



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2017 – 07:48 AM EDT

PDB ID : 2F86
Title : The Association Domain of C. elegans CaMKII
Authors : Rosenberg, O.S.; Kuriyan, J.
Deposited on : unknown
Resolution : 2.64 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
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

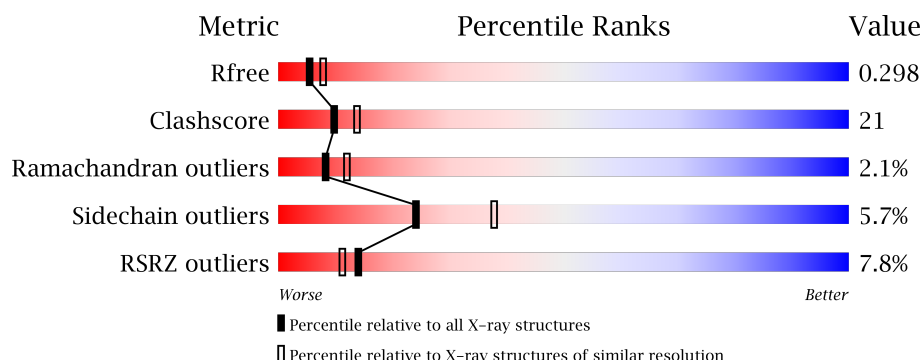
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.64 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}	100719	1044 (2.66-2.62)
Clashscore	112137	1092 (2.66-2.62)
Ramachandran outliers	110173	1077 (2.66-2.62)
Sidechain outliers	110143	1077 (2.66-2.62)
RSRZ outliers	101464	1047 (2.66-2.62)

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	B	143	<div> <div>10%</div> <div>60%</div> <div>27%</div> <div>•</div> <div>10%</div> </div>
1	D	143	<div> <div>8%</div> <div>54%</div> <div>32%</div> <div>•</div> <div>10%</div> </div>
1	F	143	<div> <div>8%</div> <div>55%</div> <div>32%</div> <div>•</div> <div>10%</div> </div>
1	H	143	<div> <div>6%</div> <div>52%</div> <div>35%</div> <div>•</div> <div>10%</div> </div>
1	J	143	<div> <div>9%</div> <div>57%</div> <div>29%</div> <div>•</div> <div>10%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	L	143	<div><div>6%</div><div><div></div><div>63%</div><div>22%</div><div>5%</div><div>10%</div></div></div>
1	N	143	<div><div>3%</div><div><div></div><div>55%</div><div>34%</div><div>•</div><div>10%</div></div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7335 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 Hypothetical protein K11E8.1d.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	129	Total	C	N	O	S	0	0	0
			1045	647	192	199	7			
1	D	129	Total	C	N	O	S	0	0	0
			1045	647	192	199	7			
1	F	129	Total	C	N	O	S	0	0	0
			1045	647	192	199	7			
1	H	129	Total	C	N	O	S	0	0	0
			1045	647	192	199	7			
1	J	129	Total	C	N	O	S	0	0	0
			1045	647	192	199	7			
1	L	129	Total	C	N	O	S	0	0	0
			1045	647	192	199	7			
1	N	129	Total	C	N	O	S	0	0	0
			1045	647	192	199	7			

- Molecule 2 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	O	0	0
			3	3		
2	D	2	Total	O	0	0
			2	2		
2	F	1	Total	O	0	0
			1	1		
2	H	3	Total	O	0	0
			3	3		
2	J	3	Total	O	0	0
			3	3		
2	L	5	Total	O	0	0
			5	5		
2	N	3	Total	O	0	0
			3	3		

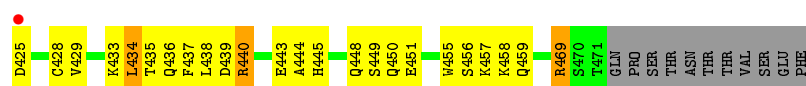
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Chain B:
-
- 10% 60% 27% 10%
- | Residue Type | Count |
|--------------|-------|
| ASP | 1 |
| ASP | 1 |
| N343 | 1 |
| D344 | 1 |
| S345 | 1 |
| E346 | 1 |
| K347 | 1 |
| D352 | 1 |
| I353 | 1 |
| V356 | 1 |
| T357 | 1 |
| Q358 | 1 |
| T359 | 1 |
| L360 | 1 |
| L361 | 1 |
| F369 | 1 |
| T373 | 1 |
| R374 | 1 |
| T381 | 1 |
| C382 | 1 |
| F383 | 1 |
| L391 | 1 |
| N405 | 1 |
| R406 | 1 |
| K407 | 1 |
| N408 | 1 |
| Q409 | 1 |
| V410 | 1 |
| H411 | 1 |
| T412 | 1 |
| T413 | 1 |
| M414 | 1 |
| L415 | 1 |
| N416 | 1 |
| E424 | 1 |
| V429 | 1 |
| L434 | 1 |
| T435 | 1 |
| Q436 | 1 |
| F437 | 1 |
| L438 | 1 |
| D439 | 1 |
| R440 | 1 |
| N441 | 1 |
- | Residue Type | Count |
|--------------|-------|
| Q448 | 1 |
| S449 | 1 |
| Q450 | 1 |
| E451 | 1 |
| W455 | 1 |
| S456 | 1 |
| K457 | 1 |
| G460 | 1 |
| R461 | 1 |
| R469 | 1 |
| S470 | 1 |
| T471 | 1 |
| GLN | 1 |
| PRO | 1 |
| SER | 1 |
| THR | 1 |
| ASN | 1 |
| THR | 1 |
| THR | 1 |
| VAL | 1 |
| SER | 1 |
| SER | 1 |
| GLU | 1 |
| PHE | 1 |

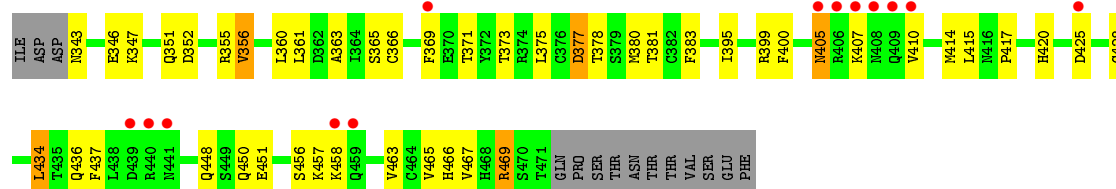
- Chain D:
-

- [illegible]

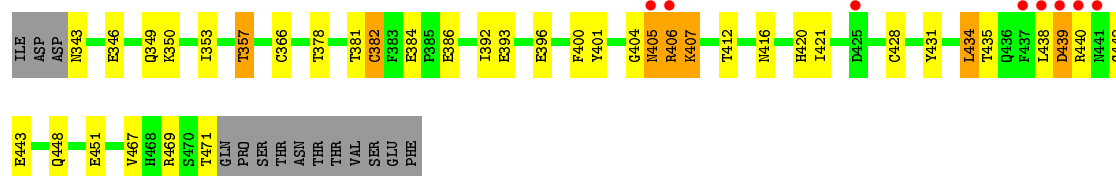
- Chain H: 



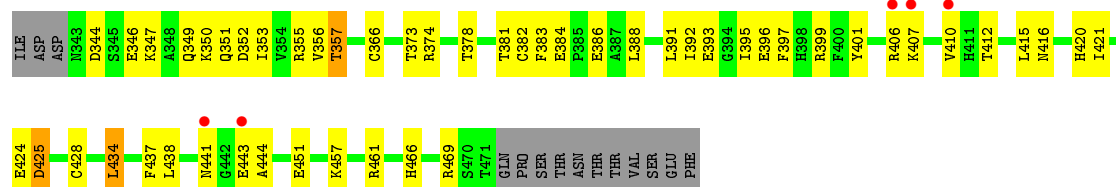
• Molecule 1: Hypothetical protein K11E8.1d



• Molecule 1: Hypothetical protein K11E8.1d



• Molecule 1: Hypothetical protein K11E8.1d



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	70.87Å 186.93Å 182.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.80 – 2.64 46.80 – 2.64	Depositor EDS
% Data completeness (in resolution range)	93.0 (46.80-2.64) 93.1 (46.80-2.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.65Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.248 , 0.301 0.248 , 0.298	Depositor DCC
R_{free} test set	3343 reflections (9.97%)	DCC
Wilson B-factor (Å ²)	45.2	Xtriage
Anisotropy	0.074	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	7335	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.43	0/1065	0.70	0/1438
1	D	0.42	0/1065	0.65	0/1438
1	F	0.38	0/1065	0.64	0/1438
1	H	0.47	0/1065	0.71	0/1438
1	J	0.39	0/1065	0.64	0/1438
1	L	0.43	0/1065	0.65	0/1438
1	N	0.44	0/1065	0.64	0/1438
All	All	0.42	0/7455	0.66	0/10066

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 [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	B	1045	0	1008	46	0
1	D	1045	0	1008	48	0
1	F	1045	0	1008	43	0
1	H	1045	0	1008	50	0
1	J	1045	0	1008	45	0
1	L	1045	0	1008	34	0
1	N	1045	0	1008	51	0
2	B	3	0	0	0	0
2	D	2	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	1	0	0	0	0
2	H	3	0	0	0	0
2	J	3	0	0	0	0
2	L	5	0	0	0	0
2	N	3	0	0	0	0
All	All	7335	0	7056	308	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 21.

All (308) 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:N:353:ILE:O	1:N:357:THR:HG22	1.56	1.05
1:H:425:ASP:HB3	1:H:457:LYS:HB3	1.03	1.02
1:H:425:ASP:HB3	1:H:457:LYS:CB	1.92	0.99
1:D:350:LYS:HE2	1:D:421:ILE:HD11	1.42	0.98
1:H:425:ASP:CB	1:H:457:LYS:HB3	1.94	0.97
1:F:451:GLU:HG2	1:F:469:ARG:HG2	1.45	0.97
1:J:469:ARG:HH11	1:J:469:ARG:HG3	1.32	0.93
1:L:353:ILE:O	1:L:357:THR:HG22	1.66	0.93
1:B:405:ASN:O	1:B:406:ARG:CB	2.16	0.93
1:D:421:ILE:HD12	1:D:421:ILE:H	1.32	0.92
1:H:412:THR:HG22	1:H:435:THR:HG23	1.51	0.91
1:L:407:LYS:H	1:L:407:LYS:HD2	1.35	0.91
1:J:366:CYS:HA	1:J:407:LYS:HG2	1.53	0.90
1:F:353:ILE:O	1:F:357:THR:HG23	1.74	0.88
1:H:348:ALA:HA	1:H:351:GLN:HE21	1.37	0.87
1:B:405:ASN:O	1:B:406:ARG:HB2	1.71	0.87
1:L:451:GLU:HG2	1:L:469:ARG:HG2	1.56	0.86
1:D:425:ASP:HB3	1:D:457:LYS:HB3	1.57	0.85
1:D:451:GLU:OE2	1:D:469:ARG:HD3	1.78	0.82
1:D:350:LYS:CE	1:D:421:ILE:HD11	2.12	0.80
1:F:381:THR:HG22	1:F:393:GLU:OE1	1.81	0.79
1:H:414:MET:HG2	1:H:417:PRO:HG3	1.64	0.78
1:F:352:ASP:HA	1:F:355:ARG:HH11	1.46	0.78
1:B:406:ARG:O	1:B:407:LYS:HG3	1.83	0.78
1:N:381:THR:CG2	1:N:391:LEU:HD11	2.14	0.77
1:H:469:ARG:HH11	1:H:469:ARG:HG3	1.50	0.76
1:B:353:ILE:O	1:B:357:THR:HG23	1.84	0.76
1:F:380:MET:HA	1:F:465:VAL:O	1.86	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:451:GLU:HG2	1:J:469:ARG:HG2	1.67	0.76
1:H:440:ARG:HD3	1:H:440:ARG:H	1.51	0.76
1:J:369:PHE:HB3	1:J:399:ARG:NH2	2.03	0.74
1:B:406:ARG:O	1:B:407:LYS:CG	2.35	0.74
1:D:357:THR:HG21	1:D:429:VAL:HG11	1.68	0.74
1:H:415:LEU:HD11	1:H:434:LEU:HD22	1.69	0.73
1:D:421:ILE:N	1:D:421:ILE:HD12	2.03	0.73
1:B:405:ASN:O	1:B:406:ARG:CG	2.36	0.73
1:L:407:LYS:HD2	1:L:407:LYS:N	2.04	0.72
1:J:469:ARG:HH11	1:J:469:ARG:CG	2.03	0.72
1:L:439:ASP:OD1	1:L:439:ASP:N	2.23	0.71
1:N:346:GLU:HG2	1:N:350:LYS:HE3	1.71	0.71
1:B:469:ARG:HG3	1:B:469:ARG:HH11	1.55	0.71
1:D:386:GLU:HB3	1:D:401:TYR:OH	1.91	0.70
1:D:451:GLU:HG2	1:D:469:ARG:HG2	1.74	0.70
1:J:380:MET:HA	1:J:465:VAL:O	1.91	0.69
1:D:396:GLU:OE1	1:D:399:ARG:NH2	2.24	0.69
1:L:440:ARG:O	1:L:443:GLU:HG2	1.92	0.69
1:H:448:GLN:HE21	1:H:450:GLN:HE21	1.37	0.69
1:H:349:GLN:HB3	1:H:421:ILE:HD11	1.73	0.69
1:B:369:PHE:O	1:B:373:THR:HG23	1.92	0.69
1:H:439:ASP:HB2	1:H:443:GLU:CG	2.23	0.69
1:B:405:ASN:O	1:B:406:ARG:HG3	1.92	0.69
1:D:420:HIS:HB2	1:D:428:CYS:SG	2.33	0.68
1:N:366:CYS:HB3	1:N:407:LYS:HE3	1.76	0.68
1:F:437:PHE:CE1	1:F:445:HIS:HB2	2.29	0.67
1:B:357:THR:HG22	1:B:455:TRP:CZ2	2.30	0.66
1:H:348:ALA:HA	1:H:351:GLN:NE2	2.10	0.66
1:N:352:ASP:OD1	1:N:355:ARG:NH2	2.28	0.66
1:F:357:THR:HG21	1:F:429:VAL:HG11	1.76	0.66
1:F:352:ASP:HA	1:F:355:ARG:NH1	2.11	0.66
1:D:357:THR:HG22	1:D:455:TRP:CZ2	2.31	0.65
1:L:400:PHE:CZ	1:N:438:LEU:HD22	2.31	0.65
1:N:386:GLU:HB3	1:N:401:TYR:OH	1.96	0.65
1:J:369:PHE:HD2	1:J:399:ARG:NE	1.95	0.65
1:L:366:CYS:HB2	1:L:407:LYS:HE2	1.80	0.64
1:F:366:CYS:HB3	1:F:407:LYS:CE	2.28	0.63
1:H:420:HIS:HB2	1:H:428:CYS:SG	2.39	0.63
1:J:415:LEU:HD11	1:J:434:LEU:HD22	1.78	0.63
1:F:419:VAL:HG12	1:F:420:HIS:N	2.14	0.63
1:H:349:GLN:HB3	1:H:421:ILE:CD1	2.29	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:377:ASP:OD1	1:J:378:THR:N	2.34	0.61
1:H:438:LEU:HA	1:H:443:GLU:O	2.00	0.61
1:D:386:GLU:HG2	1:D:401:TYR:OH	2.01	0.60
1:J:373:THR:HG23	1:J:399:ARG:HH22	1.64	0.60
1:J:410:VAL:HG13	1:J:436:GLN:O	2.01	0.60
1:H:469:ARG:HH11	1:H:469:ARG:CG	2.15	0.60
1:D:469:ARG:HG3	1:D:469:ARG:HH11	1.67	0.60
1:F:438:LEU:HA	1:F:443:GLU:O	2.00	0.60
1:L:400:PHE:HZ	1:N:438:LEU:HD22	1.66	0.60
1:J:373:THR:CG2	1:J:399:ARG:HH22	2.15	0.60
1:N:381:THR:HG22	1:N:466:HIS:CE1	2.37	0.59
1:F:443:GLU:HG3	1:F:445:HIS:NE2	2.16	0.59
1:L:386:GLU:HB3	1:L:401:TYR:OH	2.03	0.59
1:J:369:PHE:HB3	1:J:399:ARG:CZ	2.33	0.58
1:D:346:GLU:OE2	1:D:421:ILE:HD13	2.04	0.58
1:N:381:THR:HG23	1:N:391:LEU:HD11	1.84	0.58
1:B:352:ASP:O	1:B:356:VAL:HG22	2.04	0.58
1:D:381:THR:HG23	1:D:391:LEU:HD21	1.85	0.58
1:D:360:LEU:O	1:D:364:ILE:HG13	2.03	0.58
1:F:438:LEU:HD12	1:F:438:LEU:H	1.68	0.58
1:B:439:ASP:HB2	1:B:443:GLU:HG3	1.84	0.58
1:D:369:PHE:O	1:D:373:THR:HG23	2.04	0.57
1:L:382:CYS:HB2	1:L:467:VAL:HG13	1.85	0.57
1:D:412:THR:HG22	1:D:435:THR:OG1	2.03	0.57
1:H:369:PHE:O	1:H:373:THR:HG23	2.05	0.57
1:H:438:LEU:HD23	1:H:444:ALA:HA	1.86	0.57
1:L:431:TYR:CE1	1:L:451:GLU:HB2	2.39	0.57
1:N:381:THR:HB	1:N:466:HIS:ND1	2.21	0.56
1:J:410:VAL:HG13	1:J:437:PHE:HB3	1.87	0.56
1:D:386:GLU:HG2	1:D:401:TYR:CZ	2.40	0.56
1:J:352:ASP:O	1:J:356:VAL:HG22	2.06	0.56
1:N:469:ARG:HH11	1:N:469:ARG:HG3	1.71	0.56
1:B:357:THR:HG22	1:B:455:TRP:CE2	2.40	0.56
1:D:459:GLN:OE1	1:D:459:GLN:HA	2.06	0.56
1:N:451:GLU:HG3	1:N:469:ARG:HG3	1.88	0.56
1:B:411:HIS:O	1:B:435:THR:HA	2.06	0.56
1:H:439:ASP:HB2	1:H:443:GLU:HG2	1.87	0.56
1:N:373:THR:HG22	1:N:395:ILE:HG21	1.88	0.55
1:J:366:CYS:HA	1:J:407:LYS:CG	2.33	0.55
1:J:343:ASN:O	1:J:346:GLU:HB3	2.07	0.55
1:L:412:THR:HG22	1:L:435:THR:OG1	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:451:GLU:CG	1:N:469:ARG:HG3	2.37	0.55
1:D:352:ASP:O	1:D:356:VAL:HG22	2.07	0.55
1:L:349:GLN:NE2	1:L:421:ILE:HD12	2.22	0.54
1:L:405:ASN:O	1:L:406:ARG:C	2.46	0.54
1:N:349:GLN:NE2	1:N:421:ILE:HD12	2.22	0.54
1:H:439:ASP:HB2	1:H:443:GLU:HG3	1.88	0.54
1:B:405:ASN:C	1:B:406:ARG:HG3	2.28	0.54
1:B:361:LEU:HD12	1:B:414:MET:HE2	1.89	0.54
1:B:374:ARG:HD2	1:B:461:ARG:NH1	2.22	0.54
1:J:373:THR:CG2	1:J:399:ARG:NH2	2.71	0.54
1:B:410:VAL:HA	1:B:436:GLN:O	2.07	0.54
1:D:425:ASP:CB	1:D:457:LYS:HB3	2.34	0.54
1:B:438:LEU:HA	1:B:443:GLU:O	2.07	0.54
1:L:384:GLU:OE2	1:L:469:ARG:NH1	2.41	0.54
1:D:381:THR:CG2	1:D:391:LEU:HD11	2.38	0.53
1:F:366:CYS:HB3	1:F:407:LYS:HE3	1.90	0.53
1:H:369:PHE:CZ	1:H:399:ARG:HG3	2.43	0.53
1:H:357:THR:HG21	1:H:429:VAL:HG11	1.90	0.53
1:B:357:THR:HG21	1:B:429:VAL:HG11	1.91	0.53
1:J:448:GLN:HE21	1:J:450:GLN:HE21	1.57	0.53
1:L:434:LEU:CD1	1:L:448:GLN:HG3	2.39	0.53
1:D:421:ILE:CD1	1:D:421:ILE:H	2.13	0.53
1:D:346:GLU:HG3	1:D:421:ILE:HG12	1.91	0.52
1:J:352:ASP:HA	1:J:355:ARG:NH2	2.24	0.52
1:N:346:GLU:O	1:N:350:LYS:HG3	2.08	0.52
1:J:369:PHE:HD2	1:J:399:ARG:CD	2.22	0.52
1:F:353:ILE:O	1:F:356:VAL:HG22	2.09	0.52
1:H:425:ASP:O	1:H:456:SER:HA	2.10	0.52
1:N:415:LEU:HD11	1:N:434:LEU:HD22	1.91	0.52
1:D:357:THR:HG22	1:D:455:TRP:HZ2	1.73	0.52
1:B:381:THR:HG23	1:B:391:LEU:HD21	1.91	0.52
1:J:347:LYS:O	1:J:351:GLN:HG3	2.10	0.51
1:B:374:ARG:HD2	1:B:461:ARG:HH12	1.74	0.51
1:N:425:ASP:OD2	1:N:457:LYS:HB3	2.10	0.51
1:D:386:GLU:CG	1:D:401:TYR:OH	2.59	0.51
1:F:415:LEU:O	1:F:417:PRO:HD3	2.10	0.51
1:F:404:GLY:O	1:F:406:ARG:N	2.43	0.51
1:J:373:THR:HG21	1:J:399:ARG:NH2	2.25	0.51
1:D:353:ILE:O	1:D:357:THR:HG23	2.11	0.51
1:H:353:ILE:O	1:H:357:THR:HG23	2.10	0.51
1:D:381:THR:HG21	1:D:391:LEU:HD11	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:434:LEU:HD23	1:N:397:PHE:HE2	1.76	0.50
1:D:381:THR:HG22	1:D:382:CYS:N	2.27	0.50
1:N:381:THR:CG2	1:N:466:HIS:CE1	2.95	0.50
1:F:346:GLU:HG3	1:F:421:ILE:HG13	1.94	0.49
1:J:420:HIS:HB2	1:J:428:CYS:SG	2.52	0.49
1:H:448:GLN:NE2	1:H:450:GLN:HE21	2.07	0.49
1:L:382:CYS:SG	1:L:384:GLU:HG2	2.52	0.49
1:F:451:GLU:HG2	1:F:469:ARG:CG	2.31	0.49
1:J:469:ARG:HG3	1:J:469:ARG:NH1	2.12	0.49
1:N:381:THR:CG2	1:N:466:HIS:ND1	2.74	0.49
1:D:355:ARG:HH12	1:D:356:VAL:HG13	1.77	0.49
1:L:405:ASN:O	1:L:406:ARG:O	2.31	0.49
1:F:353:ILE:HA	1:F:356:VAL:HG22	1.95	0.49
1:F:419:VAL:CG1	1:F:420:HIS:N	2.75	0.49
1:J:361:LEU:HD12	1:J:414:MET:HE3	1.94	0.49
1:D:386:GLU:CB	1:D:401:TYR:OH	2.59	0.49
1:N:382:CYS:HB3	1:N:392:ILE:HB	1.94	0.49
1:F:413:THR:HG22	1:F:415:LEU:HD23	1.94	0.49
1:B:451:GLU:HG3	1:B:469:ARG:HG3	1.95	0.48
1:D:350:LYS:HE2	1:D:421:ILE:CD1	2.29	0.48
1:N:441:ASN:HB2	1:N:443:GLU:HG3	1.94	0.48
1:J:377:ASP:O	1:J:395:ILE:HD11	2.14	0.48
1:B:446:THR:O	1:N:388:LEU:HD11	2.12	0.48
1:F:412:THR:HG22	1:F:435:THR:HG23	1.95	0.48
1:J:410:VAL:CG1	1:J:437:PHE:HB3	2.43	0.48
1:H:359:THR:HG22	1:H:375:LEU:HD11	1.96	0.48
1:F:437:PHE:CD1	1:F:437:PHE:C	2.87	0.47
1:H:469:ARG:NH1	1:H:469:ARG:CG	2.76	0.47
1:F:469:ARG:HG3	1:F:469:ARG:HH11	1.79	0.47
1:J:371:THR:HG22	1:J:375:LEU:HD12	1.97	0.47
1:L:382:CYS:HB2	1:L:467:VAL:CG1	2.43	0.47
1:L:343:ASN:O	1:L:346:GLU:N	2.48	0.47
1:N:366:CYS:CB	1:N:407:LYS:HE3	2.45	0.47
1:B:424:GLU:O	1:B:424:GLU:HG2	2.15	0.47
1:N:352:ASP:O	1:N:356:VAL:HG22	2.15	0.47
1:B:469:ARG:CG	1:B:469:ARG:HH11	2.25	0.47
1:H:422:ILE:HG22	1:H:423:GLY:N	2.29	0.47
1:J:360:LEU:O	1:J:363:ALA:HB3	2.15	0.47
1:B:407:LYS:O	1:B:408:ASN:HB2	2.15	0.46
1:B:451:GLU:HG3	1:B:469:ARG:CG	2.46	0.46
1:H:347:LYS:O	1:H:351:GLN:HG3	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:458:LYS:HD2	1:J:463:VAL:HG21	1.97	0.46
1:N:469:ARG:HH11	1:N:469:ARG:CG	2.27	0.46
1:F:381:THR:HB	1:F:391:LEU:HD21	1.96	0.46
1:N:420:HIS:HB2	1:N:428:CYS:SG	2.55	0.46
1:D:349:GLN:NE2	1:D:421:ILE:HG23	2.31	0.46
1:H:350:LYS:O	1:H:354:VAL:HG23	2.16	0.46
1:B:356:VAL:HG23	1:B:357:THR:H	1.81	0.46
1:H:369:PHE:CE2	1:H:399:ARG:HG3	2.51	0.46
1:B:441:ASN:HD22	1:B:443:GLU:CD	2.18	0.46
1:H:373:THR:HG22	1:H:395:ILE:HD12	1.98	0.46
1:H:448:GLN:HG2	1:H:449:SER:N	2.31	0.46
1:N:438:LEU:HD13	1:N:444:ALA:HA	1.97	0.46
1:B:457:LYS:HE3	1:B:460:GLY:O	2.16	0.46
1:N:349:GLN:HE21	1:N:421:ILE:HD12	1.81	0.46
1:F:371:THR:O	1:F:375:LEU:HG	2.16	0.46
1:N:451:GLU:HG3	1:N:469:ARG:CG	2.46	0.46
1:B:439:ASP:HB3	1:B:440:ARG:H	1.62	0.45
1:N:347:LYS:O	1:N:347:LYS:HG2	2.15	0.45
1:N:374:ARG:HD2	1:N:461:ARG:HH12	1.81	0.45
1:L:440:ARG:C	1:L:442:GLY:H	2.19	0.45
1:H:357:THR:HG22	1:H:455:TRP:CZ2	2.51	0.45
1:B:356:VAL:O	1:B:359:THR:HB	2.16	0.45
1:F:366:CYS:HB3	1:F:407:LYS:HE2	1.99	0.45
1:H:433:LYS:HD3	1:H:451:GLU:OE2	2.17	0.45
1:D:412:THR:HA	1:D:434:LEU:O	2.17	0.45
1:D:405:ASN:O	1:D:406:ARG:C	2.55	0.44
1:B:448:GLN:NE2	1:B:450:GLN:NE2	2.65	0.44
1:F:360:LEU:O	1:F:363:ALA:HB3	2.18	0.44
1:F:410:VAL:HG12	1:F:411:HIS:N	2.32	0.44
1:D:422:ILE:O	1:D:426:ALA:HB3	2.17	0.44
1:H:451:GLU:HG2	1:H:469:ARG:HG3	2.00	0.44
1:N:346:GLU:CG	1:N:350:LYS:HE3	2.42	0.44
1:N:381:THR:HG22	1:N:382:CYS:N	2.32	0.44
1:B:391:LEU:HD23	1:B:391:LEU:C	2.38	0.44
1:H:381:THR:HA	1:H:392:ILE:O	2.17	0.44
1:J:434:LEU:HA	1:J:434:LEU:HD12	1.88	0.44
1:L:439:ASP:OD2	1:L:443:GLU:HG3	2.17	0.44
1:B:438:LEU:HD23	1:B:443:GLU:C	2.38	0.43
1:L:420:HIS:HB2	1:L:428:CYS:SG	2.58	0.43
1:D:370:GLU:HA	1:D:370:GLU:OE1	2.18	0.43
1:N:396:GLU:OE1	1:N:399:ARG:NH1	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:406:ARG:O	1:B:407:LYS:HG2	2.18	0.43
1:F:399:ARG:O	1:F:400:PHE:C	2.55	0.43
1:H:357:THR:O	1:H:361:LEU:HG	2.18	0.43
1:L:406:ARG:HB3	1:L:407:LYS:HD2	2.01	0.43
1:F:356:VAL:HG23	1:F:357:THR:N	2.33	0.43
1:F:469:ARG:HG3	1:F:469:ARG:NH1	2.33	0.43
1:J:381:THR:O	1:J:466:HIS:HA	2.17	0.43
1:B:343:ASN:O	1:B:347:LYS:N	2.46	0.43
1:F:407:LYS:HB2	1:F:407:LYS:HE3	1.79	0.43
1:L:353:ILE:O	1:L:357:THR:CG2	2.51	0.43
1:F:457:LYS:HE2	1:F:460:GLY:O	2.18	0.43
1:D:422:ILE:O	1:D:423:GLY:C	2.57	0.43
1:H:384:GLU:OE2	1:H:469:ARG:NH2	2.52	0.43
1:N:410:VAL:HG22	1:N:437:PHE:HB2	2.00	0.43
1:D:417:PRO:HA	1:D:431:TYR:HB3	2.01	0.43
1:H:357:THR:HG22	1:H:455:TRP:NE1	2.33	0.43
1:J:369:PHE:CD2	1:J:399:ARG:HD3	2.54	0.42
1:J:425:ASP:HA	1:J:457:LYS:HB3	2.01	0.42
1:N:384:GLU:OE2	1:N:469:ARG:NH2	2.52	0.42
1:D:461:ARG:HH11	1:D:461:ARG:HG2	1.84	0.42
1:L:400:PHE:CZ	1:N:438:LEU:CD2	3.00	0.42
1:F:352:ASP:CA	1:F:355:ARG:NH1	2.81	0.42
1:J:369:PHE:CD2	1:J:399:ARG:CD	3.02	0.42
1:N:434:LEU:HA	1:N:434:LEU:HD12	1.83	0.42
1:F:421:ILE:C	1:F:422:ILE:HG13	2.39	0.42
1:L:346:GLU:O	1:L:350:LYS:HG3	2.19	0.42
1:N:347:LYS:O	1:N:351:GLN:HG3	2.19	0.42
1:B:406:ARG:C	1:B:407:LYS:HG3	2.39	0.42
1:B:408:ASN:C	1:B:409:GLN:HG3	2.40	0.42
1:D:457:LYS:HE2	1:D:460:GLY:O	2.19	0.42
1:B:356:VAL:HG23	1:B:357:THR:N	2.34	0.42
1:B:448:GLN:HE21	1:B:450:GLN:HE21	1.67	0.42
1:F:401:TYR:CE1	1:H:436:GLN:NE2	2.88	0.42
1:J:355:ARG:HB3	1:J:355:ARG:CZ	2.49	0.42
1:H:437:PHE:CZ	1:H:445:HIS:HB2	2.55	0.42
1:H:369:PHE:HA	1:H:372:TYR:HB3	2.02	0.42
1:H:434:LEU:HA	1:H:434:LEU:HD12	1.84	0.42
1:H:357:THR:HG22	1:H:455:TRP:CE2	2.54	0.42
1:N:441:ASN:HB2	1:N:443:GLU:CG	2.49	0.42
1:F:401:TYR:HE1	1:H:436:GLN:NE2	2.18	0.41
1:J:469:ARG:CG	1:J:469:ARG:NH1	2.67	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:373:THR:HG22	1:N:395:ILE:HD13	2.01	0.41
1:B:434:LEU:HD23	1:N:397:PHE:CE2	2.54	0.41
1:H:353:ILE:O	1:H:356:VAL:HG22	2.20	0.41
1:L:381:THR:HA	1:L:392:ILE:O	2.19	0.41
1:N:424:GLU:O	1:N:424:GLU:HG2	2.20	0.41
1:N:374:ARG:HD2	1:N:461:ARG:NH1	2.35	0.41
1:J:410:VAL:HG22	1:J:437:PHE:HB2	2.03	0.41
1:L:434:LEU:HD12	1:L:434:LEU:HA	1.84	0.41
1:L:471:THR:O	1:L:471:THR:CG2	2.68	0.41
1:B:412:THR:HG22	1:B:435:THR:HG23	2.01	0.41
1:H:443:GLU:HG2	1:H:443:GLU:H	1.68	0.41
1:L:404:GLY:O	1:L:406:ARG:N	2.54	0.41
1:F:352:ASP:O	1:F:356:VAL:HG13	2.21	0.41
1:F:404:GLY:C	1:F:406:ARG:H	2.23	0.41
1:J:369:PHE:HD2	1:J:399:ARG:CZ	2.34	0.41
1:J:456:SER:O	1:J:463:VAL:HG22	2.20	0.41
1:F:433:LYS:HD3	1:F:451:GLU:OE2	2.20	0.41
1:N:381:THR:CG2	1:N:382:CYS:N	2.83	0.41
1:N:392:ILE:HG22	1:N:393:GLU:N	2.36	0.41
1:D:357:THR:O	1:D:361:LEU:HG	2.21	0.41
1:D:383:PHE:CE2	1:D:391:LEU:HB2	2.56	0.41
1:B:434:LEU:HA	1:B:434:LEU:HD12	1.90	0.41
1:J:414:MET:HG2	1:J:417:PRO:HG3	2.02	0.41
1:N:412:THR:HA	1:N:434:LEU:O	2.20	0.41
1:D:387:ALA:O	1:D:390:ASN:HB2	2.21	0.40
1:J:369:PHE:HD1	1:J:369:PHE:H	1.65	0.40
1:J:451:GLU:OE2	1:J:469:ARG:HD3	2.20	0.40
1:J:400:PHE:CZ	1:L:438:LEU:HG	2.57	0.40
1:N:349:GLN:NE2	1:N:421:ILE:HG23	2.37	0.40
1:D:469:ARG:NH1	1:D:469:ARG:HG3	2.33	0.40
1:F:415:LEU:O	1:F:416:ASN:C	2.59	0.40
1:L:381:THR:HG22	1:L:393:GLU:HG2	2.03	0.40
1:D:381:THR:HB	1:D:466:HIS:ND1	2.37	0.40
1:H:458:LYS:HB3	1:H:459:GLN:OE1	2.22	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	B	127/143 (89%)	116 (91%)	9 (7%)	2 (2%)	11	16
1	D	127/143 (89%)	117 (92%)	5 (4%)	5 (4%)	3	4
1	F	127/143 (89%)	116 (91%)	7 (6%)	4 (3%)	5	7
1	H	127/143 (89%)	117 (92%)	9 (7%)	1 (1%)	22	34
1	J	127/143 (89%)	115 (91%)	10 (8%)	2 (2%)	11	16
1	L	127/143 (89%)	112 (88%)	12 (9%)	3 (2%)	7	9
1	N	127/143 (89%)	120 (94%)	5 (4%)	2 (2%)	11	16
All	All	889/1001 (89%)	813 (92%)	57 (6%)	19 (2%)	8	12

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	406	ARG
1	D	406	ARG
1	F	405	ASN
1	F	440	ARG
1	L	405	ASN
1	L	406	ARG
1	N	406	ARG
1	B	407	LYS
1	D	388	LEU
1	D	405	ASN
1	J	377	ASP
1	J	405	ASN
1	F	400	PHE
1	L	416	ASN
1	N	416	ASN
1	D	416	ASN
1	F	416	ASN
1	H	422	ILE
1	D	389	GLY

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	B	116/130 (89%)	111 (96%)	5 (4%)	33	53
1	D	116/130 (89%)	110 (95%)	6 (5%)	27	43
1	F	116/130 (89%)	108 (93%)	8 (7%)	18	28
1	H	116/130 (89%)	109 (94%)	7 (6%)	22	35
1	J	116/130 (89%)	109 (94%)	7 (6%)	22	35
1	L	116/130 (89%)	109 (94%)	7 (6%)	22	35
1	N	116/130 (89%)	110 (95%)	6 (5%)	27	43
All	All	812/910 (89%)	766 (94%)	46 (6%)	24	38

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	383	PHE
1	B	416	ASN
1	B	434	LEU
1	B	441	ASN
1	B	469	ARG
1	D	373	THR
1	D	388	LEU
1	D	421	ILE
1	D	424	GLU
1	D	441	ASN
1	D	469	ARG
1	F	344	ASP
1	F	357	THR
1	F	378	THR
1	F	383	PHE
1	F	391	LEU
1	F	434	LEU
1	F	438	LEU
1	F	439	ASP
1	H	344	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	378	THR
1	H	399	ARG
1	H	408	ASN
1	H	434	LEU
1	H	440	ARG
1	H	469	ARG
1	J	356	VAL
1	J	365	SER
1	J	383	PHE
1	J	405	ASN
1	J	434	LEU
1	J	467	VAL
1	J	469	ARG
1	L	357	THR
1	L	378	THR
1	L	382	CYS
1	L	396	GLU
1	L	407	LYS
1	L	434	LEU
1	L	439	ASP
1	N	344	ASP
1	N	357	THR
1	N	378	THR
1	N	383	PHE
1	N	425	ASP
1	N	434	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	351	GLN
1	B	390	ASN
1	B	398	HIS
1	B	411	HIS
1	B	441	ASN
1	B	445	HIS
1	B	448	GLN
1	D	349	GLN
1	D	351	GLN
1	D	390	ASN
1	D	441	ASN
1	D	448	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	468	HIS
1	F	349	GLN
1	F	351	GLN
1	F	468	HIS
1	H	351	GLN
1	H	358	GLN
1	H	390	ASN
1	H	411	HIS
1	H	436	GLN
1	H	448	GLN
1	J	349	GLN
1	J	390	ASN
1	J	436	GLN
1	J	450	GLN
1	J	468	HIS
1	L	349	GLN
1	L	351	GLN
1	L	390	ASN
1	L	436	GLN
1	L	445	HIS
1	L	448	GLN
1	L	468	HIS
1	N	351	GLN
1	N	358	GLN
1	N	398	HIS
1	N	416	ASN
1	N	468	HIS

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	B	129/143 (90%)	0.46	14 (10%) 6 4	23, 42, 93, 102	0
1	D	129/143 (90%)	0.45	11 (8%) 11 10	26, 42, 92, 103	0
1	F	129/143 (90%)	0.45	11 (8%) 11 10	31, 54, 93, 107	0
1	H	129/143 (90%)	0.30	8 (6%) 21 19	20, 37, 88, 95	0
1	J	129/143 (90%)	0.39	13 (10%) 8 5	30, 55, 94, 102	0
1	L	129/143 (90%)	0.38	8 (6%) 21 19	25, 42, 95, 102	0
1	N	129/143 (90%)	0.25	5 (3%) 40 36	23, 42, 93, 107	0
All	All	903/1001 (90%)	0.38	70 (7%) 14 11	20, 45, 94, 107	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	438	LEU	6.9
1	B	406	ARG	5.9
1	N	407	LYS	5.3
1	B	407	LYS	5.2
1	H	424	GLU	4.7
1	B	442	GLY	4.6
1	H	425	ASP	4.6
1	F	405	ASN	4.5
1	L	439	ASP	4.3
1	L	406	ARG	4.2
1	N	406	ARG	4.2
1	B	408	ASN	4.2
1	B	409	GLN	3.9
1	F	439	ASP	3.8
1	J	369	PHE	3.8
1	F	424	GLU	3.7
1	B	405	ASN	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	N	441	ASN	3.6
1	D	408	ASN	3.6
1	F	344	ASP	3.4
1	B	441	ASN	3.4
1	D	406	ARG	3.3
1	B	439	ASP	3.2
1	L	437	PHE	3.2
1	J	407	LYS	3.2
1	F	459	GLN	3.1
1	B	440	ARG	3.1
1	H	409	GLN	3.1
1	D	441	ASN	3.0
1	B	410	VAL	2.9
1	J	406	ARG	2.9
1	D	407	LYS	2.9
1	B	343	ASN	2.8
1	J	405	ASN	2.8
1	F	410	VAL	2.8
1	D	438	LEU	2.7
1	B	344	ASP	2.7
1	J	458	LYS	2.6
1	J	459	GLN	2.6
1	F	406	ARG	2.6
1	L	440	ARG	2.5
1	D	410	VAL	2.5
1	D	409	GLN	2.5
1	H	422	ILE	2.5
1	J	439	ASP	2.4
1	N	443	GLU	2.4
1	J	408	ASN	2.3
1	D	442	GLY	2.3
1	D	443	GLU	2.2
1	J	441	ASN	2.2
1	L	405	ASN	2.2
1	H	343	ASN	2.2
1	H	410	VAL	2.2
1	L	441	ASN	2.2
1	F	393	GLU	2.2
1	J	440	ARG	2.2
1	F	409	GLN	2.1
1	B	437	PHE	2.1
1	H	345	SER	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	N	410	VAL	2.1
1	D	370	GLU	2.1
1	J	409	GLN	2.1
1	J	410	VAL	2.1
1	H	406	ARG	2.1
1	B	346	GLU	2.1
1	D	437	PHE	2.1
1	J	425	ASP	2.1
1	L	425	ASP	2.1
1	F	461	ARG	2.0
1	F	407	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no 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.