



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:03 PM GMT

PDB ID : 1IKN
Title : IKAPPABALPHA/NF-KAPPAB COMPLEX
Authors : Huxford, T.; Huang, D.-B.; Malek, S.; Ghosh, G.
Deposited on : 1998-11-13
Resolution : 2.30 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

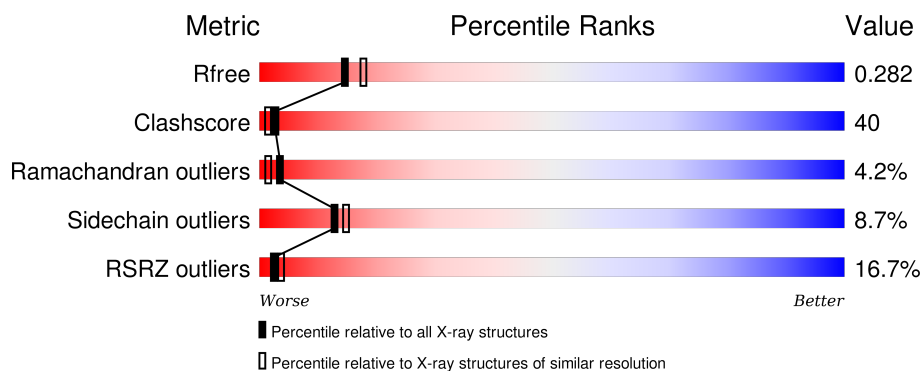
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	286	<div> <div>20%</div> <div>42%</div> <div>49%</div> <div>8%</div> </div>
2	C	119	<div> <div>7%</div> <div>50%</div> <div>44%</div> <div>5%</div> </div>
3	D	236	<div> <div>15%</div> <div>35%</div> <div>47%</div> <div>8%</div> <div>8%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4979 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 PROTEIN (NF-KAPPA-B P65 SUBUNIT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	0	1
			2262	1405	422	424	11			

- Molecule 2 is a protein called PROTEIN (NF-KAPPA-B P50D SUBUNIT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	113	Total	C	N	O	S	0	0	1
			916	584	152	177	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	216	Total	C	N	O	S	0	0	1
			1589	991	281	309	8			

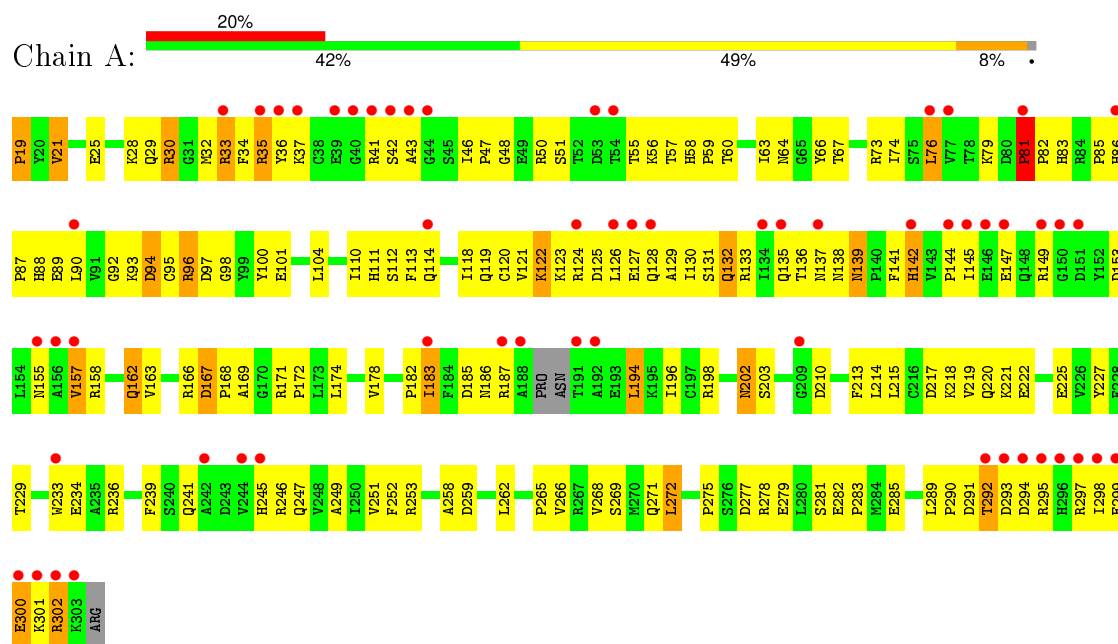
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	89	Total	O	0	0
			89	89		
4	C	53	Total	O	0	0
			53	53		
4	D	70	Total	O	0	0
			70	70		

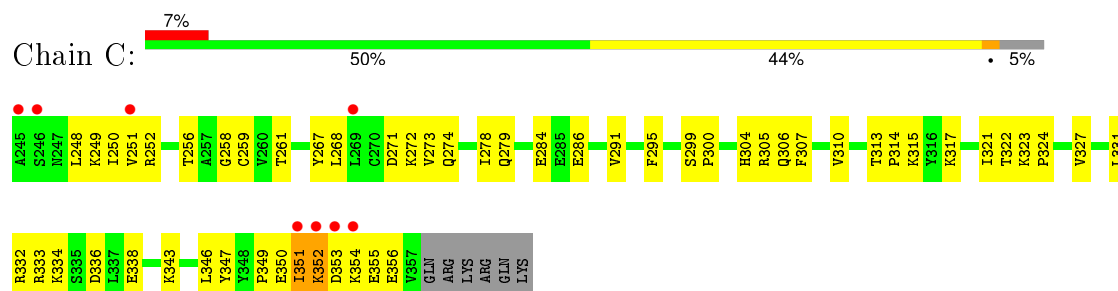
3 Residue-property plots

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.

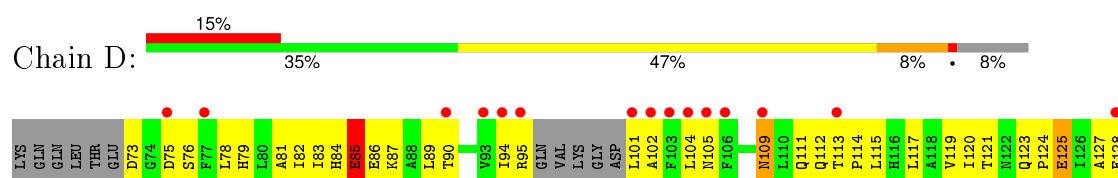
• Molecule 1: PROTEIN (NF-KAPPA-B P65 SUBUNIT)

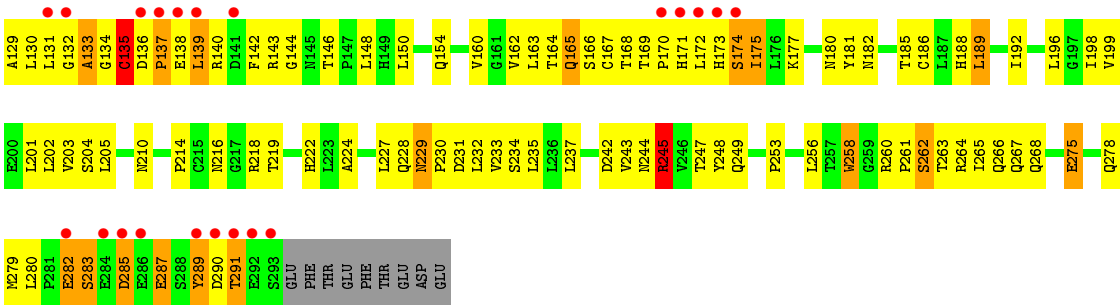


• Molecule 2: PROTEIN (NF-KAPPA-B P50D SUBUNIT)



• Molecule 3: PROTEIN (I-KAPPA-B-ALPHA)





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	124.50Å 49.30Å 120.60Å 90.00° 108.70° 90.00°	Depositor
Resolution (Å)	6.00 – 2.30 24.88 – 2.25	Depositor EDS
% Data completeness (in resolution range)	74.2 (6.00-2.30) 77.2 (24.88-2.25)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.17 (at 2.26Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.223 , 0.277 0.230 , 0.282	Depositor DCC
R_{free} test set	1199 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.268	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 92.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 25696 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4979	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.79% 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	0.35	0/2313	0.63	1/3132 (0.0%)
2	C	0.44	0/936	0.67	0/1262
3	D	0.38	0/1616	0.66	0/2209
All	All	0.38	0/4865	0.65	1/6603 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	19	PRO	N-CA-CB	5.28	109.63	103.30

There are no chirality outliers.

There are no planarity outliers.

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	2262	0	2217	191	0
2	C	916	0	896	60	0
3	D	1589	0	1510	156	0
4	A	89	0	0	8	0
4	C	53	0	0	4	0
4	D	70	0	0	10	0
All	All	4979	0	4623	380	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 40.

All (380) 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:122:LYS:HD2	1:A:122:LYS:H	1.16	1.05
3:D:105:ASN:HD22	3:D:114:PRO:HD2	1.23	1.01
1:A:87:PRO:HB2	1:A:121:VAL:HG11	1.47	0.97
1:A:79:LYS:HA	1:A:158:ARG:HD2	1.49	0.94
1:A:64:ASN:HB2	4:A:370:HOH:O	1.70	0.92
1:A:291:ASP:HB3	1:A:295:ARG:HB2	1.53	0.91
3:D:138:GLU:O	3:D:140:ARG:HG2	1.72	0.89
3:D:245:ARG:HA	3:D:245:ARG:NE	1.87	0.87
3:D:140:ARG:HD2	3:D:144:GLY:O	1.75	0.87
3:D:81:ALA:HB1	3:D:90:THR:HA	1.58	0.85
1:A:229:THR:HG22	4:A:373:HOH:O	1.77	0.84
3:D:143:ARG:HH22	3:D:150:LEU:HD21	1.42	0.83
2:C:352:LYS:HA	2:C:352:LYS:NZ	1.93	0.83
1:A:158:ARG:NH1	1:A:182:PRO:HD3	1.93	0.82
1:A:81:PRO:HB2	1:A:82:PRO:HD3	1.59	0.82
2:C:248:LEU:HD11	2:C:333:ARG:HG3	1.60	0.82
1:A:282:GLU:HG2	1:A:283:PRO:HD2	1.59	0.81
2:C:333:ARG:NH1	2:C:338:GLU:HB2	1.95	0.81
1:A:33:ARG:HB3	1:A:186:ASN:CG	2.01	0.81
2:C:324:PRO:HB2	2:C:346:LEU:HD11	1.61	0.81
3:D:172:LEU:HD13	3:D:173:HIS:N	1.94	0.81
1:A:131:SER:O	1:A:135:GLN:HG2	1.82	0.80
1:A:33:ARG:HG3	1:A:35:ARG:HH22	1.47	0.79
3:D:162:VAL:O	3:D:165:GLN:HG3	1.83	0.79
3:D:216:ASN:HD22	3:D:218:ARG:HE	1.30	0.79
3:D:210:ASN:HD21	3:D:242:ASP:H	1.31	0.79
3:D:169:THR:HA	3:D:174:SER:HB3	1.65	0.78
3:D:137:PRO:HG2	3:D:138:GLU:H	1.48	0.78
3:D:174:SER:HB2	4:D:348:HOH:O	1.83	0.78
3:D:138:GLU:C	3:D:139:LEU:HD23	2.04	0.78
1:A:290:PRO:HD3	4:A:381:HOH:O	1.82	0.78
2:C:343:LYS:HD3	4:D:304:HOH:O	1.83	0.78
2:C:274:GLN:HG3	4:C:115:HOH:O	1.82	0.77
2:C:261:THR:O	2:C:315:LYS:HG3	1.84	0.77
1:A:122:LYS:H	1:A:122:LYS:CD	1.94	0.77
1:A:32:MET:HA	1:A:33:ARG:NH2	2.01	0.76
1:A:33:ARG:HG2	1:A:35:ARG:HH12	1.51	0.76
1:A:122:LYS:HD2	1:A:122:LYS:N	2.00	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:114:PRO:HA	3:D:117:LEU:HD23	1.66	0.75
3:D:121:THR:HG22	3:D:123:GLN:HG3	1.69	0.75
1:A:187:ARG:HH12	1:A:220:GLN:NE2	1.84	0.74
2:C:249:LYS:HB3	2:C:271:ASP:OD1	1.87	0.74
1:A:194:LEU:HD22	1:A:279:GLU:HG3	1.69	0.74
3:D:185:THR:H	3:D:188:HIS:CD2	2.06	0.74
2:C:336:ASP:OD2	2:C:338:GLU:HG2	1.87	0.74
1:A:33:ARG:HB3	1:A:186:ASN:OD1	1.88	0.73
1:A:262:LEU:HD21	1:A:266:VAL:HG12	1.68	0.73
3:D:185:THR:H	3:D:188:HIS:HD2	1.35	0.73
3:D:168:THR:C	3:D:170:PRO:HD2	2.09	0.73
3:D:219:THR:H	3:D:222:HIS:HD2	1.36	0.73
1:A:167:ASP:OD2	1:A:171:ARG:HB3	1.88	0.72
3:D:138:GLU:O	3:D:139:LEU:HD23	1.89	0.72
1:A:76:LEU:HG	1:A:157:VAL:HG21	1.72	0.72
3:D:275:GLU:H	3:D:275:GLU:CD	1.91	0.72
3:D:143:ARG:NH2	3:D:150:LEU:HD21	2.04	0.72
1:A:167:ASP:HB2	1:A:171:ARG:O	1.90	0.72
1:A:291:ASP:CB	1:A:295:ARG:HB2	2.21	0.70
3:D:160:VAL:HG21	3:D:198:ILE:HD12	1.73	0.70
3:D:289:TYR:H	3:D:289:TYR:HD1	1.38	0.70
1:A:297:ARG:HH22	3:D:154:GLN:HG3	1.55	0.70
1:A:50:ARG:HH22	3:D:266:GLN:NE2	1.90	0.69
3:D:125:GLU:O	3:D:128:GLU:HB3	1.91	0.69
2:C:251:VAL:HG13	3:D:249:GLN:CG	2.23	0.68
2:C:251:VAL:HG13	3:D:249:GLN:HG2	1.75	0.68
1:A:168:PRO:HD2	4:A:362:HOH:O	1.93	0.68
2:C:350:GLU:CG	2:C:353:ASP:HB2	2.23	0.68
3:D:165:GLN:OE1	3:D:166:SER:N	2.27	0.68
1:A:171:ARG:HD2	1:A:171:ARG:C	2.14	0.68
1:A:19:PRO:HA	4:A:321:HOH:O	1.94	0.68
1:A:302:ARG:HD3	1:A:302:ARG:H	1.58	0.67
2:C:333:ARG:HH12	2:C:338:GLU:HB2	1.58	0.67
1:A:262:LEU:O	1:A:290:PRO:HB3	1.93	0.67
1:A:301:LYS:HB2	1:A:301:LYS:NZ	2.10	0.66
2:C:252:ARG:HD3	3:D:216:ASN:HB2	1.78	0.65
3:D:119:VAL:CG2	3:D:163:LEU:HD11	2.28	0.64
1:A:158:ARG:HH12	1:A:182:PRO:HD3	1.61	0.64
1:A:118:ILE:HG13	1:A:183:ILE:HD11	1.80	0.64
2:C:272:LYS:HE2	2:C:306:GLN:HG2	1.78	0.64
3:D:188:HIS:O	3:D:192:ILE:HG13	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:LYS:NZ	1:A:93:LYS:HB3	2.13	0.63
1:A:225:GLU:OE2	1:A:275:PRO:HG3	1.99	0.63
3:D:185:THR:HG22	3:D:186:CYS:N	2.13	0.63
3:D:219:THR:H	3:D:222:HIS:CD2	2.16	0.63
3:D:245:ARG:HA	3:D:245:ARG:HE	1.61	0.62
3:D:228:GLN:NE2	3:D:262:SER:H	1.97	0.62
1:A:29:GLN:NE2	1:A:222:GLU:HG2	2.14	0.62
1:A:130:ILE:HD12	1:A:131:SER:N	2.15	0.62
3:D:135:CYS:HB3	3:D:139:LEU:HB3	1.81	0.61
3:D:210:ASN:ND2	3:D:242:ASP:H	1.97	0.61
3:D:263:THR:O	3:D:267:GLN:HG3	2.01	0.61
1:A:299:GLU:N	4:A:371:HOH:O	2.33	0.61
2:C:352:LYS:HA	2:C:352:LYS:HZ1	1.65	0.61
3:D:172:LEU:C	3:D:174:SER:H	2.04	0.61
1:A:218:LYS:NZ	1:A:218:LYS:HB3	2.16	0.61
1:A:203:SER:OG	1:A:289:LEU:HD11	2.01	0.61
3:D:243:VAL:HG22	4:D:331:HOH:O	1.99	0.61
3:D:196:LEU:HG	3:D:235:LEU:HD22	1.83	0.60
1:A:41:ARG:HH21	1:A:92:GLY:H	1.46	0.60
2:C:250:ILE:HB	2:C:343:LYS:HE3	1.83	0.60
3:D:201:LEU:O	3:D:201:LEU:HD22	2.01	0.60
3:D:262:SER:OG	3:D:265:ILE:HG13	2.02	0.60
3:D:169:THR:N	3:D:170:PRO:HD2	2.17	0.59
3:D:216:ASN:ND2	3:D:218:ARG:HE	1.99	0.59
2:C:259:CYS:SG	2:C:350:GLU:HB2	2.42	0.59
1:A:33:ARG:CG	1:A:35:ARG:HH12	2.14	0.59
3:D:79:HIS:O	3:D:83:ILE:HG13	2.01	0.59
3:D:258:TRP:HZ3	3:D:278:GLN:O	1.85	0.59
3:D:119:VAL:HG22	3:D:163:LEU:HD11	1.84	0.58
3:D:125:GLU:H	3:D:125:GLU:CD	2.06	0.58
3:D:105:ASN:HB2	3:D:114:PRO:HG2	1.85	0.58
3:D:258:TRP:CZ3	3:D:278:GLN:O	2.57	0.58
3:D:216:ASN:HD22	3:D:218:ARG:NE	2.00	0.57
1:A:265:PRO:HB3	1:A:289:LEU:HD23	1.86	0.57
1:A:110:ILE:N	1:A:110:ILE:HD12	2.20	0.57
1:A:33:ARG:HG3	1:A:35:ARG:NH2	2.18	0.57
1:A:277:ASP:OD1	1:A:279:GLU:HB3	2.05	0.57
1:A:162:GLN:HE22	1:A:174:LEU:HD21	1.70	0.57
3:D:81:ALA:O	3:D:84:HIS:O	2.23	0.57
3:D:129:ALA:O	3:D:131:LEU:HG	2.05	0.57
3:D:229:ASN:O	3:D:233:VAL:HG13	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:LEU:HD13	1:A:90:LEU:HG	1.85	0.57
1:A:297:ARG:HB3	3:D:112:GLN:HE22	1.69	0.56
2:C:324:PRO:CB	2:C:346:LEU:HD11	2.31	0.56
3:D:127:ALA:O	3:D:130:LEU:HD22	2.05	0.56
1:A:194:LEU:HB3	1:A:281:SER:HB3	1.88	0.56
1:A:187:ARG:HH22	1:A:220:GLN:HE22	1.52	0.56
1:A:96:ARG:CZ	1:A:101:GLU:HB3	2.34	0.56
1:A:19:PRO:N	1:A:64:ASN:O	2.39	0.56
1:A:46:ILE:HD11	1:A:118:ILE:HG12	1.87	0.56
3:D:210:ASN:HD21	3:D:242:ASP:N	2.01	0.56
3:D:75:ASP:HA	3:D:79:HIS:ND1	2.20	0.56
2:C:295:PHE:O	2:C:314:PRO:HB3	2.05	0.56
3:D:199:VAL:O	3:D:203:VAL:HG23	2.05	0.55
3:D:172:LEU:HD11	4:D:336:HOH:O	2.06	0.55
1:A:132:GLN:O	1:A:135:GLN:HB2	2.06	0.55
1:A:297:ARG:HB3	3:D:112:GLN:NE2	2.22	0.55
2:C:352:LYS:HA	2:C:352:LYS:HZ2	1.71	0.55
1:A:58:HIS:CD2	1:A:114:GLN:HA	2.41	0.55
1:A:85:PRO:HG3	1:A:139:ASN:HA	1.87	0.55
2:C:334:LYS:HE2	4:C:1:HOH:O	2.06	0.55
2:C:351:ILE:HD12	2:C:352:LYS:N	2.22	0.54
3:D:285:ASP:N	3:D:285:ASP:OD1	2.40	0.54
1:A:219:VAL:HG22	1:A:247:GLN:O	2.06	0.54
2:C:350:GLU:HG2	2:C:353:ASP:HB2	1.88	0.54
1:A:145:ILE:HG21	4:A:309:HOH:O	2.08	0.54
1:A:87:PRO:HB2	1:A:121:VAL:CG1	2.30	0.54
2:C:272:LYS:HD3	2:C:273:VAL:N	2.22	0.54
1:A:112:SER:OG	1:A:114:GLN:NE2	2.41	0.54
1:A:123:LYS:HD2	1:A:126:LEU:HD13	1.90	0.54
1:A:167:ASP:C	1:A:169:ALA:H	2.11	0.53
1:A:196:ILE:CG1	1:A:272:LEU:HD22	2.37	0.53
1:A:236:ARG:HH11	1:A:236:ARG:HG3	1.73	0.53
3:D:135:CYS:HB3	3:D:139:LEU:CB	2.38	0.53
3:D:228:GLN:HE22	3:D:262:SER:H	1.55	0.53
2:C:353:ASP:O	2:C:354:LYS:HB2	2.07	0.53
1:A:57:THR:HG22	1:A:58:HIS:N	2.24	0.53
1:A:239:PHE:HB3	1:A:252:PHE:CB	2.38	0.53
1:A:21:VAL:O	1:A:178:VAL:HG21	2.08	0.53
3:D:144:GLY:O	3:D:180:ASN:HA	2.09	0.53
2:C:278:ILE:HD11	2:C:331:LEU:HB3	1.91	0.53
3:D:135:CYS:O	3:D:139:LEU:HD13	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:ARG:HH22	3:D:154:GLN:CG	2.20	0.53
1:A:198:ARG:NH1	2:C:310:VAL:HG11	2.24	0.53
1:A:246:ARG:HE	3:D:287:GLU:CA	2.22	0.53
2:C:321:ILE:HG13	2:C:323:LYS:H	1.74	0.52
3:D:135:CYS:O	3:D:139:LEU:HB3	2.08	0.52
1:A:251:VAL:HG11	2:C:252:ARG:NH1	2.25	0.52
3:D:244:ASN:O	3:D:245:ARG:O	2.28	0.52
1:A:96:ARG:HH11	1:A:96:ARG:CG	2.23	0.52
1:A:229:THR:CG2	1:A:269:SER:HB3	2.39	0.52
2:C:333:ARG:HH12	2:C:338:GLU:CB	2.23	0.52
1:A:33:ARG:HB3	1:A:186:ASN:ND2	2.25	0.52
3:D:73:ASP:N	4:D:347:HOH:O	2.42	0.52
3:D:136:ASP:N	3:D:137:PRO:CD	2.73	0.52
1:A:41:ARG:NH2	1:A:92:GLY:H	2.08	0.52
1:A:162:GLN:HA	1:A:162:GLN:NE2	2.25	0.52
2:C:284:GLU:O	2:C:291:VAL:HG23	2.10	0.52
3:D:111:GLN:OE1	3:D:142:PHE:HA	2.10	0.52
1:A:96:ARG:HG2	1:A:96:ARG:HH11	1.75	0.52
3:D:264:ARG:O	3:D:268:GLN:HG2	2.10	0.51
1:A:196:ILE:HG12	1:A:272:LEU:HD22	1.93	0.51
1:A:218:LYS:HZ3	1:A:218:LYS:HB3	1.75	0.51
1:A:73:ARG:NH2	1:A:138:ASN:OD1	2.43	0.51
1:A:245:HIS:NE2	2:C:307:PHE:HB3	2.25	0.51
1:A:210:ASP:O	1:A:253:ARG:HA	2.10	0.51
3:D:185:THR:HG22	3:D:186:CYS:H	1.73	0.51
1:A:233:TRP:CD1	1:A:258:ALA:HB2	2.46	0.51
3:D:172:LEU:O	3:D:174:SER:N	2.44	0.51
1:A:63:ILE:HD11	1:A:163:VAL:HG11	1.92	0.51
1:A:79:LYS:HA	1:A:158:ARG:CD	2.31	0.51
1:A:246:ARG:HH22	3:D:289:TYR:HB3	1.76	0.51
1:A:162:GLN:CA	1:A:162:GLN:HE21	2.23	0.51
1:A:277:ASP:O	1:A:278:ARG:HB2	2.11	0.51
3:D:181:TYR:C	3:D:182:ASN:HD22	2.14	0.51
2:C:299:SER:OG	2:C:300:PRO:HD2	2.10	0.51
3:D:134:GLY:O	3:D:135:CYS:C	2.49	0.51
3:D:84:HIS:O	3:D:86:GLU:HG2	2.11	0.51
1:A:58:HIS:CG	1:A:114:GLN:HA	2.46	0.51
3:D:101:LEU:O	3:D:102:ALA:HB3	2.10	0.51
3:D:85:GLU:HB3	4:D:345:HOH:O	2.10	0.51
1:A:153:ASP:OD1	1:A:155:ASN:HB2	2.11	0.50
1:A:187:ARG:HH22	1:A:220:GLN:NE2	2.09	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:LYS:CD	1:A:122:LYS:N	2.68	0.50
1:A:96:ARG:C	1:A:98:GLY:H	2.14	0.50
1:A:214:LEU:C	1:A:214:LEU:HD23	2.31	0.50
1:A:55:THR:HA	1:A:56:LYS:NZ	2.26	0.50
1:A:86:HIS:CE1	1:A:88:HIS:CD2	2.99	0.50
3:D:138:GLU:O	3:D:140:ARG:NH1	2.44	0.50
3:D:170:PRO:HG2	4:D:305:HOH:O	2.10	0.50
1:A:112:SER:CB	1:A:114:GLN:HE22	2.25	0.50
3:D:94:ILE:HG23	3:D:95:ARG:N	2.26	0.50
2:C:350:GLU:HB3	2:C:353:ASP:HB2	1.93	0.50
1:A:33:ARG:CG	1:A:35:ARG:HH22	2.21	0.50
3:D:143:ARG:HH22	3:D:150:LEU:CD2	2.21	0.49
1:A:227:TYR:CE1	1:A:234:GLU:HG3	2.47	0.49
3:D:137:PRO:CG	3:D:138:GLU:H	2.22	0.49
1:A:217:ASP:OD1	2:C:305:ARG:NH2	2.46	0.49
1:A:28:LYS:CE	1:A:51:SER:HB2	2.43	0.49
1:A:55:THR:HA	1:A:56:LYS:HZ1	1.77	0.49
3:D:113:THR:O	3:D:117:LEU:HD22	2.12	0.49
1:A:89:GLU:HB2	1:A:98:GLY:HA2	1.95	0.49
2:C:313:THR:HG22	2:C:314:PRO:O	2.12	0.49
1:A:202:ASN:HD22	1:A:202:ASN:C	2.16	0.49
1:A:162:GLN:NE2	1:A:174:LEU:HD21	2.27	0.49
2:C:324:PRO:HB2	2:C:346:LEU:CD1	2.39	0.49
1:A:167:ASP:C	1:A:169:ALA:N	2.66	0.49
1:A:32:MET:SD	1:A:46:ILE:HG12	2.54	0.48
2:C:278:ILE:HG13	2:C:279:GLN:N	2.28	0.48
2:C:256:THR:HG21	3:D:214:PRO:HB2	1.95	0.48
1:A:302:ARG:HD3	1:A:302:ARG:N	2.27	0.48
1:A:33:ARG:H	1:A:33:ARG:CZ	2.27	0.48
1:A:94:ASP:HB2	1:A:100:TYR:CE2	2.48	0.48
1:A:246:ARG:HH21	3:D:287:GLU:CB	2.27	0.48
1:A:221:LYS:CE	3:D:280:LEU:HD23	2.44	0.48
1:A:118:ILE:HD12	1:A:157:VAL:HG11	1.95	0.48
3:D:218:ARG:NH1	4:D:361:HOH:O	2.44	0.48
3:D:243:VAL:O	3:D:253:PRO:HD2	2.13	0.48
3:D:282:GLU:HB2	4:D:346:HOH:O	2.13	0.48
3:D:117:LEU:O	3:D:121:THR:HB	2.13	0.47
1:A:229:THR:HG22	1:A:269:SER:HB3	1.95	0.47
1:A:112:SER:HB3	1:A:114:GLN:HE22	1.79	0.47
2:C:251:VAL:O	3:D:248:TYR:HB2	2.15	0.47
1:A:66:TYR:CD1	1:A:67:THR:N	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:LEU:HD22	1:A:111:HIS:CD2	2.50	0.47
3:D:168:THR:N	3:D:170:PRO:HD2	2.29	0.47
1:A:132:GLN:O	1:A:136:THR:HG22	2.14	0.47
2:C:284:GLU:HB2	2:C:327:VAL:HG12	1.95	0.47
3:D:169:THR:N	3:D:170:PRO:CD	2.76	0.47
3:D:135:CYS:SG	3:D:139:LEU:HA	2.55	0.47
1:A:81:PRO:O	1:A:83:HIS:N	2.47	0.47
1:A:33:ARG:O	1:A:35:ARG:NH1	2.47	0.47
1:A:132:GLN:HA	1:A:135:GLN:CG	2.45	0.47
1:A:171:ARG:HD2	1:A:172:PRO:C	2.35	0.47
1:A:129:ALA:O	1:A:133:ARG:HG2	2.15	0.47
1:A:86:HIS:CG	1:A:87:PRO:HD2	2.50	0.47
1:A:233:TRP:HZ3	1:A:268:VAL:HG11	1.79	0.47
2:C:351:ILE:HG12	3:D:111:GLN:HG3	1.97	0.46
1:A:25:GLU:OE2	1:A:57:THR:HG21	2.15	0.46
1:A:301:LYS:HZ2	1:A:301:LYS:HB2	1.80	0.46
3:D:124:PRO:O	3:D:128:GLU:N	2.40	0.46
2:C:352:LYS:HD2	3:D:109:ASN:OD1	2.15	0.46
3:D:172:LEU:HD21	4:D:336:HOH:O	2.15	0.46
1:A:259:ASP:HB3	1:A:262:LEU:HD13	1.98	0.46
1:A:162:GLN:HE22	1:A:174:LEU:CD2	2.28	0.46
1:A:291:ASP:HB2	1:A:295:ARG:NE	2.31	0.45
3:D:279:MET:HG2	3:D:280:LEU:N	2.31	0.45
2:C:321:ILE:HD12	2:C:322:THR:H	1.80	0.45
3:D:119:VAL:HG12	3:D:154:GLN:HE22	1.81	0.45
2:C:350:GLU:CB	2:C:353:ASP:HB2	2.47	0.45
3:D:234:SER:HB3	3:D:268:GLN:HE22	1.81	0.45
1:A:113:PHE:N	1:A:113:PHE:CD1	2.84	0.45
3:D:185:THR:O	3:D:189:LEU:HD22	2.16	0.45
1:A:128:GLN:O	1:A:131:SER:HB3	2.17	0.45
3:D:235:LEU:O	3:D:235:LEU:HG	2.15	0.45
2:C:321:ILE:O	2:C:349:PRO:HB3	2.16	0.45
3:D:230:PRO:HB2	3:D:264:ARG:NE	2.32	0.45
3:D:282:GLU:O	3:D:283:SER:C	2.55	0.45
1:A:221:LYS:O	1:A:241:GLN:HG2	2.17	0.45
1:A:185:ASP:OD1	1:A:186:ASN:N	2.46	0.45
3:D:282:GLU:HG2	3:D:282:GLU:O	2.17	0.45
1:A:300:GLU:N	1:A:300:GLU:OE1	2.50	0.45
3:D:173:HIS:O	3:D:174:SER:O	2.34	0.44
3:D:289:TYR:N	3:D:289:TYR:CD1	2.84	0.44
1:A:28:LYS:HE3	1:A:48:GLY:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:PRO:HB2	1:A:82:PRO:CD	2.40	0.44
1:A:126:LEU:O	1:A:130:ILE:HG13	2.17	0.44
1:A:213:PHE:CE2	2:C:252:ARG:HG2	2.52	0.44
3:D:119:VAL:HG12	3:D:154:GLN:NE2	2.32	0.44
3:D:140:ARG:NH1	3:D:146:THR:HG22	2.32	0.44
1:A:127:GLU:O	1:A:130:ILE:HD11	2.17	0.44
1:A:236:ARG:NH1	4:A:334:HOH:O	2.49	0.44
1:A:76:LEU:HG	1:A:157:VAL:CG2	2.45	0.44
1:A:56:LYS:NZ	1:A:56:LYS:H	2.16	0.44
1:A:35:ARG:HB3	1:A:35:ARG:CZ	2.47	0.44
3:D:125:GLU:HA	3:D:128:GLU:HB3	1.99	0.44
2:C:258:GLY:O	2:C:347:TYR:HA	2.17	0.44
1:A:202:ASN:HD22	1:A:202:ASN:H	1.65	0.43
1:A:290:PRO:HB2	1:A:292:THR:HG23	2.00	0.43
3:D:185:THR:N	3:D:188:HIS:HD2	2.09	0.43
2:C:272:LYS:CE	2:C:306:GLN:HG2	2.47	0.43
3:D:275:GLU:CD	3:D:275:GLU:N	2.66	0.43
2:C:268:LEU:C	2:C:268:LEU:HD23	2.38	0.43
1:A:86:HIS:ND1	1:A:87:PRO:HD2	2.34	0.43
1:A:198:ARG:HB3	2:C:267:TYR:OH	2.19	0.43
1:A:59:PRO:O	1:A:113:PHE:HD1	2.01	0.43
1:A:162:GLN:HA	1:A:162:GLN:HE21	1.83	0.43
2:C:323:LYS:HD2	3:D:138:GLU:HG3	2.01	0.43
3:D:86:GLU:HB3	3:D:89:LEU:CB	2.49	0.43
3:D:290:ASP:O	3:D:291:THR:CB	2.66	0.43
3:D:76:SER:C	3:D:78:LEU:H	2.22	0.43
1:A:50:ARG:NH2	3:D:266:GLN:NE2	2.64	0.42
1:A:96:ARG:NH1	1:A:96:ARG:CG	2.81	0.42
1:A:141:PHE:O	1:A:142:HIS:C	2.57	0.42
1:A:37:LYS:HB2	1:A:119:GLN:CD	2.39	0.42
1:A:187:ARG:HH11	1:A:187:ARG:HG2	1.84	0.42
2:C:305:ARG:O	2:C:306:GLN:HB2	2.18	0.42
3:D:201:LEU:O	3:D:204:SER:HB3	2.19	0.42
3:D:177:LYS:HD2	3:D:177:LYS:N	2.34	0.42
3:D:164:THR:HG21	3:D:205:LEU:CD1	2.49	0.42
3:D:113:THR:O	3:D:114:PRO:C	2.58	0.42
3:D:185:THR:CG2	3:D:186:CYS:N	2.82	0.42
3:D:120:ILE:HA	3:D:154:GLN:OE1	2.20	0.42
3:D:133:ALA:HB1	3:D:136:ASP:OD1	2.20	0.42
3:D:198:ILE:O	3:D:202:LEU:HG	2.20	0.42
1:A:93:LYS:HB3	1:A:93:LYS:HZ3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:ILE:HG13	1:A:272:LEU:HD22	2.01	0.42
2:C:284:GLU:HA	4:C:87:HOH:O	2.18	0.42
1:A:25:GLU:HB3	1:A:60:THR:HB	2.01	0.42
1:A:272:LEU:HD12	1:A:272:LEU:HA	1.82	0.42
1:A:302:ARG:HG3	1:A:302:ARG:HH11	1.84	0.42
3:D:260:ARG:HG3	3:D:260:ARG:HH11	1.84	0.42
3:D:171:HIS:HB2	3:D:174:SER:OG	2.20	0.42
3:D:115:LEU:HD11	3:D:163:LEU:HD21	2.01	0.42
3:D:182:ASN:N	3:D:182:ASN:HD22	2.17	0.42
1:A:202:ASN:ND2	1:A:202:ASN:C	2.73	0.42
2:C:315:LYS:HD2	2:C:315:LYS:N	2.34	0.41
1:A:297:ARG:NH1	3:D:154:GLN:OE1	2.53	0.41
3:D:175:ILE:HG13	3:D:175:ILE:H	1.64	0.41
1:A:36:TYR:CE1	1:A:120:CYS:SG	3.13	0.41
1:A:225:GLU:CD	1:A:275:PRO:HG3	2.41	0.41
3:D:229:ASN:HB3	3:D:232:LEU:HB3	2.02	0.41
1:A:25:GLU:HG2	1:A:58:HIS:O	2.20	0.41
1:A:124:ARG:NH1	1:A:125:ASP:OD2	2.54	0.41
3:D:105:ASN:ND2	3:D:114:PRO:HD2	2.08	0.41
3:D:105:ASN:HB2	3:D:114:PRO:CG	2.50	0.41
1:A:268:VAL:CG1	1:A:269:SER:N	2.82	0.41
3:D:168:THR:HG23	3:D:171:HIS:HD2	1.85	0.41
3:D:222:HIS:CE1	3:D:247:THR:HG23	2.56	0.41
3:D:132:GLY:O	3:D:134:GLY:N	2.54	0.41
1:A:268:VAL:HG12	1:A:269:SER:N	2.36	0.41
1:A:28:LYS:HB3	1:A:47:PRO:HG2	2.03	0.41
1:A:124:ARG:O	1:A:124:ARG:HD3	2.20	0.41
1:A:128:GLN:O	1:A:132:GLN:HG2	2.21	0.41
3:D:196:LEU:HD21	3:D:231:ASP:HB3	2.02	0.41
1:A:30:ARG:NH1	1:A:222:GLU:OE1	2.53	0.41
3:D:224:ALA:CB	3:D:233:VAL:HG12	2.51	0.41
1:A:25:GLU:CD	1:A:57:THR:HG21	2.41	0.41
1:A:57:THR:HG22	1:A:58:HIS:H	1.86	0.41
1:A:74:ILE:HD11	1:A:113:PHE:CE2	2.55	0.41
3:D:148:LEU:HB3	3:D:175:ILE:HG21	2.02	0.41
3:D:172:LEU:O	3:D:173:HIS:HB3	2.21	0.41
2:C:313:THR:HG23	2:C:314:PRO:HD2	2.02	0.41
3:D:140:ARG:HH11	3:D:146:THR:HG22	1.85	0.41
3:D:168:THR:HA	3:D:171:HIS:CD2	2.55	0.41
2:C:251:VAL:CG1	3:D:249:GLN:HG2	2.48	0.41
1:A:214:LEU:O	1:A:249:ALA:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:78:LEU:O	3:D:82:ILE:N	2.39	0.41
1:A:144:PRO:HG2	1:A:147:GLU:CG	2.51	0.41
3:D:172:LEU:C	3:D:174:SER:N	2.72	0.40
1:A:132:GLN:HA	1:A:135:GLN:HB2	2.04	0.40
1:A:285:GLU:H	1:A:285:GLU:CD	2.25	0.40
1:A:215:LEU:HB3	2:C:304:HIS:CD2	2.56	0.40
1:A:135:GLN:C	1:A:137:ASN:H	2.24	0.40
1:A:34:PHE:HB2	1:A:185:ASP:OD2	2.20	0.40
1:A:262:LEU:HD21	1:A:266:VAL:CG1	2.43	0.40
1:A:36:TYR:HD2	1:A:122:LYS:NZ	2.20	0.40
1:A:93:LYS:C	1:A:95:CYS:H	2.25	0.40
1:A:56:LYS:H	1:A:56:LYS:CE	2.35	0.40
1:A:35:ARG:HG2	1:A:35:ARG:HH11	1.86	0.40
2:C:332:ARG:HD2	4:C:19:HOH:O	2.19	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	279/286 (98%)	242 (87%)	28 (10%)	9 (3%)	5	3
2	C	111/119 (93%)	101 (91%)	9 (8%)	1 (1%)	21	24
3	D	212/236 (90%)	171 (81%)	26 (12%)	15 (7%)	1	0
All	All	602/641 (94%)	514 (85%)	63 (10%)	25 (4%)	3	1

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	ARG
1	A	292	THR
3	D	135	CYS

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Mol	Chain	Res	Type
3	D	137	PRO
3	D	174	SER
3	D	287	GLU
1	A	42	SER
1	A	43	ALA
1	A	142	HIS
1	A	298	ILE
2	C	355	GLU
3	D	85	GLU
3	D	87	LYS
3	D	133	ALA
3	D	167	CYS
3	D	139	LEU
3	D	245	ARG
3	D	262	SER
3	D	283	SER
3	D	291	THR
1	A	94	ASP
1	A	97	ASP
3	D	175	ILE
3	D	261	PRO
1	A	81	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	251/256 (98%)	228 (91%)	23 (9%)	11	13
2	C	101/108 (94%)	96 (95%)	5 (5%)	30	41
3	D	165/204 (81%)	148 (90%)	17 (10%)	9	10
All	All	517/568 (91%)	472 (91%)	45 (9%)	13	15

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	VAL
1	A	30	ARG
1	A	33	ARG
1	A	35	ARG
1	A	76	LEU
1	A	81	PRO
1	A	96	ARG
1	A	122	LYS
1	A	132	GLN
1	A	139	ASN
1	A	157	VAL
1	A	162	GLN
1	A	166	ARG
1	A	167	ASP
1	A	183	ILE
1	A	194	LEU
1	A	202	ASN
1	A	271	GLN
1	A	272	LEU
1	A	293	ASP
1	A	294	ASP
1	A	300	GLU
1	A	302	ARG
2	C	286	GLU
2	C	317	LYS
2	C	351	ILE
2	C	352	LYS
2	C	356	GLU
3	D	85	GLU
3	D	104	LEU
3	D	109	ASN
3	D	125	GLU
3	D	135	CYS
3	D	165	GLN
3	D	189	LEU
3	D	227	LEU
3	D	229	ASN
3	D	237	LEU
3	D	245	ARG
3	D	256	LEU
3	D	258	TRP
3	D	275	GLU
3	D	282	GLU

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Mol	Chain	Res	Type
3	D	285	ASP
3	D	289	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	114	GLN
1	A	128	GLN
1	A	162	GLN
1	A	202	ASN
1	A	220	GLN
1	A	271	GLN
3	D	105	ASN
3	D	112	GLN
3	D	171	HIS
3	D	182	ASN
3	D	188	HIS
3	D	210	ASN
3	D	216	ASN
3	D	222	HIS
3	D	228	GLN
3	D	229	ASN
3	D	249	GLN
3	D	266	GLN
3	D	267	GLN
3	D	268	GLN
3	D	271	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	283/286 (98%)	1.04	58 (20%) 1 2	20, 52, 71, 81	0
2	C	113/119 (94%)	0.46	8 (7%) 19 26	20, 39, 69, 77	0
3	D	216/236 (91%)	1.06	36 (16%) 2 4	19, 46, 70, 79	0
All	All	612/641 (95%)	0.94	102 (16%) 2 4	19, 47, 70, 81	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	101	LEU	14.2
1	A	298	ILE	12.1
3	D	102	ALA	10.3
1	A	188	ALA	10.1
3	D	291	THR	8.0
3	D	172	LEU	7.9
3	D	293	SER	7.5
3	D	292	GLU	7.2
1	A	292	THR	7.1
3	D	131	LEU	7.1
1	A	54	THR	7.1
3	D	285	ASP	6.6
2	C	353	ASP	6.4
3	D	77	PHE	6.3
2	C	246	SER	6.3
1	A	297	ARG	6.1
1	A	43	ALA	5.8
2	C	352	LYS	5.8
3	D	106	PHE	5.5
1	A	42	SER	5.4
1	A	187	ARG	5.1
1	A	40	GLY	5.1
3	D	170	PRO	5.1

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Mol	Chain	Res	Type	RSRZ
3	D	137	PRO	4.9
3	D	95	ARG	4.9
1	A	191	THR	4.9
3	D	289	TYR	4.9
3	D	173	HIS	4.8
3	D	290	ASP	4.8
2	C	245	ALA	4.8
1	A	293	ASP	4.2
1	A	145	ILE	4.1
1	A	37	LYS	4.1
2	C	351	ILE	4.1
1	A	124	ARG	4.1
1	A	299	GLU	4.0
1	A	76	LEU	4.0
1	A	150	GLY	3.9
1	A	81	PRO	3.8
1	A	127	GLU	3.8
1	A	302	ARG	3.8
3	D	104	LEU	3.7
3	D	94	ILE	3.7
3	D	93	VAL	3.6
1	A	41	ARG	3.4
1	A	294	ASP	3.4
1	A	137	ASN	3.3
3	D	171	HIS	3.3
1	A	33	ARG	3.3
1	A	53	ASP	3.2
1	A	135	GLN	3.1
3	D	282	GLU	3.1
1	A	126	LEU	3.1
3	D	139	LEU	3.1
1	A	146	GLU	3.0
1	A	303	LYS	3.0
1	A	147	GLU	3.0
3	D	128	GLU	3.0
3	D	286	GLU	2.9
3	D	75	ASP	2.9
1	A	192	ALA	2.9
3	D	103	PHE	2.9
1	A	142	HIS	2.8
3	D	174	SER	2.8
1	A	77	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
3	D	132	GLY	2.7
1	A	296	HIS	2.7
1	A	149	ARG	2.7
1	A	295	ARG	2.7
3	D	138	GLU	2.6
2	C	269	LEU	2.6
1	A	86	HIS	2.5
1	A	128	GLN	2.5
1	A	183	ILE	2.5
3	D	113	THR	2.5
1	A	157	VAL	2.5
1	A	114	GLN	2.5
1	A	301	LYS	2.4
1	A	242	ALA	2.4
1	A	155	ASN	2.4
3	D	90	THR	2.4
1	A	209	GLY	2.4
1	A	233	TRP	2.3
1	A	300	GLU	2.3
1	A	144	PRO	2.3
1	A	35	ARG	2.3
2	C	251	VAL	2.2
1	A	36	TYR	2.2
1	A	156	ALA	2.2
3	D	141	ASP	2.2
3	D	105	ASN	2.2
1	A	44	GLY	2.2
2	C	354	LYS	2.2
1	A	151	ASP	2.1
1	A	39	GLU	2.1
1	A	134	ILE	2.1
1	A	90	LEU	2.1
1	A	244	VAL	2.1
3	D	109	ASN	2.1
3	D	136	ASP	2.1
1	A	245	HIS	2.1
3	D	284	GLU	2.0

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

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.