



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:05 PM GMT

PDB ID : 1NFI  
Title : I-KAPPA-B-ALPHA/NF-KAPPA-B COMPLEX  
Authors : Jacobs, M.D.; Harrison, S.C.  
Deposited on : 1998-08-25  
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

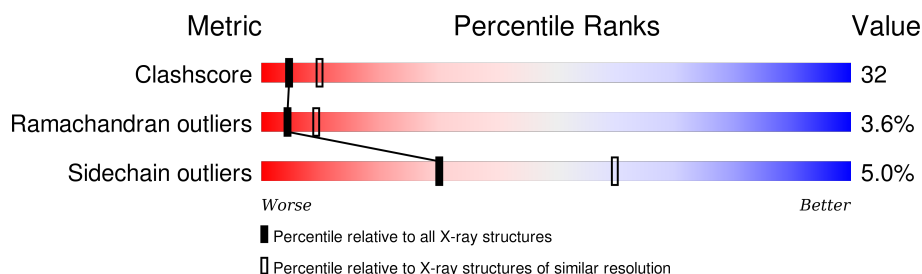
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	301	
1	C	301	
2	B	107	
2	D	107	
3	E	213	
3	F	213	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9890 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 NF-KAPPA-B P65.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	295	Total	C	N	O	S	0	0	0
			2380	1483	443	441	13			
1	C	301	Total	C	N	O	S	0	0	0
			2423	1511	450	449	13			

- Molecule 2 is a protein called NF-KAPPA-B P50.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	107	Total	C	N	O	S	0	0	0
			875	562	145	165	3			
2	D	107	Total	C	N	O	S	0	0	0
			875	562	145	165	3			

- Molecule 3 is a protein called I-KAPPA-B-ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	213	Total	C	N	O	S	0	0	0
			1633	1026	287	311	9			
3	F	213	Total	C	N	O	S	0	0	0
			1633	1026	287	311	9			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	11	Total	O	0	0
			11	11		
4	B	9	Total	O	0	0
			9	9		
4	C	11	Total	O	0	0
			11	11		
4	D	8	Total	O	0	0
			8	8		

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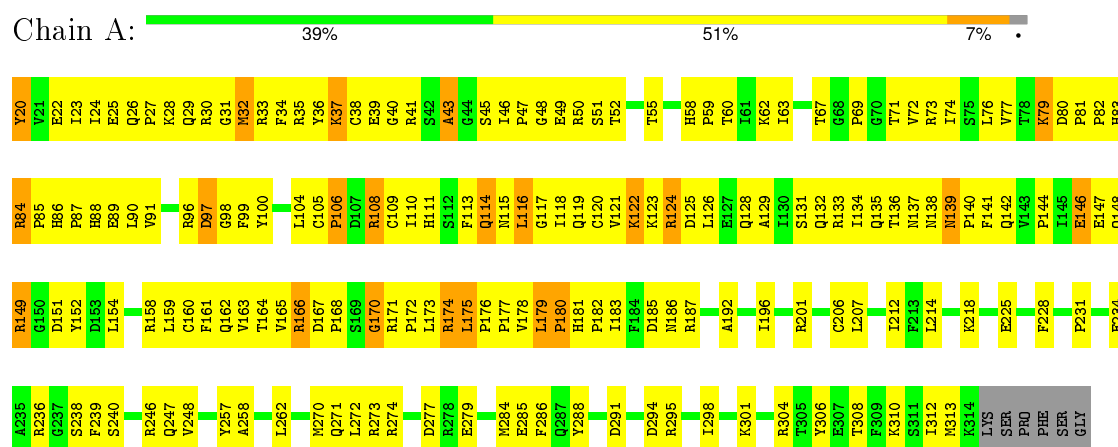
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	15	Total	O	0	0
			15	15		
4	F	17	Total	O	0	0
			17	17		

### 3 Residue-property plots

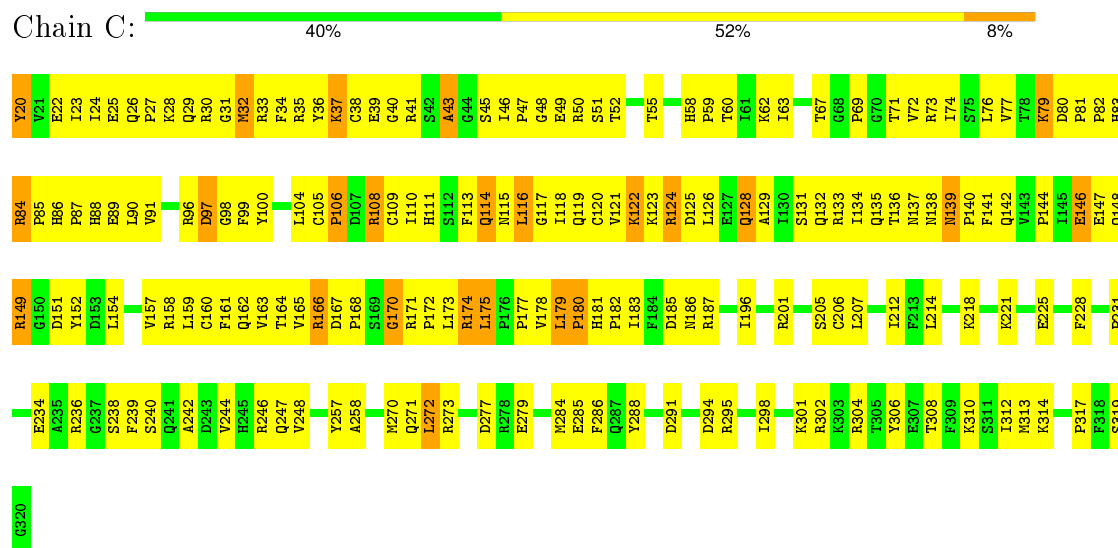
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

#### • Molecule 1: NF-KAPPA-B P65

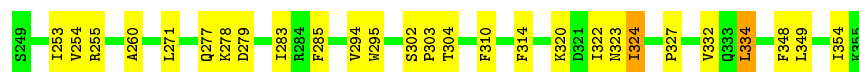


#### • Molecule 1: NF-KAPPA-B P65



#### • Molecule 2: NF-KAPPA-B P50

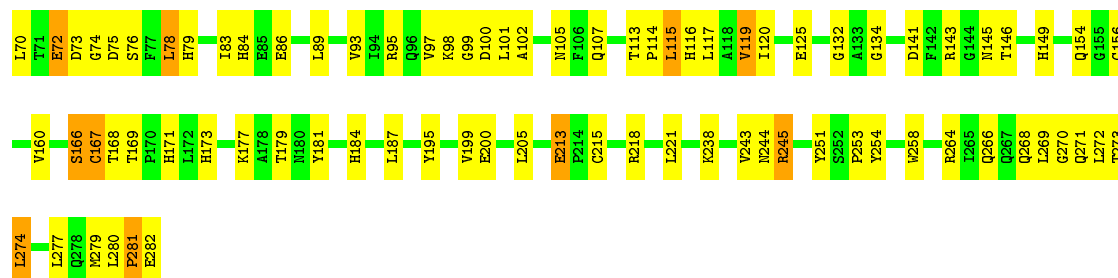




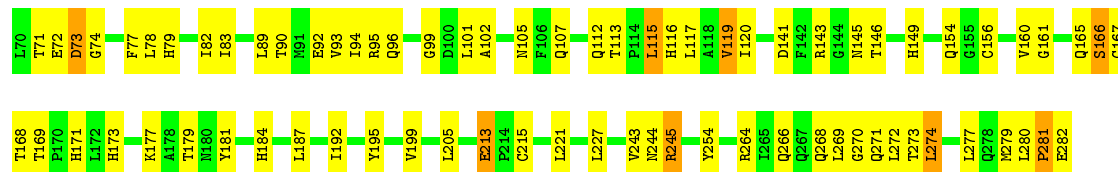
• Molecule 2: NF-KAPPA-B P50



• Molecule 3: I-KAPPA-B-ALPHA



• Molecule 3: I-KAPPA-B-ALPHA



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.09 Å 91.08 Å 190.98 Å 90.00° 96.32° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70	Depositor
% Data completeness (in resolution range)	90.9 (20.00-2.70)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.05	Depositor
Refinement program	CNS 0.5	Depositor
R, $R_{free}$	0.223 , 0.265	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9890	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

## 5 Model quality [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.44	0/2436	0.73	0/3296
1	C	0.45	0/2481	0.73	1/3356 (0.0%)
2	B	0.57	0/895	0.83	0/1207
2	D	0.60	0/895	0.84	0/1207
3	E	0.52	0/1663	0.79	1/2268 (0.0%)
3	F	0.49	0/1663	0.78	0/2268
All	All	0.49	0/10033	0.77	2/13602 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	218	ARG	NE-CZ-NH1	-5.31	117.64	120.30
1	C	272	LEU	CA-CB-CG	5.19	127.24	115.30

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	2380	0	2351	218	0
1	C	2423	0	2393	220	0
2	B	875	0	864	23	0
2	D	875	0	864	23	0
3	E	1633	0	1626	80	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	1633	0	1626	80	0
4	A	11	0	0	1	0
4	B	9	0	0	0	0
4	C	11	0	0	1	0
4	D	8	0	0	0	0
4	E	15	0	0	5	0
4	F	17	0	0	3	0
All	All	9890	0	9724	623	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 32.

All (623) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:71:THR:HG22	3:F:72:GLU:H	1.11	1.10
3:E:254:TYR:HB2	3:E:272:LEU:HD21	1.42	1.01
3:F:254:TYR:HB2	3:F:272:LEU:HD21	1.43	0.99
1:A:159:LEU:O	1:A:180:PRO:HD3	1.64	0.97
1:C:76:LEU:HG	1:C:90:LEU:HG	1.48	0.96
1:A:76:LEU:HG	1:A:90:LEU:HG	1.49	0.95
1:C:159:LEU:O	1:C:180:PRO:HD3	1.66	0.95
1:A:73:ARG:HB3	1:A:162:GLN:HB2	1.49	0.94
1:C:73:ARG:HB3	1:C:162:GLN:HB2	1.49	0.93
1:C:89:GLU:HG3	1:C:98:GLY:HA2	1.53	0.91
1:C:295:ARG:HH21	3:E:154:GLN:HB3	1.36	0.91
1:C:132:GLN:HA	1:C:135:GLN:HE21	1.36	0.91
1:C:74:ILE:HB	1:C:100:TYR:HB3	1.53	0.90
1:A:74:ILE:HB	1:A:100:TYR:HB3	1.54	0.89
1:C:50:ARG:HH22	3:E:279:MET:H	1.21	0.89
2:B:277:GLN:NE2	2:B:279:ASP:H	1.72	0.88
1:A:132:GLN:HA	1:A:135:GLN:HE21	1.37	0.88
1:A:89:GLU:HG3	1:A:98:GLY:HA2	1.54	0.88
1:C:108:ARG:NH1	1:C:108:ARG:HB3	1.89	0.87
1:A:295:ARG:HH21	3:F:154:GLN:HB3	1.38	0.87
1:A:108:ARG:HB3	1:A:108:ARG:NH1	1.90	0.87
3:E:272:LEU:HD22	4:E:288:HOH:O	1.74	0.86
1:C:52:THR:HG23	1:C:55:THR:H	1.41	0.86
1:A:52:THR:HG23	1:A:55:THR:H	1.41	0.85
1:A:207:LEU:HD22	1:A:291:ASP:OD2	1.77	0.84
1:A:35:ARG:HD3	1:A:39:GLU:HG2	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:124:ARG:NH1	1:A:125:ASP:HB2	1.92	0.83
1:C:207:LEU:HD22	1:C:291:ASP:OD2	1.77	0.83
1:C:35:ARG:HD3	1:C:39:GLU:HG2	1.60	0.83
1:C:26:GLN:HE21	1:C:27:PRO:HD2	1.43	0.82
1:A:26:GLN:HE21	1:A:27:PRO:HD2	1.43	0.81
2:D:277:GLN:NE2	2:D:279:ASP:H	1.77	0.81
3:F:71:THR:HG22	3:F:72:GLU:N	1.93	0.81
1:C:124:ARG:NH1	1:C:125:ASP:HB2	1.95	0.80
1:A:158:ARG:NH1	1:A:182:PRO:HD3	1.97	0.79
1:C:308:THR:O	1:C:312:ILE:HG13	1.82	0.79
1:A:90:LEU:HD22	1:A:116:LEU:HD11	1.66	0.77
1:C:108:ARG:HB3	1:C:108:ARG:HH11	1.49	0.77
1:C:90:LEU:HD22	1:C:116:LEU:HD11	1.65	0.77
1:C:158:ARG:NH1	1:C:182:PRO:HD3	2.00	0.76
1:A:285:GLU:H	1:A:285:GLU:CD	1.89	0.76
1:C:82:PRO:HB2	1:C:84:ARG:HD2	1.67	0.75
1:C:76:LEU:HD21	1:C:90:LEU:HD21	1.69	0.75
1:A:76:LEU:HD21	1:A:90:LEU:HD21	1.68	0.75
1:A:108:ARG:HH11	1:A:108:ARG:HB3	1.50	0.75
1:C:141:PHE:CZ	1:C:179:LEU:HD21	2.22	0.75
3:E:254:TYR:HB2	3:E:272:LEU:CD2	2.17	0.75
1:C:285:GLU:CD	1:C:285:GLU:H	1.90	0.74
3:E:89:LEU:O	3:E:93:VAL:HG23	1.87	0.74
1:A:31:GLY:HA2	1:A:186:ASN:HD21	1.53	0.74
1:A:82:PRO:HB2	1:A:84:ARG:HD2	1.70	0.74
3:F:254:TYR:HB2	3:F:272:LEU:CD2	2.17	0.73
3:E:281:PRO:O	3:E:282:GLU:HB2	1.87	0.73
1:C:76:LEU:CG	1:C:90:LEU:HG	2.19	0.73
1:A:80:ASP:HB3	1:A:81:PRO:HD2	1.71	0.73
1:A:32:MET:HE3	1:A:32:MET:HA	1.71	0.72
3:E:187:LEU:HD11	3:E:199:VAL:HG13	1.70	0.72
1:C:141:PHE:HZ	1:C:179:LEU:HD21	1.54	0.72
3:F:71:THR:CG2	3:F:72:GLU:H	1.96	0.71
1:A:62:LYS:HA	1:A:109:CYS:O	1.91	0.71
1:C:26:GLN:HE22	1:C:180:PRO:HB2	1.54	0.71
1:A:89:GLU:HG3	1:A:98:GLY:CA	2.21	0.71
1:C:80:ASP:HB3	1:C:81:PRO:HD2	1.71	0.71
1:C:228:PHE:CZ	1:C:270:MET:HE2	2.24	0.71
1:C:32:MET:HE3	1:C:32:MET:HA	1.71	0.71
1:C:89:GLU:HG3	1:C:98:GLY:CA	2.19	0.71
1:A:76:LEU:CG	1:A:90:LEU:HG	2.20	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:GLN:HE22	1:A:180:PRO:HB2	1.57	0.70
1:A:50:ARG:HH22	3:F:279:MET:H	1.39	0.70
1:A:141:PHE:CZ	1:A:179:LEU:HD21	2.27	0.70
3:F:271:GLN:HG3	3:F:271:GLN:O	1.92	0.70
1:C:31:GLY:HA2	1:C:186:ASN:HD21	1.55	0.70
3:F:101:LEU:HD12	3:F:105:ASN:HD21	1.56	0.69
3:E:271:GLN:O	3:E:271:GLN:HG3	1.91	0.69
3:F:272:LEU:HD22	4:F:15:HOH:O	1.91	0.69
2:B:327:PRO:HB3	2:B:349:LEU:HD11	1.75	0.69
3:E:269:LEU:O	3:E:272:LEU:HD23	1.93	0.69
1:C:46:ILE:HD12	1:C:116:LEU:HD12	1.74	0.69
1:C:295:ARG:NH2	3:E:154:GLN:HB3	2.05	0.69
1:C:124:ARG:C	1:C:124:ARG:HD2	2.13	0.69
1:A:124:ARG:C	1:A:124:ARG:HD2	2.14	0.68
3:F:269:LEU:O	3:F:272:LEU:HD23	1.93	0.68
1:C:62:LYS:HA	1:C:109:CYS:O	1.93	0.68
1:A:295:ARG:NH2	3:F:154:GLN:HB3	2.09	0.68
3:F:89:LEU:O	3:F:93:VAL:HG23	1.94	0.68
1:C:85:PRO:HB2	1:C:133:ARG:HG3	1.76	0.67
3:E:245:ARG:HG2	3:E:245:ARG:HH11	1.58	0.67
3:E:279:MET:O	3:E:280:LEU:HD23	1.94	0.67
1:A:124:ARG:O	1:A:124:ARG:HD2	1.93	0.67
1:A:46:ILE:HD12	1:A:116:LEU:HD12	1.76	0.67
3:F:279:MET:O	3:F:280:LEU:HD23	1.95	0.67
1:C:295:ARG:O	1:C:298:ILE:HG22	1.95	0.66
3:E:101:LEU:HD12	3:E:105:ASN:HD21	1.60	0.66
1:A:158:ARG:CZ	1:A:182:PRO:HD3	2.26	0.66
3:F:77:PHE:CZ	3:F:89:LEU:HD21	2.30	0.66
1:C:124:ARG:O	1:C:124:ARG:HD2	1.96	0.66
3:F:187:LEU:HD11	3:F:199:VAL:HG13	1.76	0.66
1:A:141:PHE:HZ	1:A:179:LEU:HD21	1.59	0.65
1:C:87:PRO:O	1:C:121:VAL:HG21	1.96	0.65
1:C:26:GLN:HE22	1:C:180:PRO:CB	2.08	0.65
1:A:87:PRO:O	1:A:121:VAL:HG21	1.97	0.65
1:C:122:LYS:HB3	1:C:124:ARG:NH1	2.11	0.65
1:A:122:LYS:HB3	1:A:124:ARG:NH1	2.11	0.65
3:F:245:ARG:HH11	3:F:245:ARG:HG2	1.62	0.65
1:A:295:ARG:O	1:A:298:ILE:HG22	1.97	0.64
1:A:85:PRO:HB2	1:A:133:ARG:HG3	1.79	0.64
1:C:52:THR:HG23	1:C:55:THR:N	2.10	0.64
1:C:228:PHE:CE2	1:C:270:MET:HE2	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:254:TYR:CB	3:E:272:LEU:HD21	2.25	0.64
1:A:52:THR:HG23	1:A:55:THR:N	2.11	0.63
1:A:26:GLN:HE22	1:A:180:PRO:CB	2.11	0.63
1:A:28:LYS:HE3	1:A:48:GLY:O	1.99	0.63
2:B:332:VAL:HG23	2:B:348:PHE:HB2	1.81	0.63
1:C:165:VAL:O	1:C:173:LEU:N	2.31	0.63
1:A:310:LYS:HA	1:A:313:MET:CE	2.29	0.63
1:A:165:VAL:O	1:A:173:LEU:N	2.32	0.62
1:A:86:HIS:HD2	1:A:88:HIS:HB2	1.64	0.62
1:C:36:TYR:HB3	1:C:37:LYS:HD3	1.82	0.62
1:C:158:ARG:CZ	1:C:182:PRO:HD3	2.29	0.62
1:C:108:ARG:CB	1:C:108:ARG:HH11	2.11	0.62
1:C:86:HIS:HD2	1:C:88:HIS:HB2	1.64	0.62
1:A:277:ASP:CG	1:A:279:GLU:HG3	2.20	0.62
2:D:332:VAL:HG23	2:D:348:PHE:HB2	1.81	0.62
1:C:28:LYS:HE3	1:C:48:GLY:O	2.00	0.61
1:C:52:THR:CG2	1:C:55:THR:H	2.11	0.61
1:A:122:LYS:HB3	1:A:124:ARG:HH12	1.66	0.61
3:E:213:GLU:HG2	4:E:289:HOH:O	2.01	0.61
2:D:327:PRO:HB3	2:D:349:LEU:HD11	1.82	0.61
1:C:26:GLN:NE2	1:C:180:PRO:HB2	2.15	0.61
1:A:108:ARG:HH11	1:A:108:ARG:CB	2.12	0.61
1:A:52:THR:CG2	1:A:55:THR:H	2.11	0.61
1:A:141:PHE:HZ	1:A:179:LEU:HD11	1.66	0.60
2:D:253:ILE:HD11	2:D:334:LEU:HD13	1.83	0.60
1:A:228:PHE:CZ	1:A:270:MET:HE2	2.36	0.60
1:A:179:LEU:N	1:A:179:LEU:HD22	2.16	0.60
1:A:36:TYR:HB3	1:A:37:LYS:HD3	1.82	0.60
1:C:25:GLU:O	1:C:59:PRO:HA	2.01	0.60
1:C:35:ARG:HH11	1:C:39:GLU:HG3	1.66	0.60
1:C:236:ARG:HH11	1:C:236:ARG:HG3	1.66	0.60
1:A:25:GLU:O	1:A:59:PRO:HA	2.01	0.60
1:A:67:THR:HG22	1:A:109:CYS:SG	2.42	0.60
1:C:122:LYS:HB3	1:C:124:ARG:HH12	1.66	0.60
3:F:213:GLU:OE2	3:F:215:CYS:HB2	2.02	0.60
1:A:174:ARG:O	1:A:175:LEU:HB2	2.01	0.60
1:C:20:TYR:HA	1:C:175:LEU:CD1	2.31	0.59
1:C:141:PHE:HZ	1:C:179:LEU:HD11	1.66	0.59
1:A:35:ARG:CD	1:A:39:GLU:HG2	2.31	0.59
1:C:35:ARG:O	1:C:119:GLN:HA	2.02	0.59
1:C:174:ARG:O	1:C:175:LEU:HB2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ARG:HG3	1:A:33:ARG:O	2.03	0.59
1:A:306:TYR:O	1:A:310:LYS:HG3	2.03	0.59
3:F:107:GLN:HG2	3:F:113:THR:HG22	1.84	0.59
1:A:96:ARG:O	1:A:98:GLY:N	2.34	0.59
1:A:35:ARG:HH11	1:A:39:GLU:HG3	1.67	0.59
1:C:179:LEU:HD22	1:C:179:LEU:N	2.18	0.59
3:E:213:GLU:OE2	3:E:215:CYS:HB2	2.02	0.59
1:A:80:ASP:C	1:A:82:PRO:HD2	2.23	0.59
1:A:167:ASP:HB2	1:A:168:PRO:CD	2.33	0.59
1:A:26:GLN:NE2	1:A:180:PRO:HB2	2.17	0.59
1:A:228:PHE:CE2	1:A:270:MET:HE2	2.38	0.59
1:A:236:ARG:HH11	1:A:236:ARG:HG3	1.66	0.59
1:C:141:PHE:CZ	1:C:179:LEU:HD11	2.37	0.58
3:F:254:TYR:CE1	3:F:266:GLN:HG3	2.39	0.58
3:F:254:TYR:CB	3:F:272:LEU:HD21	2.25	0.58
1:C:22:GLU:OE2	1:C:62:LYS:HE3	2.04	0.58
3:E:254:TYR:CE1	3:E:266:GLN:HG3	2.37	0.58
1:C:171:ARG:HB3	1:C:172:PRO:HD2	1.85	0.58
1:A:45:SER:OG	1:A:115:ASN:HA	2.04	0.58
1:C:35:ARG:HH11	1:C:39:GLU:CG	2.17	0.58
2:B:253:ILE:HD11	2:B:334:LEU:HD13	1.86	0.58
2:B:254:VAL:O	2:B:255:ARG:HB2	2.04	0.58
2:B:277:GLN:HE22	2:B:279:ASP:H	1.51	0.57
1:A:35:ARG:HH11	1:A:39:GLU:CG	2.17	0.57
1:C:35:ARG:CD	1:C:39:GLU:HG2	2.32	0.57
1:C:45:SER:OG	1:C:115:ASN:HA	2.04	0.57
3:F:79:HIS:O	3:F:83:ILE:HG13	2.04	0.57
3:E:274:LEU:HA	3:E:277:LEU:HD12	1.86	0.57
1:C:302:ARG:HG3	3:E:84:HIS:CD2	2.39	0.57
1:C:80:ASP:C	1:C:82:PRO:HD2	2.24	0.57
1:A:159:LEU:HB2	1:A:180:PRO:HG3	1.87	0.57
3:E:213:GLU:CG	4:E:289:HOH:O	2.52	0.57
1:C:277:ASP:CG	1:C:279:GLU:HG3	2.25	0.57
1:A:20:TYR:HA	1:A:175:LEU:CD1	2.35	0.57
1:C:159:LEU:HB2	1:C:180:PRO:HG3	1.87	0.57
1:A:26:GLN:O	1:A:49:GLU:N	2.38	0.57
1:A:26:GLN:HB2	1:A:49:GLU:HB2	1.86	0.57
1:A:141:PHE:CZ	1:A:179:LEU:HD11	2.39	0.57
1:A:196:ILE:HG21	1:A:284:MET:HG3	1.86	0.57
1:C:167:ASP:HB2	1:C:168:PRO:CD	2.35	0.57
1:C:132:GLN:HA	1:C:135:GLN:HG2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:GLN:CA	1:A:135:GLN:HE21	2.15	0.56
1:C:26:GLN:HB2	1:C:49:GLU:HB2	1.87	0.56
1:C:140:PRO:O	1:C:177:PRO:HG2	2.04	0.56
1:C:33:ARG:HG3	1:C:33:ARG:O	2.05	0.56
1:A:146:GLU:HA	1:A:149:ARG:NH1	2.21	0.56
2:B:295:TRP:CD1	2:B:320:LYS:HB3	2.40	0.56
1:A:171:ARG:HB3	1:A:172:PRO:HD2	1.86	0.56
1:A:22:GLU:OE2	1:A:62:LYS:HE3	2.05	0.56
1:C:26:GLN:O	1:C:49:GLU:N	2.38	0.56
1:A:158:ARG:HH12	1:A:182:PRO:HD3	1.70	0.56
1:A:310:LYS:HA	1:A:313:MET:HE3	1.87	0.56
1:C:46:ILE:CD1	1:C:116:LEU:HD12	2.35	0.56
3:E:169:THR:C	3:E:171:HIS:H	2.08	0.56
1:A:35:ARG:O	1:A:119:GLN:HA	2.06	0.56
1:A:139:ASN:HB3	1:A:142:GLN:HA	1.88	0.56
1:C:26:GLN:NE2	1:C:27:PRO:HD2	2.19	0.55
2:D:254:VAL:O	2:D:255:ARG:HB2	2.06	0.55
3:E:187:LEU:CD1	3:E:199:VAL:HG13	2.37	0.55
3:F:169:THR:C	3:F:171:HIS:H	2.09	0.55
1:A:132:GLN:HA	1:A:135:GLN:HG2	1.88	0.55
1:C:185:ASP:OD1	1:C:187:ARG:HG2	2.07	0.55
1:C:88:HIS:HE1	1:C:154:LEU:HB3	1.72	0.55
1:C:20:TYR:HA	1:C:175:LEU:HD13	1.89	0.55
3:E:269:LEU:O	3:E:271:GLN:N	2.32	0.55
1:C:270:MET:HE3	1:C:286:PHE:HB2	1.89	0.55
1:C:146:GLU:HA	1:C:149:ARG:NH1	2.22	0.55
3:F:269:LEU:O	3:F:271:GLN:N	2.35	0.54
1:A:26:GLN:NE2	1:A:181:HIS:H	2.05	0.54
1:C:132:GLN:HA	1:C:135:GLN:NE2	2.16	0.54
1:C:158:ARG:HH12	1:C:182:PRO:HD3	1.71	0.54
1:C:166:ARG:HA	1:C:171:ARG:O	2.07	0.54
3:E:213:GLU:OE2	3:E:215:CYS:N	2.40	0.54
1:C:96:ARG:O	1:C:98:GLY:N	2.39	0.54
1:A:79:LYS:HA	1:A:158:ARG:HD2	1.88	0.54
1:C:79:LYS:HA	1:C:158:ARG:HD2	1.89	0.54
1:C:139:ASN:HB3	1:C:142:GLN:HA	1.88	0.54
1:A:31:GLY:CA	1:A:186:ASN:HD21	2.20	0.54
1:C:24:ILE:HD11	1:C:62:LYS:HB2	1.89	0.54
1:C:67:THR:HG22	1:C:109:CYS:SG	2.47	0.54
1:A:166:ARG:HA	1:A:171:ARG:O	2.08	0.54
3:E:115:LEU:O	3:E:119:VAL:HG12	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:132:GLN:CA	1:C:135:GLN:HE21	2.13	0.54
3:F:243:VAL:CG2	3:F:272:LEU:HB3	2.38	0.54
1:A:24:ILE:HD11	1:A:62:LYS:HB2	1.90	0.54
1:A:306:TYR:HB3	1:A:310:LYS:HE3	1.91	0.54
1:C:246:ARG:HG3	2:D:310:PHE:CD1	2.43	0.53
1:A:246:ARG:O	1:A:247:GLN:HG3	2.09	0.53
1:A:84:ARG:HB3	1:A:85:PRO:HD2	1.90	0.53
1:C:135:GLN:HG3	1:C:136:THR:HG23	1.90	0.53
1:A:86:HIS:NE2	1:A:88:HIS:ND1	2.57	0.53
1:C:196:ILE:HG21	1:C:284:MET:HG3	1.89	0.53
1:A:301:LYS:HA	1:A:304:ARG:HG2	1.91	0.53
1:C:45:SER:CB	1:C:115:ASN:HA	2.38	0.53
1:A:46:ILE:CD1	1:A:116:LEU:HD12	2.37	0.53
1:C:27:PRO:HB2	1:C:183:ILE:HD11	1.89	0.53
1:C:47:PRO:HB2	1:C:51:SER:HB3	1.91	0.53
1:A:45:SER:CB	1:A:115:ASN:HA	2.39	0.53
2:D:295:TRP:CD1	2:D:320:LYS:HB3	2.42	0.53
1:C:116:LEU:HD13	1:C:117:GLY:N	2.24	0.53
1:C:140:PRO:HB3	1:C:160:CYS:SG	2.49	0.53
3:F:141:ASP:OD2	3:F:145:ASN:HB2	2.09	0.53
1:C:84:ARG:HB3	1:C:85:PRO:HD2	1.91	0.52
1:A:185:ASP:OD1	1:A:187:ARG:HG2	2.09	0.52
1:C:71:THR:O	1:C:163:VAL:HA	2.09	0.52
1:A:132:GLN:HA	1:A:135:GLN:NE2	2.18	0.52
1:A:109:CYS:HA	1:A:111:HIS:CE1	2.44	0.52
2:D:278:LYS:HD2	2:D:303:PRO:HB2	1.91	0.52
3:F:274:LEU:HA	3:F:277:LEU:HD12	1.91	0.52
1:C:31:GLY:CA	1:C:186:ASN:HD21	2.22	0.52
1:C:246:ARG:O	1:C:247:GLN:HG3	2.10	0.52
1:C:82:PRO:CG	1:C:84:ARG:HH11	2.23	0.52
2:B:332:VAL:CG2	2:B:348:PHE:HB2	2.40	0.52
1:A:146:GLU:OE2	1:A:147:GLU:HG3	2.10	0.52
1:C:26:GLN:NE2	1:C:181:HIS:H	2.07	0.52
3:F:213:GLU:OE2	3:F:215:CYS:N	2.43	0.52
1:C:82:PRO:HB2	1:C:84:ARG:CD	2.40	0.52
3:E:141:ASP:OD2	3:E:145:ASN:HB2	2.10	0.52
3:E:107:GLN:HG2	3:E:113:THR:HG22	1.91	0.52
1:A:116:LEU:HD13	1:A:117:GLY:N	2.24	0.52
1:A:77:VAL:HG21	1:A:179:LEU:HD12	1.92	0.52
1:C:86:HIS:NE2	1:C:88:HIS:ND1	2.56	0.52
1:A:159:LEU:O	1:A:180:PRO:CD	2.49	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:HIS:HE1	1:A:154:LEU:HB3	1.75	0.52
2:D:332:VAL:CG2	2:D:348:PHE:HB2	2.40	0.51
3:E:167:CYS:O	3:E:167:CYS:SG	2.67	0.51
3:F:167:CYS:O	3:F:167:CYS:SG	2.68	0.51
3:F:116:HIS:O	3:F:120:ILE:HG13	2.10	0.51
1:C:77:VAL:HG21	1:C:179:LEU:HD12	1.91	0.51
1:A:27:PRO:HB2	1:A:183:ILE:HD11	1.92	0.51
2:B:253:ILE:CG1	2:B:334:LEU:HD13	2.41	0.51
3:F:156:CYS:O	3:F:160:VAL:HG23	2.11	0.51
1:A:32:MET:CE	1:A:32:MET:HA	2.39	0.51
3:F:101:LEU:H	3:F:101:LEU:HD22	1.74	0.51
3:E:156:CYS:O	3:E:160:VAL:HG23	2.10	0.51
1:C:32:MET:CE	1:C:32:MET:HA	2.41	0.51
1:C:109:CYS:HA	1:C:111:HIS:CE1	2.45	0.51
1:C:201:ARG:HG2	1:C:212:ILE:HG12	1.93	0.51
1:C:27:PRO:CB	1:C:183:ILE:HD11	2.41	0.51
3:E:101:LEU:H	3:E:101:LEU:HD22	1.76	0.51
1:C:23:ILE:HD13	1:C:180:PRO:HB3	1.92	0.51
1:C:166:ARG:HG3	1:C:170:GLY:O	2.10	0.51
1:A:246:ARG:HG3	2:B:310:PHE:CD1	2.46	0.51
1:A:140:PRO:O	1:A:177:PRO:HG2	2.11	0.51
1:A:135:GLN:HG3	1:A:136:THR:HG23	1.92	0.51
3:F:279:MET:C	3:F:280:LEU:HD23	2.32	0.51
3:F:101:LEU:HD22	3:F:101:LEU:N	2.26	0.51
3:F:167:CYS:C	3:F:169:THR:H	2.15	0.51
1:A:257:TYR:CG	1:A:258:ALA:N	2.79	0.51
1:C:74:ILE:HG22	1:C:90:LEU:CD1	2.40	0.50
1:C:35:ARG:HD2	1:C:39:GLU:HB3	1.93	0.50
1:A:23:ILE:HD13	1:A:180:PRO:HB3	1.94	0.50
1:A:26:GLN:NE2	1:A:27:PRO:HD2	2.20	0.50
1:A:47:PRO:HB2	1:A:51:SER:HB3	1.92	0.50
3:E:97:VAL:HG12	3:E:100:ASP:HB3	1.93	0.50
1:A:82:PRO:CG	1:A:84:ARG:HH11	2.25	0.50
1:C:113:PHE:O	1:C:114:GLN:O	2.30	0.50
1:C:301:LYS:HA	1:C:304:ARG:HG2	1.93	0.50
1:A:71:THR:O	1:A:163:VAL:HA	2.12	0.50
1:A:20:TYR:HA	1:A:175:LEU:HD13	1.93	0.50
1:C:298:ILE:HD11	3:E:117:LEU:HD22	1.92	0.50
2:B:278:LYS:HD2	2:B:303:PRO:HB2	1.93	0.50
3:F:173:HIS:O	3:F:177:LYS:HB2	2.12	0.50
3:E:279:MET:C	3:E:280:LEU:HD23	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:167:CYS:C	3:E:169:THR:H	2.15	0.49
3:E:97:VAL:CG1	3:E:100:ASP:HB3	2.42	0.49
3:E:244:ASN:HD21	3:E:273:THR:H	1.58	0.49
1:A:74:ILE:HG22	1:A:90:LEU:CD1	2.42	0.49
2:B:277:GLN:NE2	2:B:279:ASP:N	2.51	0.49
1:A:298:ILE:HD11	3:F:117:LEU:HD22	1.94	0.49
1:C:271:GLN:HG2	4:C:327:HOH:O	2.11	0.49
3:E:243:VAL:CG2	3:E:272:LEU:HB3	2.42	0.49
1:C:206:CYS:HA	1:C:288:TYR:CD1	2.47	0.49
1:C:34:PHE:HB2	1:C:185:ASP:OD2	2.13	0.49
1:A:201:ARG:HG2	1:A:212:ILE:HG12	1.94	0.49
3:E:173:HIS:O	3:E:177:LYS:HB2	2.11	0.49
1:A:125:ASP:O	1:A:125:ASP:OD1	2.31	0.49
1:C:228:PHE:CZ	1:C:270:MET:CE	2.95	0.49
1:C:34:PHE:HB3	1:C:120:CYS:SG	2.52	0.49
1:A:34:PHE:HB3	1:A:120:CYS:SG	2.52	0.49
2:D:294:VAL:HG23	2:D:294:VAL:O	2.11	0.49
1:A:37:LYS:HG2	1:A:38:CYS:SG	2.52	0.49
3:E:179:THR:HA	3:E:184:HIS:O	2.11	0.49
3:F:244:ASN:HD21	3:F:273:THR:H	1.60	0.49
1:C:125:ASP:OD1	1:C:125:ASP:O	2.31	0.49
3:F:187:LEU:CD1	3:F:199:VAL:HG13	2.43	0.49
3:F:245:ARG:HH11	3:F:245:ARG:CG	2.26	0.49
1:C:72:VAL:HG11	1:C:113:PHE:HE1	1.78	0.49
1:A:82:PRO:HB2	1:A:84:ARG:CD	2.42	0.49
1:A:178:VAL:O	1:A:178:VAL:HG23	2.13	0.49
1:C:97:ASP:OD2	1:C:136:THR:HG21	2.12	0.49
3:F:115:LEU:O	3:F:119:VAL:HG12	2.12	0.49
2:B:323:ASN:O	2:B:324:ILE:C	2.50	0.49
1:A:27:PRO:CB	1:A:183:ILE:HD11	2.42	0.49
1:C:164:THR:HG22	1:C:166:ARG:NH2	2.28	0.49
1:C:314:LYS:O	1:C:317:PRO:HD3	2.12	0.49
1:C:35:ARG:NE	1:C:43:ALA:HB1	2.28	0.48
1:A:86:HIS:CD2	1:A:88:HIS:HB2	2.47	0.48
3:F:107:GLN:HG2	3:F:113:THR:CG2	2.44	0.48
1:A:35:ARG:HD2	1:A:39:GLU:HB3	1.93	0.48
2:B:354:ILE:HG23	2:B:354:ILE:O	2.12	0.48
1:C:50:ARG:NH1	3:E:258:TRP:CE2	2.81	0.48
3:E:98:LYS:O	3:E:99:GLY:C	2.52	0.48
1:C:108:ARG:HD3	1:C:110:ILE:CG2	2.44	0.48
2:D:277:GLN:NE2	2:D:279:ASP:N	2.55	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:THR:HG22	1:A:166:ARG:NH2	2.29	0.48
1:A:72:VAL:HG11	1:A:113:PHE:HE1	1.78	0.48
3:E:101:LEU:N	3:E:101:LEU:HD22	2.28	0.48
1:A:228:PHE:CZ	1:A:270:MET:CE	2.97	0.48
1:A:166:ARG:HG3	1:A:170:GLY:O	2.14	0.48
3:E:274:LEU:HA	3:E:277:LEU:CD1	2.43	0.48
1:C:28:LYS:HB3	1:C:47:PRO:HG2	1.95	0.48
1:A:35:ARG:NE	1:A:43:ALA:HB1	2.29	0.48
1:C:82:PRO:HB2	1:C:84:ARG:HH11	1.79	0.48
1:A:28:LYS:HB3	1:A:47:PRO:HG2	1.95	0.48
1:C:26:GLN:HE22	1:C:180:PRO:CA	2.27	0.48
1:C:85:PRO:HB2	1:C:133:ARG:CG	2.42	0.48
1:C:218:LYS:HA	1:C:247:GLN:O	2.14	0.48
3:F:92:GLU:OE2	3:F:96:GLN:HB2	2.14	0.48
1:C:310:LYS:HA	1:C:313:MET:CE	2.43	0.48
1:C:40:GLY:O	1:C:41:ARG:HB2	2.14	0.48
1:C:46:ILE:O	1:C:59:PRO:HD3	2.14	0.48
2:D:253:ILE:CG1	2:D:334:LEU:HD13	2.43	0.48
1:A:113:PHE:O	1:A:114:GLN:O	2.32	0.48
1:A:126:LEU:HD22	1:A:126:LEU:N	2.28	0.48
3:F:264:ARG:O	3:F:268:GLN:HG3	2.13	0.48
1:C:46:ILE:HD11	1:C:118:ILE:HG13	1.96	0.47
1:A:108:ARG:HD3	1:A:110:ILE:CG2	2.45	0.47
1:A:85:PRO:HB2	1:A:133:ARG:CG	2.44	0.47
3:E:245:ARG:CG	3:E:245:ARG:HH11	2.25	0.47
1:C:146:GLU:OE2	1:C:147:GLU:HG3	2.13	0.47
2:D:354:ILE:O	2:D:354:ILE:HG23	2.14	0.47
1:A:46:ILE:HD11	1:A:118:ILE:HG13	1.97	0.47
3:E:166:SER:O	3:E:168:THR:N	2.47	0.47
1:A:26:GLN:HE22	1:A:180:PRO:CA	2.28	0.47
1:A:48:GLY:H	1:A:51:SER:HB2	1.80	0.47
1:A:46:ILE:O	1:A:59:PRO:HD3	2.15	0.47
1:C:73:ARG:HG2	1:C:162:GLN:OE1	2.14	0.47
1:A:129:ALA:O	1:A:133:ARG:HB2	2.15	0.47
1:C:60:THR:HG23	1:C:111:HIS:O	2.15	0.47
2:D:323:ASN:O	2:D:324:ILE:C	2.52	0.47
1:A:105:CYS:HA	1:A:106:PRO:HD3	1.78	0.47
1:C:48:GLY:H	1:C:51:SER:HB2	1.79	0.47
1:C:80:ASP:CB	1:C:81:PRO:HD2	2.39	0.47
1:C:76:LEU:HG	1:C:90:LEU:CG	2.32	0.47
2:D:285:PHE:CD2	2:D:332:VAL:HG22	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:70:LEU:HD12	3:E:76:SER:HB2	1.95	0.47
1:C:294:ASP:OD2	3:E:143:ARG:NH2	2.48	0.47
1:C:50:ARG:NH2	3:E:279:MET:HG2	2.31	0.46
1:C:129:ALA:O	1:C:133:ARG:HB2	2.14	0.46
1:A:218:LYS:HA	1:A:247:GLN:O	2.15	0.46
1:C:161:PHE:HB2	1:C:178:VAL:CG2	2.45	0.46
1:A:271:GLN:HG2	4:A:322:HOH:O	2.14	0.46
1:A:73:ARG:HG2	1:A:162:GLN:OE1	2.15	0.46
3:F:213:GLU:HG2	4:F:19:HOH:O	2.15	0.46
3:E:169:THR:C	3:E:171:HIS:N	2.69	0.46
3:E:116:HIS:O	3:E:120:ILE:HG13	2.15	0.46
3:F:271:GLN:CG	3:F:271:GLN:O	2.62	0.46
1:C:63:ILE:HG13	1:C:104:LEU:HD13	1.97	0.46
1:C:257:TYR:CG	1:C:258:ALA:N	2.83	0.46
3:F:179:THR:HA	3:F:184:HIS:O	2.15	0.46
1:C:82:PRO:CB	1:C:84:ARG:HH11	2.28	0.46
1:A:40:GLY:O	1:A:41:ARG:HB2	2.16	0.46
1:A:76:LEU:HG	1:A:90:LEU:CG	2.33	0.46
1:A:50:ARG:NH2	3:F:279:MET:HG2	2.31	0.46
1:A:86:HIS:ND1	1:A:87:PRO:HD2	2.30	0.46
1:A:91:VAL:HG11	1:A:119:GLN:CD	2.36	0.46
1:A:294:ASP:OD2	3:F:143:ARG:NH2	2.49	0.46
1:C:69:PRO:HA	1:C:106:PRO:HG3	1.96	0.46
1:A:69:PRO:HA	1:A:106:PRO:HG3	1.96	0.46
2:B:271:LEU:HD23	2:B:271:LEU:C	2.36	0.46
1:C:109:CYS:HA	1:C:111:HIS:HE1	1.81	0.46
3:E:73:ASP:HB2	3:E:75:ASP:OD1	2.16	0.46
3:F:72:GLU:HG3	3:F:73:ASP:N	2.30	0.46
1:C:79:LYS:HA	1:C:158:ARG:HG3	1.97	0.46
1:A:310:LYS:HG2	1:A:313:MET:HE2	1.98	0.46
1:C:110:ILE:HG23	1:C:110:ILE:O	2.16	0.45
1:A:82:PRO:CB	1:A:84:ARG:HH11	2.30	0.45
1:A:109:CYS:HA	1:A:111:HIS:HE1	1.80	0.45
1:A:176:PRO:HA	1:A:177:PRO:HD3	1.79	0.45
1:C:126:LEU:HD22	1:C:126:LEU:N	2.32	0.45
1:A:270:MET:HE3	1:A:286:PHE:HB2	1.98	0.45
3:F:168:THR:O	3:F:168:THR:HG22	2.16	0.45
3:E:200:GLU:OE2	3:E:238:LYS:NZ	2.49	0.45
1:A:28:LYS:CB	1:A:47:PRO:HG2	2.46	0.45
2:D:277:GLN:HE22	2:D:279:ASP:H	1.59	0.45
3:F:72:GLU:C	3:F:74:GLY:H	2.20	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:91:VAL:HG11	1:C:119:GLN:CD	2.36	0.45
3:E:101:LEU:HB3	3:E:105:ASN:ND2	2.31	0.45
1:C:134:ILE:HG21	1:C:148:GLN:OE1	2.16	0.45
1:A:140:PRO:HB3	1:A:160:CYS:SG	2.57	0.45
3:F:101:LEU:HB3	3:F:105:ASN:ND2	2.31	0.45
1:A:262:LEU:HA	1:A:262:LEU:HD12	1.74	0.45
1:A:110:ILE:HG23	1:A:110:ILE:O	2.16	0.45
1:A:35:ARG:NE	1:A:43:ALA:CB	2.80	0.45
1:C:35:ARG:NE	1:C:43:ALA:CB	2.79	0.45
1:A:79:LYS:HA	1:A:158:ARG:HG3	1.98	0.45
1:A:82:PRO:HB2	1:A:84:ARG:HH11	1.81	0.45
1:A:236:ARG:NH1	1:A:236:ARG:HG3	2.31	0.45
1:A:179:LEU:HD22	1:A:179:LEU:H	1.81	0.45
3:F:101:LEU:H	3:F:101:LEU:CD2	2.29	0.45
1:A:225:GLU:CD	1:A:236:ARG:HE	2.20	0.45
3:F:166:SER:O	3:F:168:THR:N	2.47	0.45
2:D:271:LEU:HD23	2:D:271:LEU:C	2.37	0.45
2:B:277:GLN:HE22	2:B:279:ASP:N	2.14	0.45
1:A:97:ASP:OD2	1:A:136:THR:HG21	2.16	0.45
2:B:260:ALA:HA	2:B:349:LEU:O	2.17	0.45
2:D:253:ILE:CD1	2:D:334:LEU:HD13	2.46	0.45
3:E:79:HIS:O	3:E:83:ILE:HG13	2.17	0.45
1:C:89:GLU:CG	1:C:98:GLY:HA2	2.35	0.45
1:A:31:GLY:HA2	1:A:186:ASN:ND2	2.26	0.45
1:A:24:ILE:CD1	1:A:62:LYS:HB2	2.47	0.45
1:A:34:PHE:HB2	1:A:185:ASP:OD2	2.17	0.45
3:F:94:ILE:HG22	3:F:94:ILE:O	2.16	0.45
1:C:221:LYS:HA	1:C:244:VAL:HG21	1.98	0.45
1:A:167:ASP:HB2	1:A:168:PRO:HD3	1.99	0.45
1:C:28:LYS:CB	1:C:47:PRO:HG2	2.47	0.44
1:A:158:ARG:NH2	1:A:182:PRO:HD3	2.31	0.44
1:A:133:ARG:HD3	1:A:138:ASN:ND2	2.32	0.44
1:A:108:ARG:HD3	1:A:110:ILE:HG23	1.99	0.44
1:C:236:ARG:NH1	1:C:236:ARG:HG3	2.31	0.44
1:A:148:GLN:HB2	1:A:149:ARG:NH2	2.32	0.44
1:C:63:ILE:HD11	1:C:163:VAL:HG11	1.98	0.44
1:A:192:ALA:HB3	1:A:274:ARG:NH1	2.32	0.44
3:F:82:ILE:HG12	3:F:90:THR:HG21	1.98	0.44
3:E:125:GLU:N	3:E:125:GLU:OE1	2.48	0.44
1:C:58:HIS:HB3	1:C:59:PRO:CD	2.47	0.44
1:A:96:ARG:HD3	3:E:98:LYS:HE3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:29:GLN:HB2	1:C:182:PRO:O	2.18	0.44
3:F:107:GLN:HA	3:F:112:GLN:O	2.17	0.44
1:A:206:CYS:HA	1:A:288:TYR:CD1	2.53	0.44
1:A:239:PHE:HD2	1:A:240:SER:O	2.00	0.44
1:A:89:GLU:CG	1:A:98:GLY:HA2	2.36	0.44
1:C:108:ARG:HD3	1:C:110:ILE:HG23	1.99	0.44
1:A:60:THR:HG23	1:A:111:HIS:O	2.17	0.44
1:A:25:GLU:OE1	1:A:48:GLY:HA3	2.18	0.44
1:C:108:ARG:HB2	1:C:110:ILE:HG22	2.00	0.44
1:C:205:SER:OG	1:C:207:LEU:HB2	2.17	0.44
1:A:81:PRO:N	1:A:82:PRO:HD2	2.33	0.44
3:E:264:ARG:O	3:E:268:GLN:HG3	2.18	0.44
3:F:72:GLU:HG3	3:F:73:ASP:H	1.82	0.44
3:F:254:TYR:CD2	3:F:277:LEU:HD23	2.53	0.44
1:C:97:ASP:CG	1:C:136:THR:HG21	2.37	0.44
1:C:24:ILE:CD1	1:C:62:LYS:HB2	2.47	0.44
1:A:167:ASP:CB	1:A:168:PRO:CD	2.95	0.44
1:A:161:PHE:HB2	1:A:178:VAL:CG2	2.47	0.44
3:F:92:GLU:O	3:F:95:ARG:N	2.40	0.44
3:F:274:LEU:HA	3:F:277:LEU:CD1	2.47	0.44
1:A:225:GLU:HG3	1:A:273:ARG:HB3	1.99	0.44
3:F:169:THR:C	3:F:171:HIS:N	2.70	0.44
1:C:45:SER:HB3	1:C:115:ASN:HA	1.99	0.44
3:F:244:ASN:ND2	3:F:272:LEU:HB2	2.33	0.44
1:A:131:SER:C	1:A:133:ARG:H	2.20	0.44
3:E:245:ARG:NH1	3:E:245:ARG:CG	2.79	0.44
1:A:86:HIS:CD2	1:A:88:HIS:H	2.36	0.44
1:C:86:HIS:CD2	1:C:88:HIS:HB2	2.47	0.43
1:A:151:ASP:OD1	1:A:152:TYR:N	2.51	0.43
1:A:310:LYS:HA	1:A:313:MET:HE2	2.00	0.43
1:C:37:LYS:HG2	1:C:38:CYS:SG	2.57	0.43
1:C:148:GLN:HB2	1:C:149:ARG:NH2	2.33	0.43
3:F:179:THR:HB	3:F:184:HIS:N	2.33	0.43
1:A:58:HIS:HB3	1:A:59:PRO:CD	2.47	0.43
1:C:86:HIS:ND1	1:C:87:PRO:HD2	2.33	0.43
1:C:158:ARG:NH2	1:C:182:PRO:HD3	2.33	0.43
1:A:166:ARG:HG2	1:C:317:PRO:HB3	1.99	0.43
3:E:168:THR:O	3:E:168:THR:HG22	2.18	0.43
3:F:243:VAL:HG21	3:F:272:LEU:HB3	1.99	0.43
1:C:77:VAL:HG21	1:C:179:LEU:CD1	2.49	0.43
1:A:138:ASN:O	1:A:139:ASN:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:GLU:CD	1:C:236:ARG:HE	2.22	0.43
2:D:263:VAL:HG21	2:D:322:ILE:HA	2.00	0.43
1:C:133:ARG:HD3	1:C:138:ASN:ND2	2.32	0.43
1:C:81:PRO:N	1:C:82:PRO:HD2	2.33	0.43
1:C:214:LEU:C	1:C:214:LEU:HD23	2.38	0.43
3:E:253:PRO:HD2	4:E:288:HOH:O	2.19	0.43
3:E:101:LEU:CD2	3:E:101:LEU:H	2.31	0.43
1:C:63:ILE:CD1	1:C:163:VAL:HG11	2.49	0.43
1:C:26:GLN:HG3	1:C:181:HIS:CE1	2.54	0.43
2:D:260:ALA:HA	2:D:349:LEU:O	2.19	0.43
3:F:213:GLU:CG	4:F:19:HOH:O	2.67	0.43
1:C:167:ASP:CB	1:C:168:PRO:CD	2.97	0.43
1:A:63:ILE:HG13	1:A:104:LEU:HD13	1.99	0.43
3:F:181:TYR:N	3:F:181:TYR:CD1	2.87	0.43
1:A:159:LEU:H	1:A:180:PRO:CG	2.32	0.42
1:C:25:GLU:OE1	1:C:48:GLY:HA3	2.18	0.42
2:B:285:PHE:CD2	2:B:332:VAL:HG22	2.54	0.42
1:C:37:LYS:HD3	1:C:37:LYS:N	2.34	0.42
3:F:96:GLN:NE2	3:F:96:GLN:HA	2.34	0.42
2:D:263:VAL:HG13	2:D:351:TYR:O	2.19	0.42
3:E:181:TYR:N	3:E:181:TYR:CD1	2.86	0.42
2:D:308:ARG:O	2:D:309:GLN:HB2	2.19	0.42
1:A:108:ARG:HB2	1:A:110:ILE:HG22	1.99	0.42
1:C:125:ASP:OD1	1:C:128:GLN:HB3	2.18	0.42
1:C:86:HIS:CD2	1:C:157:VAL:HG12	2.55	0.42
1:C:50:ARG:HH22	3:E:279:MET:N	2.02	0.42
1:C:151:ASP:OD1	1:C:152:TYR:N	2.52	0.42
1:A:308:THR:O	1:A:312:ILE:HG13	2.19	0.42
1:C:99:PHE:CD2	1:C:138:ASN:OD1	2.73	0.42
2:B:253:ILE:CD1	2:B:334:LEU:HD13	2.47	0.42
1:A:63:ILE:HD11	1:A:163:VAL:HG11	2.01	0.42
3:E:269:LEU:C	3:E:271:GLN:H	2.21	0.42
3:E:167:CYS:C	3:E:169:THR:N	2.72	0.42
3:F:192:ILE:HA	3:F:227:LEU:HD11	2.01	0.42
1:A:45:SER:HB3	1:A:115:ASN:HA	2.01	0.42
3:F:167:CYS:C	3:F:169:THR:N	2.72	0.42
3:E:254:TYR:CD2	3:E:277:LEU:HD23	2.54	0.42
3:F:269:LEU:C	3:F:271:GLN:H	2.22	0.42
1:C:246:ARG:C	1:C:247:GLN:CG	2.88	0.42
1:C:242:ALA:HB1	3:E:251:TYR:CE2	2.55	0.42
1:A:128:GLN:O	1:A:128:GLN:OE1	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:31:GLY:HA2	1:C:186:ASN:ND2	2.27	0.42
2:B:327:PRO:HB3	2:B:349:LEU:CD1	2.45	0.42
1:C:225:GLU:HG3	1:C:273:ARG:HB3	2.02	0.42
3:F:107:GLN:CG	3:F:113:THR:HG22	2.49	0.42
2:B:283:ILE:HD12	2:B:314:PHE:CD2	2.55	0.42
1:C:159:LEU:O	1:C:180:PRO:CD	2.52	0.42
1:A:97:ASP:CG	1:A:136:THR:HG21	2.39	0.42
3:F:101:LEU:O	3:F:102:ALA:C	2.58	0.42
1:C:138:ASN:O	1:C:139:ASN:C	2.57	0.42
3:E:101:LEU:O	3:E:102:ALA:C	2.57	0.42
1:C:160:CYS:SG	1:C:177:PRO:HB3	2.60	0.42
2:B:302:SER:O	2:B:304:THR:N	2.53	0.42
3:F:161:GLY:O	3:F:165:GLN:HG3	2.20	0.42
1:A:132:GLN:O	1:A:132:GLN:HG2	2.19	0.41
1:A:32:MET:HE2	1:A:33:ARG:H	1.85	0.41
1:C:228:PHE:O	1:C:234:GLU:HA	2.20	0.41
1:A:69:PRO:HB3	1:C:319:SER:HB2	2.01	0.41
1:C:178:VAL:HG23	1:C:178:VAL:O	2.19	0.41
3:E:244:ASN:HD21	3:E:273:THR:N	2.18	0.41
1:C:128:GLN:OE1	1:C:128:GLN:O	2.39	0.41
1:A:26:GLN:HG3	1:A:181:HIS:CE1	2.55	0.41
1:A:228:PHE:O	1:A:234:GLU:HA	2.20	0.41
3:E:244:ASN:ND2	3:E:272:LEU:HB2	2.34	0.41
1:C:159:LEU:H	1:C:180:PRO:CG	2.34	0.41
3:E:86:GLU:HB3	3:E:89:LEU:HB3	2.02	0.41
3:E:78:LEU:HD13	3:E:114:PRO:HG2	2.02	0.41
1:A:125:ASP:OD1	1:A:128:GLN:HB3	2.20	0.41
1:C:131:SER:C	1:C:133:ARG:H	2.22	0.41
1:C:167:ASP:HB2	1:C:168:PRO:HD3	2.01	0.41
3:E:107:GLN:HG2	3:E:113:THR:CG2	2.50	0.41
3:E:72:GLU:C	3:E:74:GLY:H	2.24	0.41
1:C:132:GLN:HG2	1:C:132:GLN:O	2.20	0.41
1:C:105:CYS:HA	1:C:106:PRO:HD3	1.79	0.41
1:C:74:ILE:HG22	1:C:90:LEU:HD13	2.03	0.41
1:C:310:LYS:HA	1:C:313:MET:HE2	2.02	0.41
1:A:99:PHE:HD2	1:A:138:ASN:OD1	2.04	0.41
1:A:77:VAL:HG21	1:A:179:LEU:CD1	2.49	0.41
1:C:86:HIS:HA	1:C:87:PRO:HD3	1.97	0.41
3:F:245:ARG:CG	3:F:245:ARG:NH1	2.81	0.41
1:C:37:LYS:HD3	1:C:37:LYS:H	1.86	0.41
3:F:244:ASN:HD21	3:F:273:THR:N	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:PHE:CD2	1:A:138:ASN:OD1	2.74	0.41
1:A:37:LYS:HD3	1:A:37:LYS:N	2.35	0.41
1:A:134:ILE:HG21	1:A:148:GLN:OE1	2.20	0.41
1:C:187:ARG:HH11	1:C:187:ARG:HG3	1.85	0.41
3:E:156:CYS:CB	4:E:296:HOH:O	2.68	0.41
1:A:214:LEU:C	1:A:214:LEU:HD23	2.42	0.41
3:F:281:PRO:O	3:F:282:GLU:HB3	2.21	0.41
1:C:99:PHE:HD2	1:C:138:ASN:OD1	2.03	0.41
1:C:239:PHE:HD2	1:C:240:SER:O	2.04	0.41
3:E:272:LEU:O	3:E:273:THR:C	2.60	0.40
1:A:26:GLN:HE22	1:A:181:HIS:H	1.69	0.40
1:A:29:GLN:HB2	1:A:182:PRO:O	2.21	0.40
1:A:87:PRO:HD3	1:A:152:TYR:CD2	2.56	0.40
1:A:246:ARG:C	1:A:247:GLN:CG	2.89	0.40
1:A:187:ARG:HH11	1:A:187:ARG:HG3	1.86	0.40
3:E:146:THR:O	3:E:149:HIS:HB2	2.21	0.40
3:E:78:LEU:HD13	3:E:114:PRO:CG	2.50	0.40
2:B:294:VAL:HG23	2:B:294:VAL:O	2.21	0.40
1:C:87:PRO:HD3	1:C:152:TYR:CD2	2.56	0.40
3:E:132:GLY:C	3:E:134:GLY:H	2.24	0.40
3:F:146:THR:O	3:F:149:HIS:HB2	2.21	0.40
2:D:257:ASP:OD1	2:D:269:ILE:HG23	2.22	0.40
3:F:245:ARG:NH1	3:F:245:ARG:HG2	2.34	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	293/301 (97%)	237 (81%)	42 (14%)	14 (5%)	<b>3</b> <b>5</b>
1	C	299/301 (99%)	237 (79%)	48 (16%)	14 (5%)	<b>3</b> <b>5</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	105/107 (98%)	96 (91%)	7 (7%)	2 (2%)	10	25
2	D	105/107 (98%)	97 (92%)	6 (6%)	2 (2%)	10	25
3	E	211/213 (99%)	188 (89%)	17 (8%)	6 (3%)	6	15
3	F	211/213 (99%)	191 (90%)	14 (7%)	6 (3%)	6	15
All	All	1224/1242 (99%)	1046 (86%)	134 (11%)	44 (4%)	4	9

All (44) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	ALA
1	A	97	ASP
1	A	114	GLN
1	A	137	ASN
1	A	174	ARG
1	C	43	ALA
1	C	97	ASP
1	C	114	GLN
1	C	137	ASN
1	C	174	ARG
1	A	122	LYS
1	C	122	LYS
2	D	324	ILE
3	E	166	SER
3	E	195	TYR
3	E	270	GLY
3	F	99	GLY
3	F	195	TYR
3	F	281	PRO
2	B	324	ILE
1	C	79	LYS
3	F	166	SER
3	F	270	GLY
1	A	79	LYS
1	A	83	HIS
1	A	106	PRO
1	A	123	LYS
1	A	139	ASN
1	C	83	HIS
1	C	106	PRO
1	C	139	ASN
3	E	72	GLU

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Mol	Chain	Res	Type
1	C	123	LYS
3	E	167	CYS
3	E	281	PRO
3	F	73	ASP
1	A	231	PRO
1	A	170	GLY
1	C	170	GLY
1	C	231	PRO
1	A	175	LEU
2	B	322	ILE
1	C	175	LEU
2	D	322	ILE

### 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	266/271 (98%)	249 (94%)	17 (6%)	22	47
1	C	271/271 (100%)	252 (93%)	19 (7%)	19	42
2	B	97/97 (100%)	96 (99%)	1 (1%)	82	94
2	D	97/97 (100%)	96 (99%)	1 (1%)	82	94
3	E	181/181 (100%)	172 (95%)	9 (5%)	30	60
3	F	181/181 (100%)	173 (96%)	8 (4%)	35	65
All	All	1093/1098 (100%)	1038 (95%)	55 (5%)	30	60

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	TYR
1	A	30	ARG
1	A	32	MET
1	A	37	LYS
1	A	84	ARG
1	A	108	ARG

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Mol	Chain	Res	Type
1	A	116	LEU
1	A	124	ARG
1	A	144	PRO
1	A	146	GLU
1	A	149	ARG
1	A	166	ARG
1	A	179	LEU
1	A	180	PRO
1	A	238	SER
1	A	248	VAL
1	A	272	LEU
2	B	334	LEU
1	C	20	TYR
1	C	30	ARG
1	C	32	MET
1	C	37	LYS
1	C	84	ARG
1	C	108	ARG
1	C	116	LEU
1	C	124	ARG
1	C	128	GLN
1	C	144	PRO
1	C	146	GLU
1	C	149	ARG
1	C	166	ARG
1	C	179	LEU
1	C	180	PRO
1	C	238	SER
1	C	248	VAL
1	C	272	LEU
1	C	306	TYR
2	D	334	LEU
3	E	78	LEU
3	E	95	ARG
3	E	115	LEU
3	E	119	VAL
3	E	205	LEU
3	E	213	GLU
3	E	221	LEU
3	E	245	ARG
3	E	274	LEU
3	F	78	LEU

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Mol	Chain	Res	Type
3	F	115	LEU
3	F	119	VAL
3	F	205	LEU
3	F	213	GLU
3	F	221	LEU
3	F	245	ARG
3	F	274	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	29	GLN
1	A	119	GLN
1	A	135	GLN
1	A	138	ASN
1	A	139	ASN
1	A	186	ASN
1	A	220	GLN
1	A	247	GLN
2	B	277	GLN
1	C	26	GLN
1	C	29	GLN
1	C	119	GLN
1	C	135	GLN
1	C	139	ASN
1	C	186	ASN
1	C	247	GLN
2	D	277	GLN
3	E	109	ASN
3	E	111	GLN
3	E	184	HIS
3	E	188	HIS
3	E	244	ASN
3	E	266	GLN
3	F	96	GLN
3	F	109	ASN
3	F	184	HIS
3	F	244	ASN
3	F	266	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 carbohydrates in this entry.

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

There are no ligands in this entry.

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

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.