



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:09 PM GMT

PDB ID : 4KR4
Title : Salmonella typhi OmpF complex with Ampicillin
Authors : Madhuranayaki, T.; Balasubramaniam, D.; Krishnaswamy, S.
Deposited on : 2013-05-16
Resolution : 3.80 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

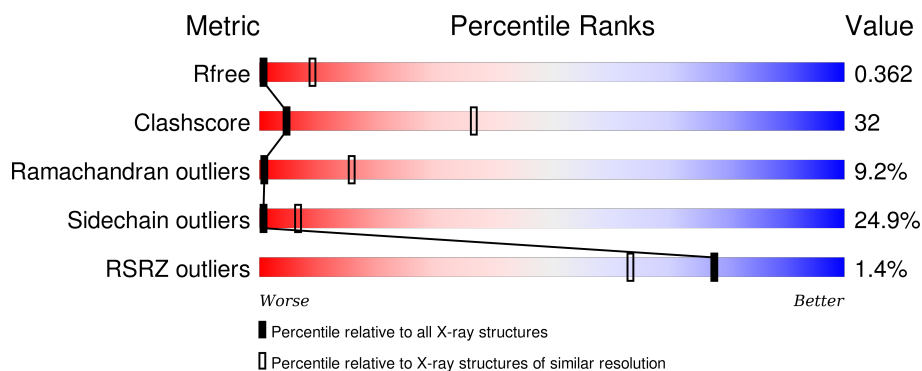
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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	1317 (4.10-3.50)
Clashscore	102246	1458 (4.10-3.50)
Ramachandran outliers	100387	1397 (4.10-3.50)
Sidechain outliers	100360	1392 (4.10-3.50)
RSRZ outliers	91569	1325 (4.10-3.50)

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	341	<div> <div></div> <div>45%</div> <div>43%</div> <div>12%</div> <div>..</div> </div>
1	B	341	<div> <div></div> <div>42%</div> <div>44%</div> <div>12%</div> <div>.</div> </div>
1	C	341	<div> <div></div> <div>42%</div> <div>40%</div> <div>16%</div> <div>..</div> </div>

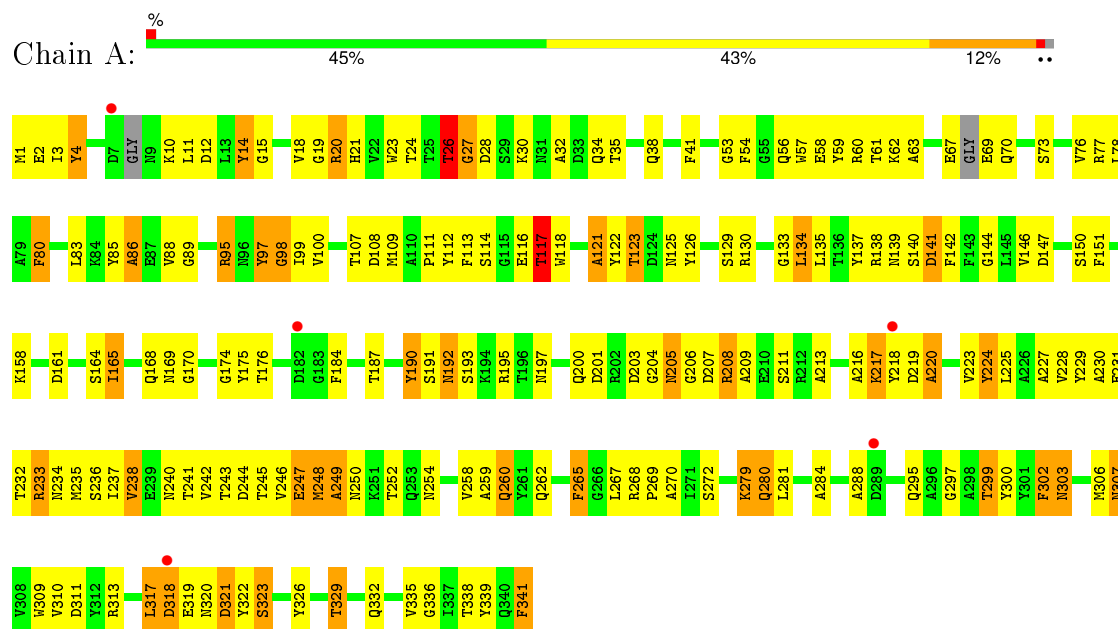
The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	AIC	C	401	-	-	-	X

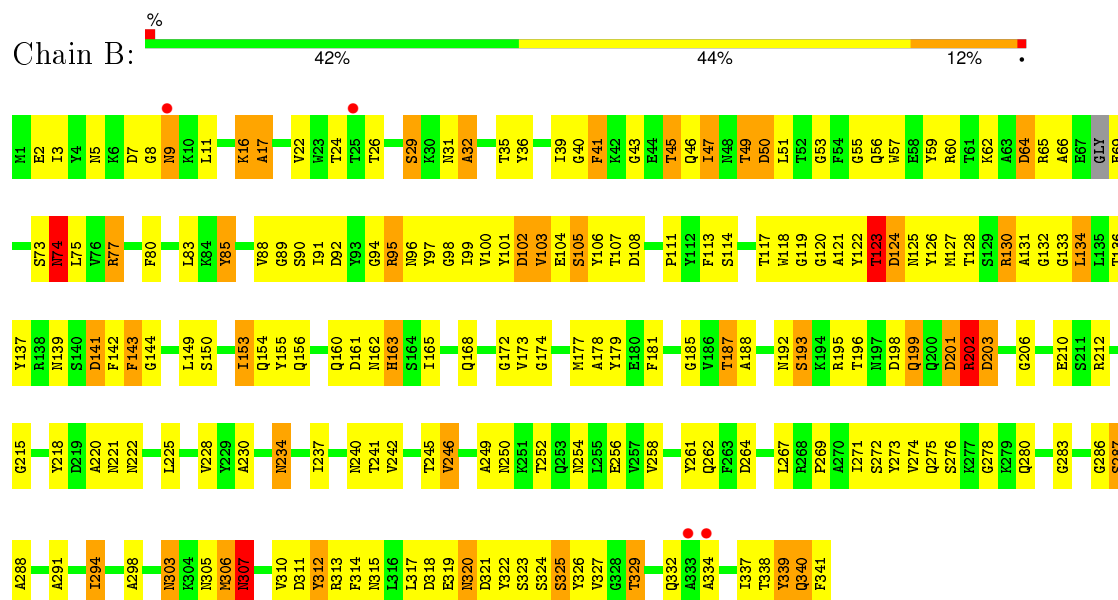
3 Residue-property plots

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.

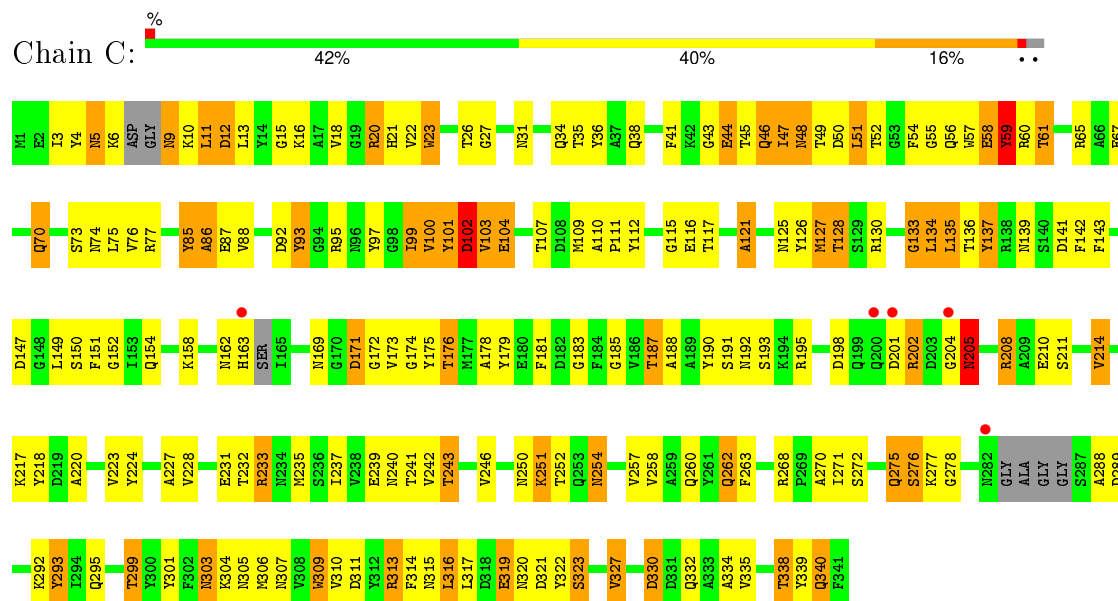
• Molecule 1: Outer membrane protein F



• Molecule 1: Outer membrane protein F



● Molecule 1: Outer membrane protein F



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.12Å 138.48Å 150.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.80 44.14 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-3.80) 99.8 (44.14-3.80)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.97 (at 3.77Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.286 , 0.366 0.284 , 0.362	Depositor DCC
R_{free} test set	929 reflections (5.39%)	DCC
Wilson B-factor (Å ²)	89.6	Xtriage
Anisotropy	0.588	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.21 , 36.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 18151 reflections	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	7501	wwPDB-VP
Average B, all atoms (Å ²)	105.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.69% 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

Bond lengths and bond angles in the following residue types are not validated in this section: AIC

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	0.52	0/2546	0.68	0/3463
1	B	0.50	0/2552	0.68	0/3474
1	C	0.53	0/2524	0.69	0/3431
All	All	0.52	0/7622	0.68	0/10368

There are no bond length outliers.

There are no bond angle outliers.

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	2498	0	2127	158	0
1	B	2503	0	2128	152	0
1	C	2476	0	2123	157	0
2	C	24	0	18	1	0
All	All	7501	0	6396	446	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 (446) 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:B:339:TYR:O	1:B:339:TYR:HD2	1.22	1.21
1:B:123:THR:HG21	1:C:67:GLU:HG3	1.33	1.09
1:B:339:TYR:O	1:B:339:TYR:CD2	2.06	1.07
1:A:20:ARG:HH11	1:A:20:ARG:HG3	1.18	1.04
1:B:102:ASP:O	1:B:103:VAL:HB	1.69	0.91
1:A:195:ARG:HH21	1:A:248:MET:HG3	1.36	0.90
1:C:306:MET:SD	1:C:339:TYR:HB2	2.11	0.90
1:A:60:ARG:HD2	1:A:77:ARG:NH2	1.86	0.89
1:A:232:THR:HG21	1:A:236:SER:HB2	1.53	0.89
1:A:235:MET:SD	1:A:248:MET:SD	2.71	0.89
1:A:18:VAL:HG22	1:A:338:THR:HG23	1.53	0.88
1:B:47:ILE:HG13	1:B:51:LEU:HB3	1.55	0.87
1:B:131:ALA:HB3	1:B:134:LEU:HD21	1.56	0.86
1:A:76:VAL:O	1:A:76:VAL:HG23	1.76	0.86
1:C:26:THR:HB	1:C:330:ASP:HB3	1.57	0.86
1:C:310:VAL:HG12	1:C:335:VAL:HG12	1.56	0.86
1:A:61:THR:HG21	1:C:59:TYR:HE2	1.42	0.83
1:A:61:THR:HG21	1:C:59:TYR:CE2	2.13	0.83
1:B:123:THR:CG2	1:C:67:GLU:HG3	2.09	0.82
1:B:141:ASP:HA	1:B:149:LEU:O	1.80	0.82
1:A:20:ARG:HG3	1:A:20:ARG:NH1	1.90	0.82
1:C:227:ALA:HB2	1:C:257:VAL:HG23	1.61	0.82
1:A:2:GLU:HA	1:A:12:ASP:HB3	1.61	0.81
1:B:240:ASN:HD21	1:B:283:GLY:HA3	1.46	0.81
1:B:315:ASN:HD21	1:B:317:LEU:HB3	1.44	0.80
1:B:303:ASN:HB3	1:B:305:ASN:H	1.47	0.80
1:C:60:ARG:HB2	1:C:77:ARG:HD2	1.64	0.79
1:C:11:LEU:CD1	1:C:12:ASP:H	1.95	0.79
1:C:47:ILE:HD12	1:C:47:ILE:H	1.47	0.79
1:A:20:ARG:CG	1:A:20:ARG:HH11	1.95	0.78
1:C:87:GLU:O	1:C:143:PHE:HA	1.85	0.77
1:A:207:ASP:O	1:A:208:ARG:HB2	1.83	0.77
1:B:45:THR:HG22	1:B:53:GLY:HA3	1.67	0.77
1:B:339:TYR:C	1:B:339:TYR:HD2	1.89	0.76
1:A:1:MET:HG3	1:A:341:PHE:HB2	1.67	0.76
1:A:195:ARG:NH2	1:A:248:MET:HG3	2.00	0.75
1:C:11:LEU:HD12	1:C:12:ASP:H	1.49	0.75
1:A:111:PRO:HG3	1:A:299:THR:HB	1.69	0.74
1:C:126:TYR:OH	1:C:169:ASN:HA	1.87	0.74
1:B:339:TYR:C	1:B:339:TYR:CD2	2.61	0.74
1:B:39:ILE:HG22	1:B:40:GLY:N	2.02	0.73
1:C:178:ALA:HA	1:C:187:THR:OG1	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:GLY:HA3	1:B:137:TYR:HE1	1.52	0.72
1:C:231:GLU:HA	1:C:252:THR:O	1.89	0.72
1:B:286:GLY:O	1:B:287:SER:HB3	1.89	0.71
1:B:160:GLN:HG3	1:B:168:GLN:HE21	1.53	0.71
1:B:39:ILE:HG22	1:B:40:GLY:H	1.54	0.71
1:C:11:LEU:O	1:C:12:ASP:HB2	1.89	0.71
1:B:177:MET:HB2	1:B:188:ALA:HB3	1.73	0.71
1:A:252:THR:HG22	1:A:254:ASN:ND2	2.05	0.71
1:B:306:MET:O	1:B:307:ASN:HB3	1.90	0.70
1:A:122:TYR:CE2	1:A:237:ILE:HB	2.27	0.70
1:A:35:THR:HB	1:A:63:ALA:HB3	1.74	0.70
1:B:73:SER:O	1:B:74:ASN:HB2	1.92	0.68
1:A:60:ARG:HD2	1:A:77:ARG:HH22	1.57	0.68
1:A:318:ASP:HA	1:A:329:THR:HG23	1.74	0.68
1:C:242:VAL:HG23	1:C:243:THR:H	1.59	0.68
1:C:313:ARG:HG2	1:C:332:GLN:H	1.60	0.67
1:A:122:TYR:HE2	1:A:237:ILE:HB	1.59	0.67
1:B:172:GLY:HA3	1:B:193:SER:HA	1.74	0.67
1:B:273:TYR:CE2	1:B:275:GLN:HB2	2.29	0.67
1:C:232:THR:HG23	1:C:252:THR:OG1	1.95	0.67
1:C:174:GLY:HA2	1:C:190:TYR:O	1.95	0.67
1:C:233:ARG:O	1:C:250:ASN:HA	1.95	0.66
1:C:126:TYR:HB2	1:C:235:MET:SD	2.35	0.66
1:C:99:ILE:HG22	1:C:127:MET:HB3	1.78	0.66
1:C:20:ARG:HD3	1:C:36:TYR:HE2	1.60	0.66
1:B:117:THR:O	1:B:119:GLY:N	2.27	0.66
1:C:126:TYR:C	1:C:128:THR:H	1.98	0.66
1:B:258:VAL:HG13	1:B:272:SER:HB3	1.77	0.66
1:C:208:ARG:HH21	1:C:208:ARG:HA	1.61	0.66
1:B:95:ARG:HH22	1:C:67:GLU:HG2	1.61	0.65
1:A:158:LYS:HA	1:A:170:GLY:HA2	1.77	0.65
1:A:307:ASN:ND2	1:A:338:THR:HB	2.11	0.65
1:C:293:TYR:HE2	1:C:327:VAL:HG21	1.60	0.65
1:A:117:THR:O	1:A:121:ALA:HB2	1.97	0.65
1:A:267:LEU:HA	1:A:300:TYR:HD1	1.62	0.64
1:B:150:SER:OG	1:B:178:ALA:HB3	1.97	0.64
1:C:58:GLU:O	1:C:59:TYR:HB2	1.97	0.64
1:A:56:GLN:HB3	1:A:80:PHE:HE2	1.62	0.64
1:A:70:GLN:O	1:A:73:SER:OG	2.12	0.64
1:A:142:PHE:HB3	1:A:146:VAL:HG22	1.80	0.64
1:A:252:THR:CG2	1:A:254:ASN:HD21	2.11	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:THR:HA	1:A:258:VAL:HG21	1.80	0.63
1:B:322:TYR:O	1:B:324:SER:N	2.31	0.63
1:B:66:ALA:O	1:B:69:GLU:HB3	1.97	0.63
1:B:75:LEU:HB2	1:C:70:GLN:HE21	1.63	0.63
1:B:16:LYS:O	1:B:17:ALA:HB3	1.97	0.63
1:A:267:LEU:HD12	1:A:268:ARG:H	1.61	0.63
1:A:76:VAL:CG2	1:A:76:VAL:O	2.44	0.62
1:A:262:GLN:HB2	1:A:268:ARG:HH11	1.64	0.62
1:A:260:GLN:HB3	1:A:270:ALA:HA	1.80	0.62
1:C:139:ASN:ND2	1:C:142:PHE:HA	2.15	0.62
1:B:39:ILE:CG2	1:B:40:GLY:H	2.11	0.62
1:A:89:GLY:HA3	1:A:137:TYR:CE1	2.35	0.62
1:C:93:TYR:CD1	1:C:134:LEU:O	2.53	0.62
1:C:93:TYR:HE1	1:C:133:GLY:HA2	1.65	0.62
1:B:45:THR:N	1:B:53:GLY:O	2.32	0.61
1:B:77:ARG:HD3	1:B:130:ARG:NH2	2.15	0.61
1:B:123:THR:HG21	1:C:67:GLU:CG	2.18	0.61
1:A:56:GLN:HB3	1:A:80:PHE:CE2	2.34	0.61
1:B:267:LEU:HD11	1:B:298:ALA:HB1	1.82	0.61
1:A:240:ASN:HB3	1:A:245:THR:HG22	1.83	0.61
1:A:3:ILE:O	1:A:4:TYR:HB2	2.00	0.61
1:B:107:THR:HG21	1:B:228:VAL:HG22	1.83	0.61
1:C:275:GLN:HG3	1:C:276:SER:H	1.66	0.61
1:C:293:TYR:CE2	1:C:327:VAL:HG21	2.37	0.60
1:B:306:MET:CE	1:B:339:TYR:HB2	2.32	0.59
1:A:192:ASN:HD21	1:A:208:ARG:HD2	1.66	0.59
1:A:267:LEU:HD13	1:A:300:TYR:HB2	1.84	0.59
1:B:60:ARG:HE	1:B:77:ARG:NH2	2.00	0.59
1:C:116:GLU:O	1:C:121:ALA:HB2	2.01	0.59
1:B:315:ASN:ND2	1:B:317:LEU:HB3	2.17	0.59
1:B:141:ASP:O	1:B:144:GLY:N	2.31	0.59
1:B:16:LYS:O	1:B:17:ALA:CB	2.50	0.59
1:B:113:PHE:CD1	1:B:313:ARG:HB3	2.36	0.59
1:C:233:ARG:HG3	1:C:251:LYS:HG3	1.85	0.58
1:B:234:ASN:HA	1:B:249:ALA:O	2.03	0.58
1:B:39:ILE:CG2	1:B:40:GLY:N	2.66	0.58
1:A:195:ARG:HH21	1:A:248:MET:CG	2.15	0.58
1:A:209:ALA:HA	1:A:234:ASN:HB2	1.85	0.58
1:A:164:SER:O	1:A:168:GLN:HG3	2.03	0.58
1:C:185:GLY:O	1:C:217:LYS:N	2.34	0.58
1:B:111:PRO:HD2	1:B:311:ASP:OD2	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:230:ALA:HB3	1:A:254:ASN:HB2	1.86	0.58
1:C:41:PHE:CD1	1:C:41:PHE:O	2.57	0.57
1:C:15:GLY:HA2	1:C:38:GLN:O	2.05	0.57
1:A:281:LEU:HD21	1:A:288:ALA:HB3	1.85	0.57
1:C:99:ILE:HG13	1:C:154:GLN:CB	2.34	0.57
1:C:101:TYR:O	1:C:104:GLU:N	2.38	0.57
1:A:129:SER:OG	1:A:130:ARG:N	2.36	0.57
1:C:240:ASN:OD1	1:C:242:VAL:HG22	2.05	0.57
1:A:252:THR:HG22	1:A:254:ASN:HD21	1.68	0.56
1:A:67:GLU:OE1	1:C:95:ARG:NH1	2.38	0.56
1:C:23:TRP:HB3	1:C:31:ASN:HB3	1.87	0.56
1:C:301:TYR:HA	1:C:307:ASN:HB3	1.87	0.56
1:B:267:LEU:HG	1:B:269:PRO:HD3	1.87	0.56
1:A:281:LEU:HD13	1:A:284:ALA:HB3	1.87	0.56
1:A:339:TYR:CD2	1:C:55:GLY:HA3	2.40	0.56
1:A:320:ASN:H	1:A:323:SER:HB2	1.70	0.56
1:C:46:GLN:HG3	1:C:48:ASN:O	2.05	0.56
1:C:258:VAL:HG12	1:C:272:SER:CB	2.36	0.56
1:A:63:ALA:HB1	1:C:95:ARG:HB2	1.88	0.56
1:A:41:PHE:O	1:A:56:GLN:HA	2.06	0.56
1:A:281:LEU:HD22	1:A:322:TYR:CE2	2.41	0.56
1:C:18:VAL:HG22	1:C:338:THR:HB	1.86	0.56
1:B:291:ALA:HA	1:B:317:LEU:HD22	1.88	0.56
1:C:107:THR:HG22	1:C:258:VAL:HG22	1.87	0.56
1:C:299:THR:HG23	1:C:309:TRP:HB3	1.88	0.56
1:C:20:ARG:HD3	1:C:36:TYR:CE2	2.42	0.55
1:C:115:GLY:O	2:C:401:AIC:HC7	2.07	0.55
1:B:134:LEU:HD22	1:B:154:GLN:HE21	1.71	0.55
1:A:3:ILE:O	1:A:4:TYR:CB	2.54	0.55
1:A:224:TYR:O	1:A:259:ALA:HA	2.06	0.55
1:C:100:VAL:O	1:C:103:VAL:HG23	2.07	0.55
1:C:126:TYR:O	1:C:128:THR:N	2.39	0.55
1:B:89:GLY:HA3	1:B:137:TYR:CE1	2.38	0.55
1:B:122:TYR:CD2	1:B:237:ILE:HB	2.42	0.55
1:A:122:TYR:HD2	1:A:237:ILE:HD12	1.72	0.55
1:C:56:GLN:CG	1:C:57:TRP:H	2.19	0.55
1:C:34:GLN:NE2	1:C:112:TYR:OH	2.40	0.55
1:B:85:TYR:HB3	1:B:88:VAL:HB	1.88	0.54
1:A:60:ARG:HD2	1:A:77:ARG:HH21	1.71	0.54
1:A:95:ARG:HH11	1:A:95:ARG:HG3	1.72	0.54
1:B:215:GLY:HA3	1:B:228:VAL:HG12	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:TRP:CZ2	1:B:59:TYR:HB2	2.42	0.54
1:C:103:VAL:HG12	1:C:228:VAL:HG21	1.88	0.54
1:B:119:GLY:HA2	1:B:128:THR:HB	1.89	0.54
1:B:195:ARG:NH1	1:B:203:ASP:HB2	2.22	0.54
1:B:195:ARG:HH12	1:B:203:ASP:HB2	1.73	0.54
1:C:43:GLY:O	1:C:44:GLU:HB2	2.08	0.54
1:B:134:LEU:HD22	1:B:154:GLN:NE2	2.23	0.54
1:C:48:ASN:ND2	1:C:51:LEU:H	2.06	0.54
1:A:272:SER:H	1:A:295:GLN:HE21	1.55	0.54
1:B:102:ASP:O	1:B:103:VAL:CB	2.49	0.54
1:A:111:PRO:CG	1:A:299:THR:HB	2.38	0.53
1:A:142:PHE:CB	1:A:146:VAL:HG22	2.38	0.53
1:C:56:GLN:HG2	1:C:57:TRP:H	1.73	0.53
1:B:306:MET:HE2	1:B:339:TYR:HB2	1.89	0.53
1:B:108:ASP:HA	1:B:114:SER:HB2	1.90	0.53
1:A:140:SER:HA	1:A:150:SER:HB2	1.89	0.53
1:C:104:GLU:OE2	1:C:104:GLU:HA	2.07	0.53
1:A:208:ARG:O	1:A:234:ASN:ND2	2.39	0.53
1:A:339:TYR:CE2	1:C:43:GLY:HA3	2.44	0.53
1:B:202:ARG:HG3	1:B:245:THR:HG21	1.90	0.53
1:C:15:GLY:CA	1:C:38:GLN:O	2.56	0.53
1:B:106:TYR:CE2	1:B:187:THR:OG1	2.62	0.53
1:A:61:THR:CG2	1:C:59:TYR:HE2	2.17	0.53
1:A:57:TRP:HA	1:A:78:LEU:O	2.10	0.52
1:A:307:ASN:HD21	1:A:338:THR:CB	2.23	0.52
1:B:95:ARG:NH1	1:C:67:GLU:OE1	2.28	0.52
1:A:2:GLU:HA	1:A:12:ASP:CB	2.34	0.52
1:B:41:PHE:O	1:B:56:GLN:HG2	2.10	0.52
1:A:313:ARG:NH1	1:A:332:GLN:OE1	2.43	0.52
1:C:125:ASN:HB3	1:C:128:THR:OG1	2.10	0.52
1:C:22:VAL:HG13	1:C:334:ALA:HB2	1.90	0.52
1:B:95:ARG:NE	1:B:131:ALA:O	2.43	0.52
1:A:59:TYR:CD2	1:A:76:VAL:HG12	2.44	0.52
1:C:101:TYR:O	1:C:102:ASP:C	2.46	0.52
1:A:231:GLU:HA	1:A:252:THR:O	2.10	0.51
1:A:306:MET:SD	1:A:339:TYR:HB2	2.51	0.51
1:A:86:ALA:C	1:A:88:VAL:H	2.14	0.51
1:A:60:ARG:HH11	1:A:77:ARG:HH22	1.57	0.51
1:A:95:ARG:CG	1:A:95:ARG:HH11	2.23	0.51
1:C:59:TYR:HD1	1:C:60:ARG:N	2.09	0.51
1:A:20:ARG:HB2	1:A:34:GLN:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:310:VAL:HG12	1:C:335:VAL:CG1	2.34	0.51
1:C:252:THR:HG22	1:C:278:GLY:HA3	1.91	0.51
1:A:262:GLN:HB2	1:A:268:ARG:NH1	2.25	0.51
1:A:21:HIS:HB2	1:C:93:TYR:HE2	1.76	0.51
1:C:5:ASN:HD22	1:C:6:LYS:H	1.58	0.51
1:C:61:THR:HG22	1:C:74:ASN:OD1	2.11	0.51
1:A:15:GLY:HA2	1:A:38:GLN:O	2.11	0.50
1:B:36:TYR:HD1	1:B:60:ARG:HG3	1.75	0.50
1:B:60:ARG:HH21	1:B:77:ARG:HH22	1.60	0.50
1:C:235:MET:HG3	1:C:235:MET:O	2.12	0.50
1:A:267:LEU:HD12	1:A:268:ARG:N	2.25	0.50
1:B:250:ASN:HB2	1:B:280:GLN:HB3	1.92	0.50
1:B:340:GLN:O	1:B:341:PHE:HB3	2.12	0.50
1:A:204:GLY:C	1:A:206:GLY:H	2.13	0.50
1:B:222:ASN:HA	1:B:262:GLN:HB3	1.93	0.50
1:C:44:GLU:HA	1:C:54:PHE:HA	1.93	0.50
1:B:49:THR:HG23	1:B:50:ASP:OD1	2.12	0.50
1:A:137:TYR:HE2	1:A:151:PHE:CZ	2.30	0.50
1:B:101:TYR:O	1:B:103:VAL:N	2.44	0.50
1:C:102:ASP:OD1	1:C:102:ASP:N	2.31	0.50
1:A:99:ILE:HG23	1:A:176:THR:HB	1.93	0.50
1:A:267:LEU:CA	1:A:300:TYR:HD1	2.25	0.50
1:C:275:GLN:HG3	1:C:276:SER:N	2.27	0.50
1:C:260:GLN:HB3	1:C:270:ALA:HB2	1.94	0.50
1:B:8:GLY:O	1:B:9:ASN:HB2	2.11	0.50
1:B:92:ASP:OD2	1:B:136:THR:HB	2.13	0.49
1:B:303:ASN:HB3	1:B:305:ASN:N	2.24	0.49
1:C:86:ALA:O	1:C:87:GLU:HB2	2.12	0.49
1:C:126:TYR:C	1:C:128:THR:N	2.65	0.49
1:B:273:TYR:HE2	1:B:275:GLN:HB2	1.76	0.49
1:C:151:PHE:HA	1:C:176:THR:O	2.13	0.49
1:C:137:TYR:O	1:C:152:GLY:HA2	2.12	0.49
1:C:103:VAL:HG12	1:C:228:VAL:CG2	2.42	0.49
1:B:36:TYR:CD1	1:B:60:ARG:HG3	2.46	0.49
1:C:171:ASP:N	1:C:171:ASP:OD1	2.45	0.49
1:C:16:LYS:HB3	1:C:340:GLN:HB3	1.94	0.49
1:C:179:TYR:CE2	1:C:181:PHE:HB3	2.48	0.49
1:A:60:ARG:HB2	1:A:77:ARG:HH21	1.77	0.49
1:A:232:THR:HG22	1:A:233:ARG:H	1.77	0.48
1:A:240:ASN:O	1:A:244:ASP:N	2.46	0.48
1:C:242:VAL:HG23	1:C:243:THR:N	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:20:ARG:NH2	1:C:112:TYR:HE1	2.11	0.48
1:B:46:GLN:OE1	1:B:49:THR:HA	2.14	0.48
1:C:11:LEU:O	1:C:12:ASP:CB	2.60	0.48
1:C:70:GLN:HG3	1:C:73:SER:HB2	1.95	0.48
1:C:258:VAL:HG12	1:C:272:SER:HB3	1.94	0.48
1:B:195:ARG:HH12	1:B:203:ASP:HA	1.78	0.48
1:A:335:VAL:HG22	1:A:336:GLY:H	1.79	0.48
1:C:59:TYR:CD1	1:C:60:ARG:N	2.82	0.48
1:C:93:TYR:HB2	1:C:135:LEU:HA	1.94	0.48
1:B:31:ASN:O	1:B:32:ALA:HB2	2.14	0.48
1:C:9:ASN:HB3	1:C:45:THR:HA	1.95	0.48
1:C:201:ASP:O	1:C:202:ARG:CB	2.62	0.48
1:A:216:ALA:O	1:A:217:LYS:CB	2.60	0.48
1:B:51:LEU:HD11	1:B:83:LEU:HB3	1.95	0.47
1:A:107:THR:O	1:A:109:MET:N	2.47	0.47
1:A:218:TYR:CD2	1:A:218:TYR:C	2.88	0.47
1:B:137:TYR:HB3	1:B:153:ILE:HD12	1.96	0.47
1:C:20:ARG:CD	1:C:36:TYR:HE2	2.25	0.47
1:A:267:LEU:HG	1:A:269:PRO:HD3	1.95	0.47
1:A:62:LYS:HB2	1:A:73:SER:HB2	1.95	0.47
1:B:62:LYS:HG3	1:B:73:SER:HA	1.96	0.47
1:C:316:LEU:HD23	1:C:316:LEU:H	1.79	0.47
1:A:307:ASN:HD21	1:A:338:THR:HB	1.80	0.47
1:B:74:ASN:HD22	1:B:74:ASN:C	2.16	0.47
1:A:97:TYR:H	1:A:97:TYR:HD2	1.61	0.47
1:B:195:ARG:HH12	1:B:203:ASP:CB	2.28	0.47
1:B:91:ILE:HA	1:B:136:THR:O	2.14	0.47
1:B:90:SER:O	1:B:137:TYR:HA	2.14	0.47
1:B:24:THR:HG22	1:B:332:GLN:CB	2.45	0.47
1:A:53:GLY:HA3	1:B:306:MET:SD	2.55	0.47
1:B:55:GLY:HA3	1:C:339:TYR:HD2	1.80	0.47
1:A:320:ASN:HB2	1:A:323:SER:H	1.80	0.47
1:B:179:TYR:O	1:B:185:GLY:HA2	2.15	0.47
1:B:252:THR:HG22	1:B:278:GLY:HA2	1.97	0.47
1:A:241:THR:HG22	1:A:321:ASP:O	2.15	0.47
1:C:93:TYR:CD1	1:C:93:TYR:C	2.87	0.47
1:A:24:THR:HG22	1:A:30:LYS:H	1.78	0.47
1:B:55:GLY:HA3	1:C:339:TYR:CD2	2.50	0.47
1:A:209:ALA:HA	1:A:234:ASN:CB	2.45	0.47
1:A:309:TRP:CE2	1:A:336:GLY:HA3	2.50	0.47
1:A:38:GLN:OE1	1:A:77:ARG:NE	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:ASN:HB3	1:A:306:MET:H	1.80	0.46
1:A:165:ILE:H	1:A:165:ILE:HD12	1.81	0.46
1:A:216:ALA:N	1:A:227:ALA:O	2.48	0.46
1:B:137:TYR:HD2	1:B:153:ILE:HD11	1.80	0.46
1:A:19:GLY:HA2	1:A:35:THR:HG23	1.98	0.46
1:C:293:TYR:HA	1:C:314:PHE:O	2.15	0.46
1:B:136:THR:OG1	1:B:154:GLN:HG3	2.16	0.46
1:A:126:TYR:CE1	1:A:193:SER:HB3	2.50	0.46
1:A:126:TYR:HE1	1:A:193:SER:HB3	1.81	0.46
1:A:242:VAL:HG23	1:A:243:THR:HG23	1.97	0.46
1:B:173:VAL:CG1	1:B:174:GLY:N	2.79	0.46
1:A:151:PHE:HD2	1:A:151:PHE:H	1.64	0.46
1:B:95:ARG:HB2	1:B:132:GLY:HA2	1.97	0.46
1:C:275:GLN:HE21	1:C:275:GLN:HB2	1.55	0.46
1:B:203:ASP:OD2	1:B:206:GLY:N	2.41	0.46
1:C:292:LYS:O	1:C:316:LEU:HD23	2.16	0.46
1:B:103:VAL:HG13	1:B:104:GLU:N	2.31	0.45
1:C:271:ILE:HA	1:C:295:GLN:O	2.15	0.45
1:B:125:ASN:OD1	1:B:126:TYR:N	2.47	0.45
1:A:317:LEU:HD22	1:A:318:ASP:H	1.82	0.45
1:B:99:ILE:O	1:B:101:TYR:N	2.50	0.45
1:A:58:GLU:HB3	1:A:77:ARG:HB3	1.97	0.45
1:A:62:LYS:HE2	1:A:73:SER:HA	1.98	0.45
1:B:57:TRP:CE2	1:B:59:TYR:HB2	2.51	0.45
1:C:210:GLU:HG3	1:C:211:SER:N	2.32	0.45
1:B:320:ASN:H	1:B:320:ASN:HD22	1.64	0.45
1:C:172:GLY:HA3	1:C:193:SER:OG	2.17	0.45
1:B:240:ASN:O	1:B:242:VAL:N	2.50	0.45
1:C:254:ASN:HA	1:C:276:SER:HA	1.98	0.45
1:A:10:LYS:HG3	1:A:11:LEU:N	2.32	0.45
1:A:339:TYR:CZ	1:C:43:GLY:HA3	2.52	0.45
1:A:184:PHE:HA	1:A:218:TYR:HA	1.98	0.45
1:B:64:ASP:OD1	1:B:64:ASP:N	2.40	0.45
1:C:178:ALA:HA	1:C:187:THR:HG1	1.80	0.45
1:B:325:SER:O	1:B:326:TYR:HB2	2.17	0.45
1:B:11:LEU:HA	1:B:43:GLY:HA2	1.99	0.45
1:B:94:GLY:O	1:B:134:LEU:HD12	2.17	0.44
1:B:315:ASN:ND2	1:B:329:THR:O	2.50	0.44
1:B:160:GLN:HG3	1:B:168:GLN:NE2	2.29	0.44
1:C:56:GLN:CG	1:C:57:TRP:N	2.80	0.44
1:B:312:TYR:CD1	1:B:312:TYR:C	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:GLY:O	1:C:56:GLN:HB2	2.17	0.44
1:C:239:GLU:HA	1:C:246:VAL:HA	1.98	0.44
1:B:104:GLU:O	1:B:107:THR:N	2.50	0.44
1:A:59:TYR:CE2	1:A:76:VAL:HG12	2.52	0.44
1:A:224:TYR:HB3	1:A:260:GLN:HG3	1.97	0.44
1:A:269:PRO:HA	1:A:297:GLY:O	2.18	0.44
1:A:300:TYR:HE2	1:A:302:PHE:HE1	1.66	0.44
1:B:196:THR:C	1:B:198:ASP:H	2.21	0.44
1:B:294:ILE:O	1:B:314:PHE:N	2.47	0.44
1:B:22:VAL:HG22	1:B:334:ALA:HB2	1.99	0.44
1:A:235:MET:H	1:A:248:MET:HB3	1.81	0.44
1:A:21:HIS:CD2	1:A:32:ALA:O	2.71	0.44
1:C:109:MET:HG3	1:C:224:TYR:HE2	1.81	0.44
1:A:174:GLY:HA2	1:A:190:TYR:O	2.17	0.44
1:B:96:ASN:H	1:B:134:LEU:CD1	2.30	0.44
1:C:139:ASN:O	1:C:150:SER:OG	2.26	0.44
1:C:47:ILE:H	1:C:47:ILE:CD1	2.20	0.44
1:C:51:LEU:HA	1:C:85:TYR:HA	1.98	0.44
1:A:14:TYR:OH	1:A:56:GLN:NE2	2.50	0.44
1:A:67:GLU:O	1:A:69:GLU:N	2.51	0.44
1:C:179:TYR:HE2	1:C:181:PHE:HB3	1.83	0.44
1:A:98:GLY:HA2	1:A:134:LEU:CD1	2.47	0.44
1:B:192:ASN:HD22	1:B:210:GLU:HB3	1.83	0.44
1:B:97:TYR:CZ	1:B:130:ARG:HD2	2.52	0.44
1:A:15:GLY:N	1:A:341:PHE:CE2	2.86	0.43
1:A:225:LEU:HA	1:A:258:VAL:O	2.18	0.43
1:C:322:TYR:O	1:C:323:SER:O	2.36	0.43
1:B:261:TYR:O	1:B:269:PRO:HD2	2.19	0.43
1:A:26:THR:O	1:A:27:GLY:C	2.56	0.43
1:C:100:VAL:HG22	1:C:128:THR:HA	2.00	0.43
1:A:229:TYR:HA	1:A:254:ASN:O	2.18	0.43
1:B:107:THR:HB	1:B:256:GLU:HB3	2.00	0.43
1:C:21:HIS:CD2	1:C:23:TRP:CD1	3.06	0.43
1:B:199:GLN:O	1:B:203:ASP:HB3	2.19	0.43
1:C:305:ASN:O	1:C:339:TYR:HD1	2.00	0.43
1:A:122:TYR:HE2	1:A:237:ILE:CB	2.29	0.43
1:A:20:ARG:NH1	1:A:34:GLN:O	2.52	0.43
1:A:137:TYR:HE2	1:A:151:PHE:CE1	2.36	0.43
1:A:116:GLU:OE1	1:A:313:ARG:NH2	2.51	0.43
1:B:103:VAL:H	1:B:105:SER:HG	1.61	0.43
1:C:303:ASN:C	1:C:305:ASN:H	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:93:TYR:CE1	1:C:133:GLY:HA2	2.50	0.43
1:B:203:ASP:HB2	1:B:206:GLY:HA3	2.01	0.43
1:B:306:MET:O	1:B:307:ASN:CB	2.62	0.43
1:B:103:VAL:CG1	1:B:104:GLU:H	2.31	0.43
1:A:77:ARG:HG3	1:A:130:ARG:CZ	2.49	0.43
1:B:41:PHE:O	1:B:56:GLN:CG	2.67	0.43
1:A:24:THR:HG22	1:A:30:LYS:N	2.33	0.43
1:A:205:ASN:N	1:A:250:ASN:HD21	2.16	0.43
1:B:306:MET:HE3	1:B:339:TYR:HB2	2.01	0.42
1:A:117:THR:OG1	1:A:118:TRP:N	2.52	0.42
1:C:99:ILE:HG21	1:C:174:GLY:HA3	2.01	0.42
1:B:163:HIS:ND1	1:B:163:HIS:N	2.66	0.42
1:A:63:ALA:HB1	1:C:95:ARG:CB	2.47	0.42
1:A:85:TYR:O	1:A:88:VAL:HB	2.18	0.42
1:B:103:VAL:CG1	1:B:104:GLU:N	2.81	0.42
1:A:60:ARG:NH1	1:A:77:ARG:HH22	2.18	0.42
1:A:213:ALA:HB1	1:A:230:ALA:HA	2.00	0.42
1:A:26:THR:OG1	1:A:27:GLY:N	2.52	0.42
1:B:173:VAL:HG12	1:B:174:GLY:N	2.34	0.42
1:A:191:SER:HB3	1:A:211:SER:HB2	2.02	0.42
1:C:21:HIS:HD2	1:C:23:TRP:NE1	2.17	0.42
1:B:230:ALA:HB3	1:B:254:ASN:HB2	2.02	0.42
1:C:58:GLU:HG2	1:C:77:ARG:HH11	1.85	0.42
1:B:165:ILE:HA	1:B:168:GLN:OE1	2.18	0.42
1:B:137:TYR:HB3	1:B:153:ILE:CD1	2.50	0.42
1:A:113:PHE:CD1	1:A:313:ARG:NH2	2.88	0.42
1:B:120:GLY:O	1:B:121:ALA:HB3	2.20	0.42
1:B:139:ASN:HD21	1:B:143:PHE:HD1	1.68	0.42
1:C:188:ALA:HA	1:C:214:VAL:HA	2.01	0.42
1:B:107:THR:HG23	1:B:228:VAL:HG13	2.01	0.41
1:C:254:ASN:HD22	1:C:276:SER:HB3	1.84	0.41
1:C:262:GLN:HA	1:C:268:ARG:HG3	2.01	0.41
1:B:276:SER:HB2	1:B:291:ALA:HB3	2.01	0.41
1:C:18:VAL:O	1:C:35:THR:HG23	2.20	0.41
1:C:309:TRP:CD1	1:C:309:TRP:O	2.73	0.41
1:B:222:ASN:O	1:B:261:TYR:CD1	2.73	0.41
1:C:205:ASN:HA	1:C:205:ASN:HD22	1.66	0.41
1:A:61:THR:HG21	1:C:59:TYR:CD2	2.55	0.41
1:A:192:ASN:HD22	1:A:192:ASN:C	2.22	0.41
1:B:201:ASP:O	1:B:202:ARG:C	2.59	0.41
1:C:149:LEU:HD12	1:C:179:TYR:CD1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:ALA:CB	1:B:320:ASN:OD1	2.68	0.41
1:C:183:GLY:HA3	1:C:220:ALA:HB2	2.02	0.41
1:A:238:VAL:HG23	1:A:247:GLU:HB3	2.02	0.41
1:C:277:LYS:HG3	1:C:289:ASP:HA	2.02	0.41
1:B:162:ASN:HB2	1:C:65:ARG:HD2	2.02	0.41
1:B:98:GLY:HA3	1:B:127:MET:O	2.21	0.41
1:A:307:ASN:ND2	1:A:338:THR:CB	2.78	0.41
1:C:16:LYS:HD2	1:C:18:VAL:HG21	2.02	0.41
1:C:288:ALA:HB1	1:C:320:ASN:HD21	1.85	0.41
1:C:303:ASN:O	1:C:305:ASN:N	2.53	0.41
1:B:160:GLN:HA	1:B:168:GLN:HG2	2.03	0.41
1:B:62:LYS:HB2	1:B:73:SER:HB2	2.02	0.41
1:B:324:SER:O	1:B:325:SER:HB3	2.21	0.41
1:B:313:ARG:O	1:B:313:ARG:HG3	2.20	0.41
1:B:155:TYR:HA	1:B:173:VAL:HG22	2.02	0.41
1:C:218:TYR:CE1	1:C:220:ALA:HB3	2.55	0.41
1:C:101:TYR:C	1:C:101:TYR:CD1	2.93	0.41
1:C:16:LYS:HD2	1:C:18:VAL:CG2	2.51	0.41
1:C:134:LEU:HB3	1:C:135:LEU:H	1.73	0.40
1:C:218:TYR:O	1:C:224:TYR:HA	2.21	0.40
1:A:248:MET:O	1:A:249:ALA:C	2.58	0.40
1:A:224:TYR:HD1	1:A:268:ARG:NH2	2.18	0.40
1:A:141:ASP:OD1	1:A:144:GLY:HA2	2.21	0.40
1:B:73:SER:O	1:B:74:ASN:CB	2.60	0.40
1:C:242:VAL:CG2	1:C:243:THR:H	2.30	0.40
1:A:175:TYR:CD2	1:A:175:TYR:N	2.88	0.40
1:A:219:ASP:O	1:A:220:ALA:HB2	2.22	0.40
1:B:47:ILE:CG1	1:B:51:LEU:HB3	2.39	0.40
1:C:85:TYR:O	1:C:86:ALA:O	2.40	0.40
1:C:56:GLN:HG2	1:C:57:TRP:N	2.36	0.40
1:A:204:GLY:O	1:A:206:GLY:N	2.39	0.40
1:A:279:LYS:O	1:A:280:GLN:C	2.60	0.40
1:B:218:TYR:CE1	1:B:220:ALA:HB3	2.56	0.40
1:C:48:ASN:ND2	1:C:51:LEU:HB3	2.36	0.40
1:C:104:GLU:O	1:C:107:THR:N	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	333/341 (98%)	241 (72%)	65 (20%)	27 (8%)	1	18
1	B	336/341 (98%)	253 (75%)	47 (14%)	36 (11%)	0	11
1	C	326/341 (96%)	246 (76%)	51 (16%)	29 (9%)	1	16
All	All	995/1023 (97%)	740 (74%)	163 (16%)	92 (9%)	1	16

All (92) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	TYR
1	A	27	GLY
1	A	108	ASP
1	A	112	TYR
1	A	117	THR
1	A	121	ALA
1	A	123	THR
1	A	205	ASN
1	A	208	ARG
1	A	280	GLN
1	A	323	SER
1	B	9	ASN
1	B	16	LYS
1	B	17	ALA
1	B	74	ASN
1	B	102	ASP
1	B	103	VAL
1	B	118	TRP
1	B	123	THR
1	B	161	ASP
1	B	202	ARG
1	B	287	SER
1	B	323	SER
1	B	327	VAL

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Mol	Chain	Res	Type
1	B	329	THR
1	C	12	ASP
1	C	86	ALA
1	C	111	PRO
1	C	121	ALA
1	C	135	LEU
1	C	141	ASP
1	C	205	ASN
1	C	304	LYS
1	C	323	SER
1	A	86	ALA
1	A	125	ASN
1	A	133	GLY
1	A	217	LYS
1	B	2	GLU
1	B	29	SER
1	B	49	THR
1	B	221	ASN
1	B	241	THR
1	B	307	ASN
1	B	319	GLU
1	B	321	ASP
1	C	27	GLY
1	C	133	GLY
1	C	162	ASN
1	C	202	ARG
1	C	204	GLY
1	C	237	ILE
1	C	276	SER
1	C	319	GLU
1	A	114	SER
1	A	233	ARG
1	A	249	ALA
1	B	35	THR
1	B	142	PHE
1	B	201	ASP
1	C	4	TYR
1	C	10	LYS
1	C	44	GLU
1	C	59	TYR
1	C	102	ASP
1	A	97	TYR

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Mol	Chain	Res	Type
1	A	201	ASP
1	A	265	PHE
1	A	319	GLU
1	A	326	TYR
1	B	7	ASP
1	B	32	ALA
1	B	124	ASP
1	B	234	ASN
1	C	127	MET
1	C	195	ARG
1	C	251	LYS
1	A	26	THR
1	A	220	ALA
1	A	279	LYS
1	B	3	ILE
1	B	181	PHE
1	C	110	ALA
1	C	192	ASN
1	B	100	VAL
1	B	325	SER
1	B	340	GLN
1	C	198	ASP
1	C	327	VAL
1	B	133	GLY
1	A	98	GLY
1	B	246	VAL

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	219/272 (80%)	172 (78%)	47 (22%)	1	10
1	B	222/272 (82%)	176 (79%)	46 (21%)	1	11
1	C	217/272 (80%)	146 (67%)	71 (33%)	0	3
All	All	658/816 (81%)	494 (75%)	164 (25%)	1	6

All (164) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	TYR
1	A	20	ARG
1	A	23	TRP
1	A	26	THR
1	A	28	ASP
1	A	54	PHE
1	A	80	PHE
1	A	83	LEU
1	A	95	ARG
1	A	100	VAL
1	A	117	THR
1	A	123	THR
1	A	134	LEU
1	A	135	LEU
1	A	138	ARG
1	A	139	ASN
1	A	141	ASP
1	A	147	ASP
1	A	161	ASP
1	A	165	ILE
1	A	169	ASN
1	A	187	THR
1	A	190	TYR
1	A	192	ASN
1	A	197	ASN
1	A	200	GLN
1	A	203	ASP
1	A	223	VAL
1	A	224	TYR
1	A	228	VAL
1	A	238	VAL
1	A	246	VAL
1	A	247	GLU
1	A	248	MET
1	A	260	GLN
1	A	265	PHE
1	A	299	THR
1	A	302	PHE
1	A	303	ASN
1	A	307	ASN
1	A	310	VAL
1	A	311	ASP

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Mol	Chain	Res	Type
1	A	317	LEU
1	A	318	ASP
1	A	321	ASP
1	A	329	THR
1	A	341	PHE
1	B	5	ASN
1	B	26	THR
1	B	29	SER
1	B	41	PHE
1	B	45	THR
1	B	47	ILE
1	B	50	ASP
1	B	64	ASP
1	B	65	ARG
1	B	74	ASN
1	B	77	ARG
1	B	80	PHE
1	B	85	TYR
1	B	95	ARG
1	B	105	SER
1	B	123	THR
1	B	124	ASP
1	B	130	ARG
1	B	134	LEU
1	B	141	ASP
1	B	143	PHE
1	B	153	ILE
1	B	156	GLN
1	B	163	HIS
1	B	187	THR
1	B	193	SER
1	B	199	GLN
1	B	202	ARG
1	B	203	ASP
1	B	212	ARG
1	B	225	LEU
1	B	246	VAL
1	B	264	ASP
1	B	271	ILE
1	B	274	VAL
1	B	294	ILE
1	B	303	ASN

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Mol	Chain	Res	Type
1	B	306	MET
1	B	307	ASN
1	B	310	VAL
1	B	312	TYR
1	B	318	ASP
1	B	320	ASN
1	B	337	ILE
1	B	338	THR
1	B	339	TYR
1	C	3	ILE
1	C	5	ASN
1	C	9	ASN
1	C	11	LEU
1	C	13	LEU
1	C	20	ARG
1	C	23	TRP
1	C	46	GLN
1	C	47	ILE
1	C	48	ASN
1	C	49	THR
1	C	50	ASP
1	C	51	LEU
1	C	52	THR
1	C	58	GLU
1	C	59	TYR
1	C	61	THR
1	C	70	GLN
1	C	75	LEU
1	C	76	VAL
1	C	85	TYR
1	C	88	VAL
1	C	92	ASP
1	C	93	TYR
1	C	97	TYR
1	C	99	ILE
1	C	100	VAL
1	C	101	TYR
1	C	102	ASP
1	C	103	VAL
1	C	104	GLU
1	C	117	THR
1	C	128	THR

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Mol	Chain	Res	Type
1	C	130	ARG
1	C	134	LEU
1	C	136	THR
1	C	137	TYR
1	C	147	ASP
1	C	158	LYS
1	C	163	HIS
1	C	171	ASP
1	C	173	VAL
1	C	175	TYR
1	C	176	THR
1	C	187	THR
1	C	191	SER
1	C	205	ASN
1	C	208	ARG
1	C	214	VAL
1	C	223	VAL
1	C	233	ARG
1	C	241	THR
1	C	243	THR
1	C	254	ASN
1	C	262	GLN
1	C	263	PHE
1	C	275	GLN
1	C	293	TYR
1	C	299	THR
1	C	303	ASN
1	C	309	TRP
1	C	311	ASP
1	C	313	ARG
1	C	315	ASN
1	C	316	LEU
1	C	317	LEU
1	C	319	GLU
1	C	321	ASP
1	C	330	ASP
1	C	338	THR
1	C	340	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	9	ASN
1	A	21	HIS
1	A	46	GLN
1	A	72	ASN
1	A	74	ASN
1	A	139	ASN
1	A	166	ASN
1	A	169	ASN
1	A	192	ASN
1	A	197	ASN
1	A	260	GLN
1	A	295	GLN
1	A	303	ASN
1	A	307	ASN
1	A	315	ASN
1	A	340	GLN
1	B	9	ASN
1	B	21	HIS
1	B	72	ASN
1	B	74	ASN
1	B	222	ASN
1	B	240	ASN
1	B	307	ASN
1	B	315	ASN
1	C	5	ASN
1	C	9	ASN
1	C	34	GLN
1	C	46	GLN
1	C	48	ASN
1	C	70	GLN
1	C	156	GLN
1	C	159	ASN
1	C	205	ASN
1	C	222	ASN
1	C	254	ASN
1	C	275	GLN

5.3.3 RNA ⓘ

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	AIC	C	401	-	22,26,26	1.49	3 (13%)	32,40,40	2.37	13 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AIC	C	401	-	-	0/12/47/47	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	AIC	C5-C4	-2.61	1.49	1.52
2	C	401	AIC	C6-S1	-2.57	1.80	1.85
2	C	401	AIC	C12-N3	3.40	1.49	1.47

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	AIC	C13-C14-N1	-5.38	106.30	118.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	AIC	C13-N3-C15	-5.02	87.33	93.89
2	C	401	AIC	C13-N3-C12	-3.91	113.40	117.36
2	C	401	AIC	C16-C6-C1	-3.29	105.61	110.88
2	C	401	AIC	C12-N3-C15	-3.25	118.36	125.99
2	C	401	AIC	C13-C14-C15	-2.11	81.57	85.20
2	C	401	AIC	O4-C15-N3	-2.01	128.74	131.64
2	C	401	AIC	C16-C6-S1	2.54	113.42	109.17
2	C	401	AIC	C6-C12-N3	2.61	110.38	106.45
2	C	401	AIC	S1-C13-N3	2.86	108.95	105.09
2	C	401	AIC	C1-C6-C12	2.88	118.01	111.56
2	C	401	AIC	C14-C13-N3	3.55	92.55	87.98
2	C	401	AIC	C14-C15-N3	3.82	97.07	91.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	AIC	1	0

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 ⓘ

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	339/341 (99%)	-0.37	5 (1%) 76 62	74, 107, 127, 148	0
1	B	340/341 (99%)	-0.37	4 (1%) 81 67	64, 105, 122, 125	0
1	C	334/341 (97%)	-0.22	5 (1%) 76 62	56, 113, 131, 141	0
All	All	1013/1023 (99%)	-0.32	14 (1%) 78 63	56, 107, 125, 148	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	7	ASP	5.3
1	B	334	ALA	4.0
1	C	282	ASN	3.9
1	C	163	HIS	3.4
1	A	218	TYR	3.1
1	C	204	GLY	3.1
1	A	289	ASP	2.9
1	B	25	THR	2.7
1	A	182	ASP	2.7
1	C	201	ASP	2.5
1	B	9	ASN	2.4
1	B	333	ALA	2.4
1	A	318	ASP	2.3
1	C	200	GLN	2.2

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	AIC	C	401	24/24	0.81	0.44	3.87	100,110,113,113	0

6.5 Other polymers [i](#)

There are no such residues in this entry.