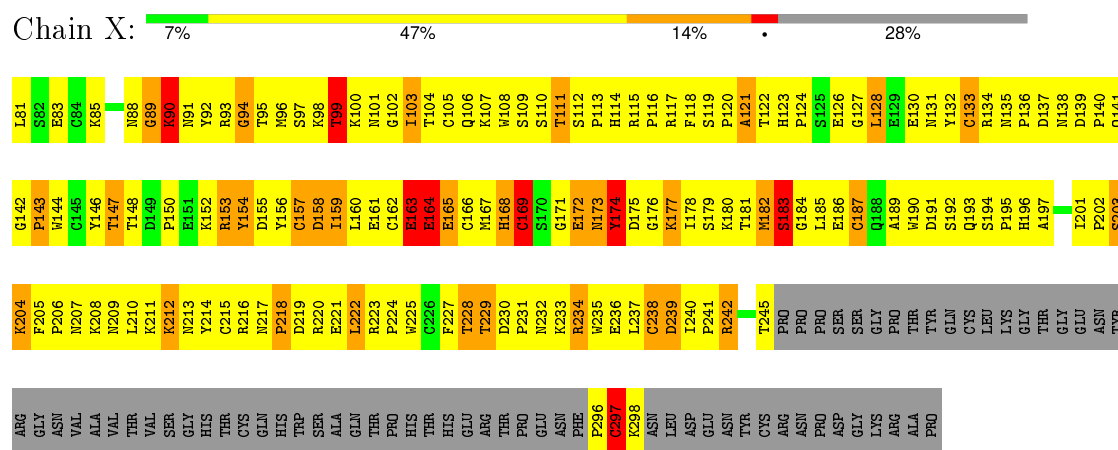
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	330	TYR	-	CLONING ARTIFACT	UNP P49054
B	330	TYR	-	CLONING ARTIFACT	UNP P49054

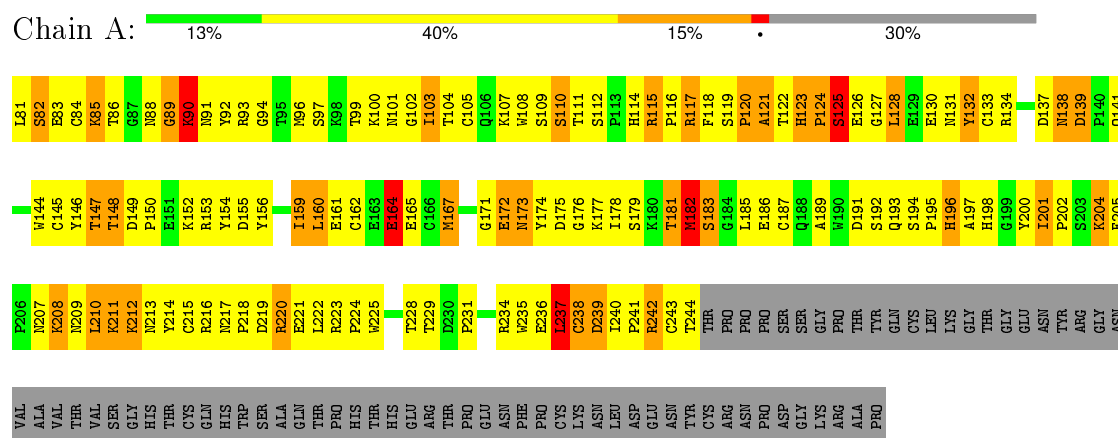
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

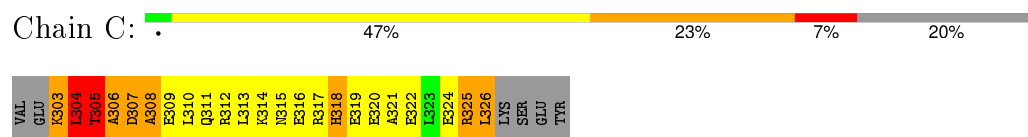
• Molecule 1: Angiostatin



• Molecule 1: Angiostatin



• Molecule 2: Plasminogen-binding group A streptococcal M-like protein PAM



• Molecule 2: Plasminogen-binding group A streptococcal M-like protein PAM

Chain B: 10% 43% 27% 20%

VAL	GLU	LYS	L304	T305	A306	D307	A308	E309	L310	Q311	R312	L313	K314	R317	H318	E319	E320	A321	E322	L323	E324	R325	L326	K327	SER	GLU	TYR
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4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	58.47Å 58.47Å 389.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 3.10 19.96 – 2.81	Depositor EDS
% Data completeness (in resolution range)	97.0 (20.00-3.10) 85.9 (19.96-2.81)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.202 , 0.296 0.203 , 0.247	Depositor DCC
R_{free} test set	1385 reflections (11.78%)	DCC
Wilson B-factor (Å ²)	77.0	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 38.1	EDS
Estimated twinning fraction	0.479 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 16262 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3064	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.01	0/1353	1.16	5/1837 (0.3%)
1	X	1.12	2/1387 (0.1%)	1.21	5/1878 (0.3%)
2	B	1.12	0/202	1.35	1/268 (0.4%)
2	C	1.06	0/202	1.38	2/268 (0.7%)
All	All	1.07	2/3144 (0.1%)	1.21	13/4251 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	133	CYS	CB-SG	-6.01	1.72	1.82
1	X	187	CYS	CB-SG	-5.07	1.73	1.81

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	326	LEU	CA-CB-CG	8.21	134.17	115.30
1	X	128	LEU	CA-CB-CG	-6.39	100.60	115.30
1	X	185	LEU	CB-CG-CD2	-6.25	100.38	111.00
2	C	304	LEU	CB-CG-CD1	6.14	121.45	111.00
1	A	181	THR	CB-CA-C	-6.07	95.22	111.60
1	X	164	GLU	N-CA-C	6.04	127.31	111.00
1	A	210	LEU	CA-CB-CG	-5.86	101.82	115.30
1	A	160	LEU	CA-CB-CG	-5.81	101.93	115.30
1	A	237	LEU	CA-CB-CG	-5.79	101.97	115.30
1	A	89	GLY	N-CA-C	5.71	127.38	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	313	LEU	CA-CB-CG	-5.48	102.69	115.30
1	X	89	GLY	N-CA-C	5.31	126.37	113.10
1	X	152	LYS	N-CA-C	-5.10	97.23	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	208	LYS	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of 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	1313	0	1182	254	0
1	X	1347	0	1225	257	0
2	B	202	0	202	37	0
2	C	202	0	202	37	0
All	All	3064	0	2811	552	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 94.

All (552) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:187:CYS:HB2	1:A:213:ASN:ND2	1.62	1.12
1:X:103:ILE:H	1:X:103:ILE:HD12	1.08	1.11
1:X:224:PRO:CG	1:X:240:ILE:HD12	1.81	1.10
1:X:195:PRO:O	1:X:196:HIS:HD2	1.32	1.10
1:X:133:CYS:O	1:X:134:ARG:HD3	1.51	1.08
1:A:174:TYR:HE2	1:A:240:ILE:HG12	1.09	1.08
1:X:164:GLU:O	1:X:164:GLU:HG3	1.52	1.05
2:B:325:ARG:HH11	2:B:325:ARG:HG2	1.19	1.03
1:X:174:TYR:CE2	1:X:176:GLY:N	2.27	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:222:LEU:O	1:X:223:ARG:HG3	1.58	1.02
1:A:174:TYR:CE1	1:A:176:GLY:HA3	1.95	1.01
1:A:174:TYR:CE2	1:A:240:ILE:HG12	1.95	1.01
1:X:242:ARG:HG3	1:X:242:ARG:HH11	1.23	1.01
1:X:194:SER:HB2	1:X:195:PRO:HA	1.44	1.00
2:B:310:LEU:HA	2:B:313:LEU:HD12	1.40	0.99
1:A:221:GLU:OE2	2:B:318:HIS:HE1	1.45	0.99
2:B:325:ARG:HH11	2:B:325:ARG:CG	1.74	0.99
1:X:174:TYR:CE2	1:X:176:GLY:CA	2.46	0.98
1:A:124:PRO:O	1:A:126:GLU:N	1.96	0.97
1:A:101:ASN:HB2	1:A:103:ILE:HD11	1.43	0.97
1:A:183:SER:OG	1:A:236:GLU:OE1	1.82	0.97
1:A:174:TYR:HE1	1:A:176:GLY:HA3	1.30	0.97
1:X:224:PRO:HG2	1:X:240:ILE:HD12	1.45	0.96
1:X:137:ASP:O	1:X:138:ASN:HB3	1.64	0.95
1:X:85:LYS:HZ1	1:A:115:ARG:HE	1.12	0.95
1:X:195:PRO:O	1:X:196:HIS:CD2	2.18	0.95
1:A:187:CYS:HB2	1:A:213:ASN:HD22	1.31	0.94
1:A:223:ARG:NH2	1:A:238:CYS:O	1.98	0.94
1:X:177:LYS:HA	1:X:214:TYR:CD1	2.02	0.94
1:A:81:LEU:O	1:A:81:LEU:HG	1.69	0.92
1:X:181:THR:O	1:X:184:GLY:N	2.03	0.92
1:A:197:ALA:O	1:A:234:ARG:NH2	2.02	0.92
1:A:164:GLU:C	1:A:164:GLU:OE2	2.07	0.92
1:A:194:SER:HA	1:A:196:HIS:N	1.85	0.92
1:X:83:GLU:HG3	1:X:83:GLU:O	1.69	0.91
1:X:195:PRO:HD3	1:X:229:THR:HG22	1.52	0.91
1:X:118:PHE:CD2	1:X:136:PRO:HB2	2.06	0.91
1:X:224:PRO:HG3	1:X:240:ILE:HD12	1.48	0.91
1:A:104:THR:HG22	1:A:105:CYS:N	1.86	0.90
1:A:104:THR:HG22	1:A:105:CYS:O	1.71	0.88
2:B:320:GLU:HG2	2:B:321:ALA:H	1.39	0.87
1:A:174:TYR:CE1	1:A:176:GLY:N	2.44	0.86
1:X:241:PRO:HB3	1:A:137:ASP:HB2	1.56	0.85
1:X:158:ASP:O	1:X:159:ILE:HG13	1.75	0.85
1:A:103:ILE:HD12	1:A:103:ILE:N	1.91	0.85
1:A:174:TYR:CE1	1:A:176:GLY:CA	2.59	0.85
2:C:303:LYS:HB2	2:C:308:ALA:HB1	1.59	0.85
1:X:147:THR:HG23	1:X:153:ARG:O	1.76	0.84
1:X:103:ILE:HD12	1:X:103:ILE:N	1.91	0.84
1:X:114:HIS:HE1	1:X:147:THR:O	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:183:SER:HB2	1:X:236:GLU:OE1	1.78	0.84
1:A:225:TRP:HB3	1:A:237:LEU:HA	1.61	0.83
1:X:229:THR:O	1:X:231:PRO:HD3	1.76	0.83
1:A:183:SER:HB2	1:A:185:LEU:HD11	1.58	0.83
1:X:296:PRO:O	1:X:297:CYS:HB2	1.79	0.83
1:X:103:ILE:H	1:X:103:ILE:CD1	1.88	0.82
1:A:240:ILE:HD12	1:A:240:ILE:N	1.93	0.82
1:A:208:LYS:O	1:A:209:ASN:HB3	1.77	0.82
2:C:317:ARG:O	2:C:320:GLU:N	2.12	0.82
1:X:121:ALA:O	1:X:124:PRO:HD3	1.78	0.82
1:X:162:CYS:O	1:X:163:GLU:O	1.97	0.82
1:X:180:LYS:HG3	1:A:141:GLN:OE1	1.78	0.82
2:C:306:ALA:O	2:C:309:GLU:N	2.12	0.82
1:A:225:TRP:HA	1:A:238:CYS:SG	2.19	0.81
1:A:124:PRO:C	1:A:126:GLU:H	1.84	0.81
2:C:324:GLU:O	2:C:326:LEU:N	2.14	0.81
1:A:123:HIS:O	1:A:128:LEU:HD11	1.81	0.81
1:X:117:ARG:O	1:X:118:PHE:HD1	1.64	0.80
1:A:194:SER:HA	1:A:195:PRO:C	2.00	0.80
1:X:163:GLU:OE2	1:X:177:LYS:HD2	1.81	0.80
2:B:320:GLU:CG	2:B:321:ALA:H	1.94	0.80
1:A:88:ASN:C	1:A:88:ASN:OD1	2.18	0.80
2:C:311:GLN:O	2:C:315:ASN:ND2	2.16	0.79
1:X:113:PRO:HG2	1:X:114:HIS:CE1	2.17	0.79
1:X:194:SER:HA	1:X:196:HIS:N	1.98	0.79
2:B:317:ARG:HA	2:B:320:GLU:OE1	1.82	0.78
1:A:175:ASP:HA	1:A:216:ARG:NH1	1.98	0.78
1:A:207:ASN:OD1	1:A:208:LYS:HD3	1.83	0.78
1:A:96:MET:O	1:A:132:TYR:HA	1.82	0.78
1:A:186:GLU:O	1:A:229:THR:HG23	1.82	0.78
1:X:177:LYS:HA	1:X:214:TYR:CE1	2.18	0.78
2:B:320:GLU:CG	2:B:321:ALA:N	2.47	0.78
1:A:178:ILE:HG22	1:A:178:ILE:O	1.82	0.78
1:X:222:LEU:C	1:X:223:ARG:HG3	2.00	0.78
1:A:97:SER:HG	1:A:132:TYR:HD1	1.29	0.78
2:C:310:LEU:HA	2:C:313:LEU:HD12	1.65	0.77
1:A:211:LYS:O	1:A:212:LYS:C	2.23	0.77
1:X:211:LYS:O	1:X:212:LYS:C	2.23	0.77
2:B:325:ARG:NH1	2:B:325:ARG:HG2	1.95	0.77
2:C:310:LEU:O	2:C:311:GLN:C	2.24	0.76
1:X:225:TRP:HB3	1:X:237:LEU:HD23	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:TYR:CZ	2:B:313:LEU:HB3	2.21	0.76
1:X:174:TYR:C	1:X:174:TYR:CD2	2.58	0.75
1:A:104:THR:HB	1:A:148:THR:HG21	1.69	0.75
1:X:118:PHE:HD2	1:X:136:PRO:HB2	1.52	0.75
1:A:124:PRO:C	1:A:126:GLU:N	2.38	0.75
1:A:104:THR:CG2	1:A:105:CYS:N	2.50	0.74
1:X:122:THR:O	1:X:124:PRO:HD2	1.87	0.74
1:A:192:SER:OG	1:A:193:GLN:N	2.21	0.74
1:X:135:ASN:HD21	1:X:139:ASP:N	1.86	0.74
1:X:164:GLU:O	1:X:166:CYS:N	2.21	0.74
1:X:85:LYS:NZ	1:A:115:ARG:HE	1.85	0.74
1:A:174:TYR:CE2	1:A:240:ILE:HG21	2.23	0.74
1:X:174:TYR:CZ	1:X:176:GLY:HA3	2.23	0.74
1:X:201:ILE:HG23	1:X:202:PRO:HD2	1.66	0.74
1:A:238:CYS:HB2	1:A:240:ILE:CD1	2.17	0.74
1:X:116:PRO:HB3	1:X:146:TYR:CE2	2.23	0.74
1:X:195:PRO:C	1:X:196:HIS:CD2	2.60	0.73
1:A:240:ILE:H	1:A:240:ILE:HD12	1.53	0.73
1:A:99:THR:OG1	1:A:103:ILE:HD13	1.87	0.73
1:A:183:SER:HB2	1:A:185:LEU:CD1	2.18	0.73
1:A:221:GLU:OE2	2:B:318:HIS:CE1	2.36	0.73
1:X:164:GLU:O	1:X:165:GLU:CB	2.34	0.73
1:X:214:TYR:O	1:X:216:ARG:HG2	1.87	0.73
1:A:182:MET:SD	1:A:239:ASP:OD2	2.46	0.73
1:X:106:GLN:HE21	1:X:110:SER:HB2	1.53	0.73
1:X:193:GLN:OE1	1:X:197:ALA:HA	1.87	0.73
2:C:306:ALA:O	2:C:309:GLU:HB2	1.88	0.73
1:X:164:GLU:O	1:X:164:GLU:CG	2.34	0.72
1:X:163:GLU:O	1:X:175:ASP:OD2	2.07	0.72
1:X:88:ASN:O	1:X:142:GLY:HA2	1.89	0.72
1:A:120:PRO:O	1:A:121:ALA:C	2.27	0.72
1:X:224:PRO:HG3	1:X:240:ILE:CD1	2.20	0.72
1:A:167:MET:O	1:A:242:ARG:HA	1.90	0.72
1:A:234:ARG:HD3	2:B:320:GLU:OE2	1.89	0.71
1:X:224:PRO:CG	1:X:240:ILE:CD1	2.66	0.71
1:A:240:ILE:H	1:A:240:ILE:CD1	2.02	0.71
1:A:164:GLU:HG2	1:A:174:TYR:CE1	2.25	0.71
1:X:227:PHE:HA	1:X:234:ARG:O	1.91	0.71
1:X:180:LYS:CG	1:A:141:GLN:OE1	2.38	0.71
1:A:179:SER:O	1:A:186:GLU:HA	1.91	0.71
1:X:189:ALA:HA	1:X:213:ASN:HB3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:TYR:HE1	1:A:176:GLY:CA	1.97	0.70
1:X:137:ASP:O	1:X:138:ASN:CB	2.39	0.70
1:A:200:TYR:CE1	2:B:313:LEU:HB3	2.26	0.70
1:A:99:THR:OG1	1:A:103:ILE:CD1	2.40	0.70
1:X:118:PHE:CE2	1:X:137:ASP:HB3	2.26	0.69
1:X:219:ASP:O	1:X:220:ARG:C	2.27	0.69
1:A:195:PRO:HG2	1:A:196:HIS:CD2	2.28	0.69
1:A:104:THR:HB	1:A:148:THR:CG2	2.22	0.69
1:A:97:SER:OG	1:A:132:TYR:HD1	1.75	0.69
1:X:155:ASP:OD1	1:X:156:TYR:N	2.25	0.69
1:X:241:PRO:CB	1:A:137:ASP:HB2	2.24	0.68
1:A:240:ILE:CD1	1:A:240:ILE:N	2.57	0.68
1:A:138:ASN:ND2	1:A:138:ASN:O	2.27	0.68
1:A:86:THR:HG23	1:A:162:CYS:SG	2.33	0.68
1:X:93:ARG:HD3	1:X:134:ARG:HE	1.59	0.68
1:X:166:CYS:HB2	1:X:241:PRO:O	1.94	0.68
1:A:174:TYR:HD2	1:A:224:PRO:HG3	1.59	0.68
1:X:181:THR:O	1:X:184:GLY:CA	2.42	0.68
1:A:209:ASN:O	1:A:210:LEU:HD23	1.94	0.67
1:A:96:MET:CB	1:A:159:ILE:HD11	2.24	0.67
1:A:139:ASP:OD2	1:A:156:TYR:OH	2.08	0.67
1:A:96:MET:HE3	1:A:159:ILE:HG13	1.77	0.67
1:A:187:CYS:CB	1:A:213:ASN:HD22	2.05	0.67
1:X:133:CYS:O	1:X:134:ARG:CD	2.38	0.67
1:A:213:ASN:O	1:A:213:ASN:CG	2.33	0.67
1:X:167:MET:N	1:X:241:PRO:O	2.27	0.67
1:X:242:ARG:NH1	1:X:242:ARG:HG3	1.99	0.67
1:A:164:GLU:OE2	1:A:165:GLU:N	2.26	0.67
1:X:242:ARG:CG	1:X:242:ARG:HH11	2.04	0.67
2:B:310:LEU:CA	2:B:313:LEU:HD12	2.23	0.67
1:X:117:ARG:O	1:X:118:PHE:CD1	2.48	0.67
2:B:317:ARG:O	2:B:320:GLU:HG2	1.95	0.67
1:A:93:ARG:HD3	1:A:134:ARG:HE	1.58	0.67
1:X:97:SER:HB2	1:X:131:ASN:OD1	1.95	0.66
1:X:95:THR:HB	1:X:132:TYR:CE1	2.30	0.66
1:X:202:PRO:HB3	1:X:210:LEU:HB2	1.75	0.66
1:A:225:TRP:CB	1:A:237:LEU:HA	2.25	0.66
1:A:124:PRO:HG2	1:A:125:SER:N	2.10	0.66
1:X:192:SER:OG	1:X:193:GLN:N	2.27	0.66
1:A:84:CYS:HB2	1:A:160:LEU:O	1.96	0.66
1:X:92:TYR:O	1:X:93:ARG:HG2	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:174:TYR:HD2	1:X:174:TYR:C	2.00	0.65
1:A:85:LYS:HG3	1:A:161:GLU:HA	1.77	0.65
1:A:164:GLU:OE1	1:A:176:GLY:CA	2.45	0.65
1:X:139:ASP:OD1	1:X:140:PRO:HD2	1.96	0.65
1:A:194:SER:HB2	1:A:195:PRO:HA	1.79	0.64
1:X:224:PRO:HG2	1:X:240:ILE:CD1	2.26	0.64
1:X:123:HIS:HB3	1:X:126:GLU:HG3	1.80	0.64
1:A:189:ALA:HA	1:A:213:ASN:CB	2.27	0.64
1:A:115:ARG:HD2	1:A:115:ARG:N	2.13	0.64
1:X:174:TYR:CE2	1:X:176:GLY:HA3	2.28	0.64
1:X:187:CYS:HB2	1:X:213:ASN:HD22	1.63	0.64
1:A:122:THR:C	1:A:123:HIS:ND1	2.51	0.64
1:X:118:PHE:HD2	1:X:136:PRO:CB	2.11	0.64
1:A:171:GLY:O	1:A:172:GLU:C	2.37	0.63
1:A:132:TYR:HB2	1:A:134:ARG:NH1	2.14	0.63
1:X:118:PHE:HE2	1:X:137:ASP:HB3	1.62	0.63
2:C:316:GLU:O	2:C:320:GLU:HG3	1.97	0.63
1:X:148:THR:O	1:X:150:PRO:HD3	1.99	0.63
1:X:174:TYR:HE2	1:X:176:GLY:CA	2.08	0.63
1:X:162:CYS:C	1:X:163:GLU:O	2.35	0.62
1:X:162:CYS:O	1:X:163:GLU:C	2.37	0.62
1:X:194:SER:HA	1:X:196:HIS:H	1.62	0.62
1:X:221:GLU:OE2	1:X:222:LEU:HB2	2.00	0.62
1:X:201:ILE:O	1:X:204:LYS:HB2	1.99	0.62
1:A:189:ALA:HA	1:A:213:ASN:HB2	1.82	0.62
1:X:221:GLU:HA	2:C:314:LYS:NZ	2.14	0.62
1:X:93:ARG:CD	1:X:134:ARG:HH21	2.12	0.62
1:X:114:HIS:CE1	1:X:147:THR:O	2.49	0.62
1:A:154:TYR:CD1	1:A:155:ASP:N	2.68	0.62
1:A:154:TYR:CG	1:A:155:ASP:N	2.62	0.62
1:X:120:PRO:HG3	1:X:128:LEU:O	1.99	0.61
1:X:113:PRO:HG2	1:X:114:HIS:ND1	2.15	0.61
1:A:194:SER:CA	1:A:196:HIS:N	2.62	0.61
1:X:83:GLU:OE2	1:X:94:GLY:HA3	2.00	0.61
1:A:210:LEU:CD2	1:A:216:ARG:HG3	2.30	0.61
1:A:209:ASN:O	1:A:216:ARG:HD2	1.99	0.61
1:A:96:MET:CE	1:A:159:ILE:HG13	2.31	0.61
1:X:93:ARG:HD3	1:X:134:ARG:HH21	1.66	0.61
1:X:174:TYR:CD2	1:X:176:GLY:N	2.60	0.61
1:A:96:MET:HB2	1:A:159:ILE:HD11	1.83	0.61
2:C:307:ASP:O	2:C:308:ALA:C	2.37	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:PRO:HG2	1:A:125:SER:H	1.66	0.60
1:A:174:TYR:CE2	1:A:240:ILE:CG1	2.79	0.60
1:A:198:HIS:ND1	1:A:200:TYR:N	2.43	0.60
1:A:101:ASN:CB	1:A:103:ILE:HD11	2.27	0.60
1:A:101:ASN:N	1:A:101:ASN:HD22	2.00	0.60
1:X:85:LYS:HB3	1:X:159:ILE:CG2	2.32	0.60
1:A:89:GLY:O	1:A:90:LYS:C	2.40	0.60
1:X:204:LYS:HB3	1:X:205:PHE:CE1	2.37	0.60
1:A:131:ASN:CG	1:A:131:ASN:O	2.34	0.60
2:B:304:LEU:N	2:B:304:LEU:HD12	2.16	0.60
1:X:85:LYS:HZ1	1:A:115:ARG:NE	1.90	0.60
1:A:164:GLU:HG2	1:A:174:TYR:HE1	1.67	0.60
1:X:217:ASN:ND2	1:X:221:GLU:O	2.33	0.59
1:X:123:HIS:N	1:X:124:PRO:CD	2.63	0.59
1:A:138:ASN:O	1:A:138:ASN:CG	2.40	0.59
2:B:325:ARG:NH1	2:B:325:ARG:CG	2.45	0.59
1:X:83:GLU:CG	1:X:83:GLU:O	2.44	0.59
1:A:84:CYS:CB	1:A:160:LEU:O	2.51	0.59
1:A:92:TYR:CZ	1:A:94:GLY:HA3	2.38	0.59
1:X:163:GLU:OE2	1:A:152:LYS:HG2	2.03	0.59
1:X:174:TYR:HE2	1:X:176:GLY:C	2.06	0.59
2:C:312:ARG:HA	2:C:315:ASN:HD22	1.67	0.59
1:X:165:GLU:OE1	1:A:146:TYR:HE1	1.85	0.59
1:X:242:ARG:CG	1:X:242:ARG:NH1	2.65	0.59
1:X:213:ASN:ND2	1:X:213:ASN:O	2.35	0.59
1:X:111:THR:O	1:X:114:HIS:O	2.21	0.59
1:X:216:ARG:O	1:X:224:PRO:HA	2.03	0.58
1:X:165:GLU:OE2	1:A:117:ARG:HB2	2.02	0.58
1:X:218:PRO:HG2	1:X:219:ASP:OD1	2.02	0.58
1:X:122:THR:C	1:X:124:PRO:CD	2.71	0.58
1:A:91:ASN:O	1:A:93:ARG:HG2	2.03	0.58
1:X:182:MET:HG3	1:X:239:ASP:OD2	2.04	0.58
1:X:159:ILE:HG22	1:X:159:ILE:O	2.02	0.58
1:X:221:GLU:OE1	2:C:318:HIS:HE1	1.86	0.58
1:A:174:TYR:CD1	1:A:175:ASP:N	2.71	0.58
1:A:164:GLU:OE1	1:A:176:GLY:HA3	2.03	0.58
1:X:225:TRP:HA	1:X:238:CYS:SG	2.43	0.58
1:X:92:TYR:CZ	1:X:159:ILE:HD13	2.39	0.58
1:X:181:THR:O	1:X:184:GLY:HA2	2.03	0.57
1:X:117:ARG:C	1:X:118:PHE:CD1	2.77	0.57
2:C:324:GLU:O	2:C:325:ARG:C	2.42	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:306:ALA:O	2:B:309:GLU:N	2.36	0.57
1:A:96:MET:HB3	1:A:159:ILE:HD11	1.87	0.57
1:A:175:ASP:HA	1:A:216:ARG:CZ	2.35	0.57
1:A:215:CYS:O	1:A:216:ARG:HG2	2.04	0.57
2:C:303:LYS:CB	2:C:308:ALA:HB1	2.33	0.57
2:C:319:GLU:O	2:C:322:GLU:HB3	2.05	0.56
1:A:221:GLU:HA	1:A:221:GLU:OE1	2.05	0.56
1:A:185:LEU:HD12	1:A:185:LEU:N	2.21	0.56
1:X:219:ASP:OD1	1:X:219:ASP:N	2.38	0.56
1:A:102:GLY:C	1:A:103:ILE:HD12	2.25	0.56
1:A:194:SER:CA	1:A:195:PRO:C	2.73	0.56
1:A:120:PRO:O	1:A:123:HIS:N	2.39	0.56
1:X:106:GLN:HG2	1:X:107:LYS:O	2.06	0.56
1:A:220:ARG:O	2:B:314:LYS:HE3	2.05	0.56
1:A:96:MET:O	1:A:132:TYR:CA	2.53	0.56
1:X:171:GLY:C	1:X:173:ASN:H	2.07	0.56
2:C:321:ALA:HA	2:C:324:GLU:OE1	2.05	0.56
1:X:104:THR:O	1:X:148:THR:HG23	2.06	0.56
1:X:230:ASP:C	1:X:230:ASP:OD1	2.44	0.56
1:X:168:HIS:O	1:X:169:CYS:CB	2.54	0.56
1:A:103:ILE:N	1:A:103:ILE:CD1	2.63	0.56
1:X:218:PRO:HG2	1:X:219:ASP:H	1.70	0.55
1:A:195:PRO:HG2	1:A:196:HIS:HD2	1.69	0.55
1:X:180:LYS:HE2	1:A:141:GLN:HG2	1.88	0.55
1:A:229:THR:O	1:A:231:PRO:HD3	2.06	0.55
1:X:158:ASP:O	1:X:159:ILE:CG1	2.49	0.55
1:X:174:TYR:CE2	1:X:216:ARG:NH1	2.74	0.55
1:X:174:TYR:CE2	1:X:176:GLY:C	2.79	0.55
1:X:85:LYS:HB3	1:X:159:ILE:HG22	1.87	0.55
1:X:221:GLU:OE1	2:C:318:HIS:CE1	2.59	0.55
1:A:124:PRO:HG2	1:A:125:SER:OG	2.06	0.55
1:A:123:HIS:O	1:A:128:LEU:CD1	2.53	0.55
1:A:115:ARG:CD	1:A:115:ARG:N	2.69	0.55
1:X:92:TYR:C	1:X:93:ARG:HG2	2.27	0.55
1:A:174:TYR:CD2	1:A:240:ILE:HG21	2.42	0.55
1:X:164:GLU:O	1:X:165:GLU:HB3	2.06	0.55
1:A:238:CYS:HB2	1:A:240:ILE:HD11	1.89	0.55
1:X:88:ASN:O	1:X:143:PRO:HD3	2.07	0.55
1:X:189:ALA:HA	1:X:213:ASN:CB	2.37	0.55
2:C:304:LEU:O	2:C:305:THR:O	2.23	0.55
1:A:179:SER:HB3	1:A:213:ASN:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:321:ALA:O	2:C:322:GLU:C	2.44	0.55
1:X:194:SER:CB	1:X:195:PRO:HA	2.14	0.54
1:A:155:ASP:OD2	1:A:156:TYR:N	2.30	0.54
1:A:118:PHE:CE2	1:A:137:ASP:HB3	2.42	0.54
1:A:221:GLU:HG3	1:A:222:LEU:N	2.23	0.54
2:B:325:ARG:O	2:B:327:LYS:N	2.40	0.54
1:X:296:PRO:O	1:X:297:CYS:CB	2.53	0.54
1:X:221:GLU:HA	2:C:314:LYS:HZ3	1.72	0.54
1:X:167:MET:HB3	1:X:240:ILE:HG21	1.90	0.54
1:X:177:LYS:CA	1:X:214:TYR:CE1	2.90	0.54
1:X:182:MET:H	1:X:238:CYS:HA	1.72	0.54
2:B:325:ARG:HH11	2:B:325:ARG:HG3	1.69	0.54
1:X:163:GLU:O	1:X:164:GLU:HB2	2.08	0.53
1:A:201:ILE:HB	1:A:204:LYS:HB2	1.90	0.53
1:A:196:HIS:CE1	1:A:234:ARG:HA	2.43	0.53
2:C:324:GLU:C	2:C:326:LEU:N	2.59	0.53
1:A:196:HIS:ND1	1:A:234:ARG:HG2	2.23	0.53
1:A:96:MET:O	1:A:133:CYS:N	2.41	0.53
1:X:174:TYR:HE2	1:X:216:ARG:HH12	1.56	0.53
1:X:122:THR:C	1:X:124:PRO:HD2	2.28	0.53
1:A:119:SER:HB2	1:A:120:PRO:CD	2.38	0.53
2:C:314:LYS:O	2:C:315:ASN:C	2.47	0.53
1:X:118:PHE:CE2	1:X:136:PRO:HB2	2.43	0.53
2:B:320:GLU:HG3	2:B:321:ALA:N	2.20	0.53
1:A:122:THR:O	1:A:123:HIS:ND1	2.42	0.53
1:X:208:LYS:HE3	1:X:218:PRO:HA	1.90	0.53
1:X:195:PRO:HD3	1:X:229:THR:CG2	2.32	0.52
1:A:132:TYR:HB2	1:A:134:ARG:HH12	1.73	0.52
1:A:210:LEU:HD23	1:A:216:ARG:HG3	1.91	0.52
1:A:93:ARG:CD	1:A:134:ARG:HE	2.23	0.52
1:A:132:TYR:N	1:A:132:TYR:CD1	2.76	0.52
2:C:317:ARG:O	2:C:318:HIS:C	2.47	0.52
1:A:179:SER:HB2	1:A:213:ASN:ND2	2.25	0.52
1:A:164:GLU:OE1	1:A:176:GLY:HA2	2.09	0.52
1:A:209:ASN:O	1:A:216:ARG:CD	2.57	0.52
1:X:174:TYR:CZ	1:X:176:GLY:CA	2.86	0.52
2:C:307:ASP:O	2:C:309:GLU:N	2.43	0.52
1:X:161:GLU:CD	1:A:114:HIS:HD2	2.13	0.51
1:A:121:ALA:O	1:A:124:PRO:HD3	2.11	0.51
1:A:164:GLU:OE2	1:A:164:GLU:O	2.28	0.51
2:B:324:GLU:O	2:B:325:ARG:C	2.48	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:130:GLU:HG3	1:X:132:TYR:CE2	2.45	0.51
1:X:96:MET:HG3	1:X:159:ILE:HG12	1.92	0.51
1:A:108:TRP:CZ2	1:A:134:ARG:HB2	2.46	0.51
1:X:135:ASN:ND2	1:X:139:ASP:N	2.58	0.51
1:X:98:LYS:HA	1:X:105:CYS:SG	2.51	0.51
1:A:193:GLN:OE1	1:A:197:ALA:HA	2.11	0.51
1:X:190:TRP:CB	1:X:210:LEU:HB3	2.41	0.51
1:A:239:ASP:O	1:A:241:PRO:HD3	2.11	0.50
1:X:122:THR:C	1:X:124:PRO:HD3	2.31	0.50
1:A:185:LEU:O	1:A:186:GLU:C	2.49	0.50
1:A:174:TYR:CZ	1:A:176:GLY:HA3	2.45	0.50
1:X:118:PHE:CZ	1:X:137:ASP:HB3	2.47	0.50
1:X:122:THR:O	1:X:124:PRO:CD	2.59	0.50
2:C:324:GLU:C	2:C:326:LEU:H	2.15	0.50
2:B:311:GLN:HA	2:B:311:GLN:OE1	2.12	0.50
1:X:161:GLU:OE1	1:A:114:HIS:HD2	1.95	0.50
1:A:174:TYR:CD1	1:A:176:GLY:N	2.78	0.50
1:X:99:THR:CG2	1:X:155:ASP:HB3	2.42	0.50
1:X:106:GLN:HE21	1:X:110:SER:CB	2.23	0.50
1:A:137:ASP:O	1:A:138:ASN:HB3	2.11	0.49
1:A:124:PRO:O	1:A:125:SER:C	2.51	0.49
1:A:228:THR:HG23	1:A:235:TRP:HA	1.94	0.49
1:A:171:GLY:O	1:A:174:TYR:N	2.43	0.49
1:X:113:PRO:CG	1:X:114:HIS:CE1	2.93	0.49
1:X:214:TYR:CB	1:X:216:ARG:NH2	2.76	0.49
1:A:92:TYR:OH	1:A:94:GLY:HA3	2.13	0.49
1:A:110:SER:O	1:A:116:PRO:HG3	2.12	0.49
2:C:307:ASP:O	2:C:311:GLN:N	2.46	0.49
1:X:168:HIS:O	1:X:169:CYS:HB2	2.12	0.49
1:A:119:SER:OG	1:A:122:THR:HG23	2.12	0.48
1:X:174:TYR:HE2	1:X:176:GLY:O	1.97	0.48
2:C:306:ALA:HB1	2:C:310:LEU:HD12	1.96	0.48
1:X:128:LEU:HD23	1:X:128:LEU:HA	1.40	0.48
1:X:93:ARG:HD3	1:X:134:ARG:NE	2.28	0.48
2:C:304:LEU:O	2:C:308:ALA:HB3	2.14	0.48
1:A:101:ASN:HB2	1:A:103:ILE:CD1	2.31	0.48
1:X:111:THR:C	1:X:114:HIS:O	2.52	0.48
1:X:171:GLY:C	1:X:173:ASN:N	2.67	0.48
1:X:214:TYR:HB2	1:X:216:ARG:NH2	2.29	0.48
1:X:166:CYS:CB	1:X:241:PRO:O	2.61	0.48
1:X:183:SER:N	1:X:236:GLU:OE1	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:219:ASP:O	1:X:221:GLU:N	2.47	0.48
2:B:310:LEU:HD23	2:B:310:LEU:HA	1.58	0.48
1:A:85:LYS:O	1:A:85:LYS:HG3	2.14	0.48
1:X:190:TRP:CD2	1:X:210:LEU:HD22	2.49	0.48
1:A:124:PRO:CG	1:A:125:SER:N	2.68	0.48
1:X:183:SER:HB2	1:X:236:GLU:CD	2.32	0.48
2:B:304:LEU:N	2:B:304:LEU:CD1	2.77	0.48
2:B:311:GLN:CD	2:B:311:GLN:N	2.67	0.48
1:X:165:GLU:OE1	1:A:146:TYR:CE1	2.65	0.47
1:A:200:TYR:CZ	2:B:313:LEU:CB	2.96	0.47
1:X:139:ASP:OD1	1:X:141:GLN:N	2.39	0.47
1:A:164:GLU:CG	1:A:174:TYR:HE1	2.27	0.47
1:X:172:GLU:OE2	1:X:220:ARG:HA	2.14	0.47
1:X:92:TYR:CZ	1:X:159:ILE:CD1	2.97	0.47
1:X:163:GLU:HB3	1:A:153:ARG:HB3	1.96	0.47
2:C:325:ARG:HG2	2:C:325:ARG:O	2.14	0.47
1:X:174:TYR:O	1:X:174:TYR:HD2	1.97	0.47
1:A:105:CYS:HA	1:A:147:THR:HA	1.95	0.47
1:A:164:GLU:OE2	1:A:165:GLU:CA	2.63	0.47
1:A:173:ASN:HD22	1:A:173:ASN:C	2.16	0.47
1:A:174:TYR:HD1	1:A:175:ASP:N	2.12	0.47
1:X:223:ARG:O	1:X:237:LEU:HD22	2.14	0.47
1:X:115:ARG:HA	1:X:116:PRO:HD3	1.64	0.47
2:B:309:GLU:HG3	2:B:312:ARG:NH2	2.30	0.47
1:A:208:LYS:HB3	1:A:218:PRO:HB3	1.96	0.47
1:X:118:PHE:O	1:X:128:LEU:HD13	2.15	0.47
1:X:108:TRP:CZ2	1:X:134:ARG:HB2	2.50	0.46
1:X:161:GLU:HG2	1:A:153:ARG:HD2	1.97	0.46
1:A:221:GLU:HG3	1:A:222:LEU:H	1.79	0.46
1:A:104:THR:CG2	1:A:105:CYS:H	2.29	0.46
1:A:99:THR:HG1	1:A:103:ILE:HD13	1.80	0.46
1:A:139:ASP:OD1	1:A:141:GLN:N	2.43	0.46
1:A:235:TRP:CE3	1:A:236:GLU:HA	2.51	0.46
1:A:147:THR:HG23	1:A:153:ARG:O	2.15	0.46
1:A:88:ASN:OD1	1:A:89:GLY:N	2.49	0.46
1:A:104:THR:O	1:A:148:THR:HG23	2.15	0.46
1:A:120:PRO:O	1:A:121:ALA:O	2.33	0.46
2:C:311:GLN:C	2:C:315:ASN:ND2	2.69	0.46
1:A:100:LYS:C	1:A:101:ASN:HD22	2.19	0.46
1:X:118:PHE:CD2	1:X:136:PRO:CB	2.84	0.46
1:A:196:HIS:N	1:A:196:HIS:CD2	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:THR:HG23	1:A:185:LEU:O	2.15	0.46
1:A:86:THR:CG2	1:A:162:CYS:HB2	2.45	0.46
1:X:212:LYS:HB2	1:X:213:ASN:H	1.27	0.46
2:C:307:ASP:C	2:C:309:GLU:N	2.68	0.46
1:X:201:ILE:CG2	1:X:202:PRO:HD2	2.42	0.46
1:A:204:LYS:O	1:A:205:PHE:CD2	2.69	0.46
1:X:206:PRO:C	1:X:208:LYS:H	2.17	0.46
1:A:179:SER:HB2	1:A:213:ASN:HD21	1.81	0.45
1:X:165:GLU:HB3	1:X:166:CYS:SG	2.56	0.45
1:X:228:THR:HG23	1:X:233:LYS:O	2.17	0.45
1:X:163:GLU:CB	1:A:153:ARG:HB3	2.46	0.45
1:X:214:TYR:O	1:X:215:CYS:C	2.55	0.45
1:A:174:TYR:CE2	1:A:240:ILE:CG2	2.96	0.45
1:A:145:CYS:O	1:A:154:TYR:HB2	2.17	0.45
1:A:118:PHE:CZ	1:A:137:ASP:HB3	2.52	0.45
1:A:85:LYS:HG2	1:A:159:ILE:O	2.16	0.45
1:X:153:ARG:HG2	1:X:154:TYR:N	2.32	0.45
1:A:133:CYS:O	1:A:134:ARG:HD3	2.17	0.45
1:X:197:ALA:O	1:X:234:ARG:NH2	2.41	0.45
1:A:187:CYS:O	1:A:213:ASN:ND2	2.50	0.45
1:A:210:LEU:HA	1:A:210:LEU:HD23	1.63	0.45
1:X:99:THR:HG21	1:X:155:ASP:HB3	1.99	0.45
2:B:322:GLU:O	2:B:326:LEU:HD13	2.17	0.45
1:X:207:ASN:OD1	1:X:207:ASN:C	2.55	0.45
1:X:139:ASP:OD1	1:X:140:PRO:CD	2.62	0.45
1:A:107:LYS:CB	1:A:110:SER:OG	2.64	0.45
1:X:144:TRP:HA	1:X:157:CYS:SG	2.57	0.45
1:A:189:ALA:HA	1:A:213:ASN:HB3	1.99	0.44
1:X:212:LYS:HG3	1:X:214:TYR:CE2	2.52	0.44
1:X:174:TYR:CD2	1:X:216:ARG:NH1	2.86	0.44
2:C:306:ALA:O	2:C:307:ASP:C	2.56	0.44
1:X:166:CYS:CA	1:X:241:PRO:O	2.65	0.44
1:A:209:ASN:C	1:A:210:LEU:HD23	2.37	0.44
1:X:219:ASP:O	2:C:314:LYS:HD2	2.18	0.44
1:X:130:GLU:HB3	1:X:131:ASN:H	1.61	0.44
1:X:93:ARG:HD2	1:X:134:ARG:HH21	1.80	0.44
1:A:215:CYS:C	1:A:216:ARG:HG2	2.38	0.44
1:X:92:TYR:CE1	1:X:159:ILE:HD13	2.53	0.44
1:X:181:THR:HG21	1:X:236:GLU:HG2	1.99	0.44
1:X:194:SER:CA	1:X:196:HIS:H	2.28	0.44
1:A:223:ARG:O	1:A:224:PRO:C	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:119:SER:C	1:X:121:ALA:N	2.68	0.44
1:A:219:ASP:O	2:B:314:LYS:CD	2.66	0.44
1:A:144:TRP:HB2	1:A:155:ASP:O	2.17	0.44
1:X:174:TYR:CD2	1:X:175:ASP:N	2.86	0.43
1:A:174:TYR:C	1:A:174:TYR:CD1	2.90	0.43
2:C:305:THR:HG22	2:C:306:ALA:H	1.83	0.43
1:X:135:ASN:ND2	1:X:139:ASP:H	2.15	0.43
1:A:201:ILE:HG22	1:A:202:PRO:HD2	2.00	0.43
1:X:177:LYS:CA	1:X:214:TYR:CD1	2.89	0.43
1:X:95:THR:HB	1:X:132:TYR:CZ	2.52	0.43
1:X:216:ARG:O	1:X:224:PRO:CA	2.66	0.43
1:X:93:ARG:HD3	1:X:134:ARG:NH2	2.31	0.43
1:X:235:TRP:N	1:X:235:TRP:CD1	2.86	0.43
1:X:122:THR:C	1:X:123:HIS:ND1	2.72	0.43
1:X:189:ALA:CA	1:X:213:ASN:HB3	2.44	0.43
2:B:305:THR:HB	2:B:308:ALA:H	1.83	0.43
1:A:181:THR:OG1	1:A:183:SER:N	2.51	0.43
1:A:217:ASN:N	1:A:218:PRO:CD	2.81	0.43
1:A:222:LEU:C	1:A:223:ARG:HG3	2.39	0.43
1:X:123:HIS:HA	1:X:124:PRO:HD2	1.60	0.43
1:A:114:HIS:C	1:A:115:ARG:HD2	2.38	0.43
1:A:207:ASN:O	1:A:207:ASN:OD1	2.35	0.43
1:A:182:MET:H	1:A:238:CYS:HA	1.82	0.43
2:C:314:LYS:HG3	2:C:317:ARG:HH21	1.83	0.43
1:X:202:PRO:O	1:X:203:SER:C	2.56	0.43
1:A:107:LYS:CB	1:A:110:SER:HG	2.31	0.43
1:X:161:GLU:OE1	1:A:114:HIS:CD2	2.71	0.43
1:A:175:ASP:CA	1:A:216:ARG:NH1	2.76	0.43
1:A:149:ASP:OD1	1:A:150:PRO:HD2	2.19	0.43
1:A:119:SER:HB2	1:A:120:PRO:HD2	2.01	0.43
1:A:221:GLU:HA	2:B:314:LYS:HE2	2.01	0.43
1:A:240:ILE:HA	1:A:241:PRO:HD2	1.63	0.43
1:A:130:GLU:OE2	1:A:130:GLU:HA	2.19	0.43
1:A:164:GLU:O	1:A:165:GLU:HG3	2.19	0.43
1:X:123:HIS:N	1:X:123:HIS:ND1	2.67	0.43
2:B:306:ALA:O	2:B:307:ASP:C	2.57	0.43
1:X:182:MET:C	1:X:184:GLY:N	2.72	0.42
1:X:201:ILE:HG22	1:X:203:SER:HB2	2.01	0.42
1:X:85:LYS:HB3	1:X:159:ILE:HG21	2.02	0.42
1:A:93:ARG:HA	1:A:134:ARG:CZ	2.49	0.42
1:A:110:SER:C	1:A:111:THR:HG23	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:HIS:NE2	1:A:153:ARG:HA	2.34	0.42
1:A:173:ASN:HD21	1:A:209:ASN:HD22	1.66	0.42
1:A:175:ASP:HB2	1:A:209:ASN:HD21	1.85	0.42
1:X:159:ILE:O	1:X:160:LEU:C	2.57	0.42
2:C:310:LEU:O	2:C:312:ARG:N	2.51	0.42
1:X:235:TRP:CE3	1:X:236:GLU:HA	2.55	0.42
1:A:127:GLY:O	1:A:134:ARG:HG3	2.19	0.42
1:A:167:MET:O	1:A:242:ARG:CG	2.68	0.42
1:X:135:ASN:CG	1:X:139:ASP:H	2.22	0.42
1:X:201:ILE:O	1:X:202:PRO:C	2.57	0.42
1:X:211:LYS:O	1:X:213:ASN:N	2.53	0.42
1:A:160:LEU:HA	1:A:160:LEU:HD23	1.35	0.42
1:X:107:LYS:HA	1:X:131:ASN:HA	2.02	0.42
1:A:92:TYR:CZ	1:A:94:GLY:CA	3.03	0.42
2:B:319:GLU:O	2:B:322:GLU:HG2	2.19	0.42
1:A:118:PHE:CE1	1:A:123:HIS:CD2	3.08	0.41
1:X:211:LYS:HB3	1:X:214:TYR:HD2	1.84	0.41
1:X:209:ASN:O	1:X:210:LEU:HD23	2.20	0.41
1:X:177:LYS:HG2	1:X:214:TYR:CZ	2.55	0.41
1:A:173:ASN:O	1:A:173:ASN:ND2	2.43	0.41
1:X:146:TYR:HA	1:X:154:TYR:HA	2.02	0.41
1:X:190:TRP:CG	1:X:210:LEU:HB3	2.56	0.41
1:A:86:THR:HG22	1:A:162:CYS:HB2	2.01	0.41
1:A:137:ASP:OD1	1:A:137:ASP:N	2.42	0.41
1:A:123:HIS:HA	1:A:124:PRO:HD2	1.81	0.41
1:X:166:CYS:HB3	1:X:241:PRO:HB2	2.03	0.41
1:A:176:GLY:N	1:A:216:ARG:HH12	2.18	0.41
1:X:210:LEU:HD23	1:X:210:LEU:HA	1.87	0.41
1:X:174:TYR:OH	1:X:178:ILE:HD12	2.20	0.41
1:A:164:GLU:HB2	1:A:165:GLU:H	1.69	0.41
2:B:310:LEU:O	2:B:313:LEU:HB2	2.21	0.41
1:A:243:CYS:O	1:A:244:THR:HB	2.20	0.41
1:X:93:ARG:HG2	1:X:93:ARG:HH11	1.86	0.41
1:A:137:ASP:O	1:A:138:ASN:CB	2.69	0.41
1:A:179:SER:CB	1:A:213:ASN:O	2.68	0.41
1:A:171:GLY:O	1:A:173:ASN:N	2.54	0.41
1:A:92:TYR:CD2	1:A:92:TYR:C	2.93	0.41
1:X:230:ASP:O	1:X:232:ASN:N	2.54	0.41
1:A:177:LYS:HG2	1:A:214:TYR:OH	2.21	0.41
1:X:211:LYS:HB3	1:X:214:TYR:CD2	2.55	0.41
1:A:221:GLU:CG	1:A:222:LEU:N	2.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:218:PRO:CG	1:X:219:ASP:H	2.33	0.41
1:A:101:ASN:N	1:A:101:ASN:ND2	2.67	0.40
1:X:163:GLU:N	1:X:175:ASP:OD2	2.54	0.40
1:X:214:TYR:HB2	1:X:216:ARG:CZ	2.50	0.40
1:A:219:ASP:O	2:B:314:LYS:HD3	2.21	0.40
1:X:89:GLY:O	1:X:90:LYS:C	2.58	0.40
1:X:181:THR:HB	1:X:236:GLU:OE1	2.21	0.40
1:X:206:PRO:C	1:X:208:LYS:N	2.73	0.40
1:A:221:GLU:CA	1:A:221:GLU:OE1	2.69	0.40
1:X:102:GLY:O	1:X:103:ILE:C	2.60	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	162/234 (69%)	113 (70%)	36 (22%)	13 (8%)	1	6
1	X	164/234 (70%)	112 (68%)	32 (20%)	20 (12%)	0	2
2	B	22/30 (73%)	14 (64%)	7 (32%)	1 (4%)	3	17
2	C	22/30 (73%)	9 (41%)	7 (32%)	6 (27%)	0	0
All	All	370/528 (70%)	248 (67%)	82 (22%)	40 (11%)	0	3

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	121	ALA
1	X	127	GLY
1	X	159	ILE
1	X	163	GLU
1	X	169	CYS

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Mol	Chain	Res	Type
1	X	204	LYS
2	C	304	LEU
2	C	305	THR
2	C	306	ALA
1	A	82	SER
1	A	83	GLU
1	A	121	ALA
1	A	124	PRO
1	A	125	SER
1	A	172	GLU
2	B	326	LEU
1	X	99	THR
1	X	153	ARG
1	X	164	GLU
1	X	182	MET
1	X	297	CYS
2	C	308	ALA
2	C	325	ARG
1	A	90	LYS
1	A	120	PRO
1	X	90	LYS
1	X	174	TYR
1	X	183	SER
2	C	307	ASP
1	A	164	GLU
1	A	182	MET
1	A	212	LYS
1	X	94	GLY
1	X	100	LYS
1	X	212	LYS
1	X	203	SER
1	X	218	PRO
1	A	112	SER
1	A	148	THR
1	X	143	PRO

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	148/212 (70%)	117 (79%)	31 (21%)	1	6
1	X	153/212 (72%)	118 (77%)	35 (23%)	1	4
2	B	21/27 (78%)	15 (71%)	6 (29%)	0	1
2	C	21/27 (78%)	18 (86%)	3 (14%)	4	17
All	All	343/478 (72%)	268 (78%)	75 (22%)	1	5

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	X	81	LEU
1	X	90	LYS
1	X	91	ASN
1	X	99	THR
1	X	101	ASN
1	X	103	ILE
1	X	109	SER
1	X	111	THR
1	X	112	SER
1	X	147	THR
1	X	154	TYR
1	X	157	CYS
1	X	158	ASP
1	X	163	GLU
1	X	165	GLU
1	X	168	HIS
1	X	169	CYS
1	X	172	GLU
1	X	173	ASN
1	X	174	TYR
1	X	177	LYS
1	X	179	SER
1	X	183	SER
1	X	186	GLU
1	X	191	ASP
1	X	222	LEU
1	X	228	THR
1	X	229	THR
1	X	234	ARG
1	X	238	CYS
1	X	239	ASP

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Mol	Chain	Res	Type
1	X	242	ARG
1	X	245	THR
1	X	297	CYS
1	X	298	LYS
2	C	303	LYS
2	C	305	THR
2	C	318	HIS
1	A	82	SER
1	A	85	LYS
1	A	90	LYS
1	A	103	ILE
1	A	109	SER
1	A	110	SER
1	A	115	ARG
1	A	117	ARG
1	A	123	HIS
1	A	125	SER
1	A	128	LEU
1	A	132	TYR
1	A	138	ASN
1	A	139	ASP
1	A	147	THR
1	A	159	ILE
1	A	164	GLU
1	A	167	MET
1	A	173	ASN
1	A	182	MET
1	A	183	SER
1	A	191	ASP
1	A	196	HIS
1	A	201	ILE
1	A	204	LYS
1	A	211	LYS
1	A	220	ARG
1	A	237	LEU
1	A	238	CYS
1	A	239	ASP
1	A	242	ARG
2	B	304	LEU
2	B	305	THR
2	B	311	GLN
2	B	312	ARG

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Mol	Chain	Res	Type
2	B	324	GLU
2	B	325	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	X	106	GLN
1	X	114	HIS
1	X	141	GLN
1	X	196	HIS
1	X	213	ASN
2	C	311	GLN
2	C	315	ASN
2	C	318	HIS
1	A	101	ASN
1	A	114	HIS
1	A	138	ASN
1	A	209	ASN
1	A	213	ASN
2	B	318	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [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	164/234 (70%)	-0.93	0 100 100	10, 33, 58, 81	0
1	X	168/234 (71%)	-0.96	0 100 100	11, 33, 55, 66	0
2	B	24/30 (80%)	-0.93	0 100 100	15, 43, 52, 70	0
2	C	24/30 (80%)	-0.80	0 100 100	13, 33, 55, 60	0
All	All	380/528 (71%)	-0.94	0 100 100	10, 33, 58, 81	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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.