



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 07:36 AM UTC

PDB ID : 4OW6 / pdb_00004ow6
Title : Crystal structure of Diphtheria Toxin at acidic pH
Authors : Leka, O.; Vallese, F.; Pirazzini, M.; Berto, P.; Montecucco, C.; Zanotti, G.
Deposited on : 2014-01-31
Resolution : 2.80 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

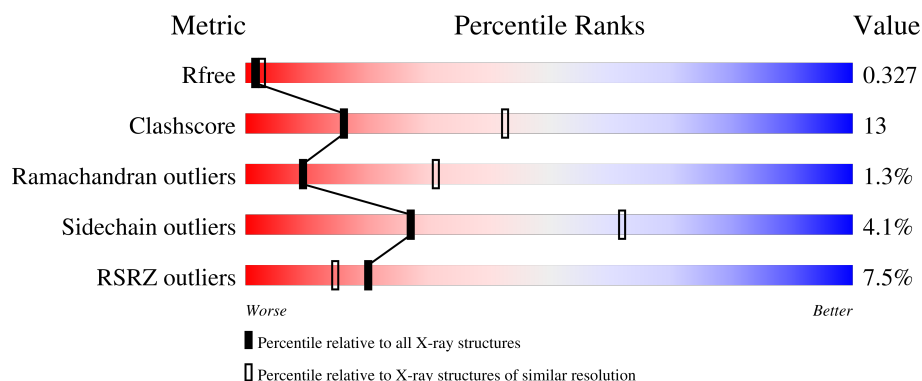
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	535	8% 61% 25% • 11%
1	B	535	6% 62% 26% • • 9%

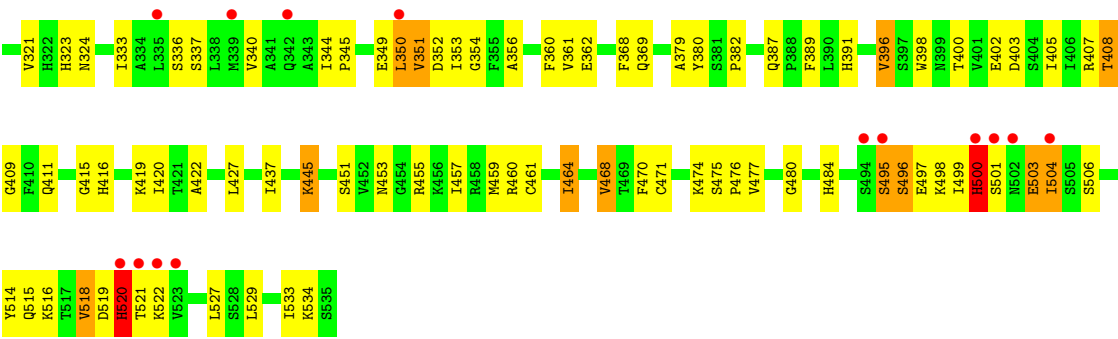
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 7374 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 Diphtheria toxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total	C	N	O	S	0	0	0
			3648	2298	620	719	11			
1	B	488	Total	C	N	O	S	0	0	0
			3726	2347	632	736	11			



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	47.44Å 141.28Å 176.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.13 – 2.80 45.13 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.2 (45.13-2.80) 94.2 (45.13-2.80)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.238 , 0.322 0.248 , 0.327	Depositor DCC
R_{free} test set	1453 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	39.1	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	7374	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% 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

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	0.66	0/3720	1.13	24/5041 (0.5%)
1	B	0.63	0/3798	1.10	18/5147 (0.3%)
All	All	0.65	0/7518	1.11	42/10188 (0.4%)

There are no bond length outliers.

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	466	GLY	N-CA-C	-11.49	98.45	115.00
1	A	272	VAL	N-CA-C	-9.74	99.20	110.21
1	B	387	GLN	CA-C-N	9.72	129.48	119.76
1	B	387	GLN	C-N-CA	9.72	129.48	119.76
1	B	260	LEU	N-CA-C	9.54	121.76	111.36
1	A	278	TYR	N-CA-C	9.24	121.35	111.28
1	A	351	VAL	N-CA-C	-9.09	97.94	109.30
1	B	503	GLU	N-CA-C	-7.67	101.08	113.19
1	A	110	LEU	N-CA-C	-7.19	104.50	113.20
1	B	437	ILE	CA-C-N	6.88	128.44	119.84
1	B	437	ILE	C-N-CA	6.88	128.44	119.84
1	A	465	ASP	N-CA-C	6.75	116.25	108.49
1	B	258	PRO	N-CA-CB	6.71	110.30	103.25
1	B	520	HIS	N-CA-C	-6.49	104.54	113.56
1	A	464	ILE	CA-C-N	-6.49	110.24	120.81
1	A	464	ILE	C-N-CA	-6.49	110.24	120.81
1	B	351	VAL	N-CA-C	6.48	117.94	109.58
1	B	495	SER	CA-C-N	6.32	133.08	121.70
1	B	495	SER	C-N-CA	6.32	133.08	121.70
1	B	500	HIS	N-CA-C	-6.18	100.84	110.42
1	A	44	GLY	N-CA-C	-6.01	106.43	114.25
1	B	324	ASN	N-CA-C	5.97	118.68	111.40
1	A	411	GLN	N-CA-C	-5.93	106.04	113.28
1	A	437	ILE	CA-C-N	5.84	125.98	119.32
1	A	437	ILE	C-N-CA	5.84	125.98	119.32

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	52	GLY	N-CA-C	5.83	119.08	110.63
1	A	434	LEU	CA-C-N	5.69	126.00	119.92
1	A	434	LEU	C-N-CA	5.69	126.00	119.92
1	A	277	ASN	CA-C-N	5.68	127.90	120.28
1	A	277	ASN	C-N-CA	5.68	127.90	120.28
1	A	272	VAL	CA-C-O	-5.64	115.86	122.13
1	B	116	GLU	N-CA-C	-5.48	104.94	111.69
1	B	518	VAL	N-CA-C	-5.33	102.03	108.53
1	A	112	GLU	CA-C-N	5.25	125.50	119.83
1	A	112	GLU	C-N-CA	5.25	125.50	119.83
1	B	468	VAL	N-CA-C	5.20	116.21	108.46
1	A	277	ASN	N-CA-C	5.04	117.78	109.72
1	A	138	LEU	CA-C-N	-5.04	114.76	119.90
1	A	138	LEU	C-N-CA	-5.04	114.76	119.90
1	A	70	GLU	N-CA-C	-5.02	107.00	113.23
1	B	464	ILE	CB-CA-C	-5.01	104.14	112.26
1	B	261	SER	N-CA-C	5.01	121.47	110.80

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	3648	0	3581	94	0
1	B	3726	0	3654	97	0
All	All	7374	0	7235	191	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 13.

All (191) 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:106:LEU:O	1:B:126:ARG:NH2	1.98	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:ASN:O	1:A:51:LYS:NZ	2.13	0.81
1:B:515:GLN:OE1	1:B:522:LYS:NZ	2.14	0.81
1:B:271:PRO:HB3	1:B:274:ALA:HA	1.64	0.79
1:B:499:ILE:HD11	1:B:503:GLU:HB2	1.67	0.77
1:A:202:ILE:HD13	1:A:321:VAL:HG21	1.66	0.76
1:A:437:ILE:HG21	1:A:440:LYS:HD2	1.67	0.76
1:A:436:THR:O	1:A:467:ASP:HB3	1.86	0.76
1:B:400:THR:HG22	1:B:402:GLU:H	1.49	0.76
1:A:86:PRO:O	1:A:133:ARG:NH2	2.20	0.74
1:A:391:HIS:HB3	1:A:527:LEU:HG	1.70	0.73
1:B:349:GLU:O	1:B:351:VAL:N	2.22	0.73
1:B:445:LYS:HD2	1:B:461:CYS:HB2	1.71	0.72
1:B:411:GLN:HG2	1:B:496:SER:HB2	1.71	0.71
1:A:103:LYS:NZ	1:A:112:GLU:O	2.23	0.69
1:A:450:ILE:HG13	1:A:459:MET:HE1	1.78	0.65
1:B:349:GLU:C	1:B:351:VAL:H	2.05	0.64
1:A:422:ALA:HB3	1:A:480:GLY:HA2	1.79	0.64
1:B:497:GLU:HG3	1:B:498:LYS:H	1.63	0.64
1:A:320:ALA:HB3	1:A:322:HIS:NE2	2.13	0.63
1:A:396:VAL:HG12	1:A:529:LEU:HD13	1.81	0.63
1:A:459:MET:HG2	1:A:471:CYS:HB3	1.80	0.63
1:A:337:SER:OG	1:A:356:ALA:O	2.14	0.62
1:B:402:GLU:HA	1:B:405:ILE:HD12	1.80	0.62
1:B:37:LYS:NZ	1:B:43:GLN:HB3	2.14	0.62
1:B:500:HIS:CD2	1:B:501:SER:N	2.69	0.61
1:A:408:THR:HG22	1:A:409:GLY:H	1.66	0.61
1:A:37:LYS:HE2	1:A:153:TRP:CD1	2.35	0.61
1:A:437:ILE:HD11	1:A:504:ILE:HG22	1.83	0.61
1:A:344:ILE:HG21	1:A:351:VAL:HB	1.83	0.60
1:B:396:VAL:HG22	1:B:420:ILE:HG12	1.82	0.60
1:A:173:ARG:HH21	1:A:207:ASP:HB2	1.66	0.60
1:B:337:SER:OG	1:B:356:ALA:O	2.19	0.59
1:A:425:THR:O	1:A:427:LEU:HD13	2.02	0.59
1:B:398:TRP:NE1	1:B:529:LEU:HG	2.18	0.58
1:A:314:MET:SD	1:A:371:VAL:HG21	2.43	0.58
1:A:323:HIS:HB3	1:A:329:VAL:HG22	1.85	0.58
1:B:267:THR:OG1	1:B:268:GLY:N	2.37	0.58
1:A:408:THR:HG21	1:A:499:ILE:HG22	1.86	0.58
1:B:42:THR:O	1:B:51:LYS:NZ	2.29	0.58
1:A:41:GLY:O	1:A:43:GLN:HG3	2.04	0.57
1:B:464:ILE:HD11	1:B:470:PHE:HB2	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:518:VAL:HG23	1:B:519:ASP:HB2	1.86	0.57
1:A:500:HIS:O	1:A:502:ASN:N	2.32	0.57
1:B:271:PRO:C	1:B:273:PHE:H	2.13	0.56
1:B:382:PRO:HG3	1:B:484:HIS:CE1	2.41	0.56
1:A:272:VAL:HG12	1:A:273:PHE:HB2	1.89	0.55
1:A:349:GLU:O	1:A:351:VAL:N	2.39	0.55
1:B:459:MET:HE3	1:B:471:CYS:HB3	1.88	0.55
1:A:165:ILE:HD11	1:A:170:ARG:HH11	1.72	0.55
1:A:352:ASP:CG	1:A:354:GLY:H	2.16	0.54
1:B:201:CYS:C	1:B:202:ILE:HG13	2.32	0.54
1:A:45:ASN:OD1	1:A:47:ASP:N	2.33	0.54
1:B:400:THR:HG22	1:B:402:GLU:N	2.21	0.54
1:B:408:THR:HG21	1:B:499:ILE:HG22	1.89	0.53
1:A:394:TYR:HB2	1:A:527:LEU:HD21	1.91	0.52
1:A:98:ASN:ND2	1:A:413:GLU:O	2.43	0.52
1:B:445:LYS:HZ1	1:B:460:ARG:HD3	1.74	0.52
1:B:260:LEU:HD12	1:B:261:SER:HA	1.90	0.52
1:B:460:ARG:HH21	1:B:474:LYS:NZ	2.07	0.52
1:A:272:VAL:O	1:A:274:ALA:N	2.37	0.52
1:B:500:HIS:CD2	1:B:501:SER:H	2.28	0.52
1:A:361:VAL:O	1:A:365:ILE:HG12	2.09	0.52
1:A:408:THR:HG22	1:A:409:GLY:N	2.24	0.52
1:B:415:GLY:C	1:B:416:HIS:CD2	2.87	0.52
1:B:445:LYS:NZ	1:B:460:ARG:HD3	2.24	0.52
1:B:206:TRP:CD1	1:B:369:GLN:HE21	2.28	0.51
1:B:284:ASN:HD21	1:B:308:PRO:HD2	1.74	0.51
1:B:408:THR:HG22	1:B:409:GLY:H	1.75	0.51
1:A:72:PRO:HG3	1:A:460:ARG:NH2	2.26	0.51
1:A:212:LYS:O	1:A:216:LYS:HG3	2.12	0.50
1:B:56:THR:HB	1:B:58:ASN:H	1.77	0.50
1:B:337:SER:HA	1:B:360:PHE:CE2	2.46	0.50
1:A:302:ALA:O	1:A:305:SER:OG	2.23	0.50
1:B:204:LEU:HD23	1:B:209:ILE:HD11	1.94	0.50
1:A:422:ALA:HB2	1:A:479:VAL:HG23	1.94	0.50
1:B:115:MET:HE2	1:B:150:ILE:HG22	1.94	0.50
1:B:337:SER:HA	1:B:360:PHE:HE2	1.76	0.50
1:B:7:ASP:OD2	1:B:10:LYS:N	2.43	0.50
1:B:314:MET:HG2	1:B:368:PHE:CE1	2.47	0.50
1:B:445:LYS:NZ	1:B:461:CYS:H	2.10	0.49
1:B:514:TYR:HE1	1:B:516:LYS:HE2	1.77	0.49
1:B:32:GLN:NE2	1:B:163:LEU:HB2	2.27	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:TYR:HB3	1:A:133:ARG:NH2	2.27	0.49
1:A:314:MET:HG2	1:A:368:PHE:CZ	2.47	0.49
1:A:437:ILE:HG23	1:A:438:PRO:HD2	1.94	0.49
1:A:449:HIS:CD2	1:A:456:LYS:HE3	2.48	0.49
1:B:94:LEU:HD11	1:B:136:LEU:HD13	1.93	0.49
1:B:283:VAL:O	1:B:287:GLN:HB2	2.13	0.48
1:A:380:TYR:CE2	1:A:419:LYS:HE2	2.48	0.48
1:B:460:ARG:HH21	1:B:474:LYS:HZ3	1.59	0.48
1:A:333:ILE:O	1:A:336:SER:HB3	2.13	0.48
1:A:170:ARG:HH21	1:A:172:LYS:NZ	2.11	0.48
1:A:90:LYS:HB2	1:A:131:ALA:HB3	1.96	0.48
1:A:49:ASP:OD1	1:A:113:PRO:HA	2.14	0.48
1:A:373:ASN:OD1	1:A:377:ARG:NE	2.39	0.47
1:B:349:GLU:HG3	1:B:350:LEU:N	2.28	0.47
1:A:395:ALA:HB3	1:A:421:THR:HB	1.96	0.47
1:B:32:GLN:HE22	1:B:163:LEU:HB2	1.79	0.47
1:B:315:GLY:HA3	1:B:323:HIS:CD2	2.49	0.47
1:B:500:HIS:HD2	1:B:501:SER:H	1.62	0.47
1:B:499:ILE:HG23	1:B:533:ILE:HG21	1.96	0.47
1:A:202:ILE:HD13	1:A:321:VAL:CG2	2.39	0.47
1:B:336:SER:O	1:B:340:VAL:HG23	2.14	0.47
1:A:184:GLN:C	1:A:186:CYS:H	2.23	0.47
1:A:131:ALA:O	1:A:133:ARG:N	2.44	0.46
1:A:170:ARG:HH21	1:A:172:LYS:HZ1	1.64	0.46
1:A:202:ILE:HG22	1:A:202:ILE:O	2.14	0.46
1:B:316:ILE:HD13	1:B:321:VAL:HA	1.96	0.46
1:A:106:LEU:O	1:A:126:ARG:NH2	2.49	0.46
1:B:457:ILE:HD12	1:B:477:VAL:HG22	1.97	0.46
1:B:519:ASP:HB3	1:B:521:THR:HB	1.96	0.46
1:A:48:ASP:HA	1:A:51:LYS:HE2	1.98	0.46
1:B:48:ASP:OD2	1:B:113:PRO:HG3	2.15	0.46
1:B:400:THR:N	1:B:403:ASP:OD2	2.48	0.46
1:B:391:HIS:HB3	1:B:527:LEU:HD23	1.98	0.46
1:B:14:MET:HE3	1:B:14:MET:HB2	1.76	0.46
1:B:389:PHE:HE2	1:B:527:LEU:HA	1.81	0.46
1:B:24:LYS:HE2	1:B:69:ASN:HD22	1.81	0.45
1:A:344:ILE:C	1:A:346:LEU:H	2.24	0.45
1:A:314:MET:HG2	1:A:368:PHE:CE1	2.52	0.45
1:A:353:ILE:H	1:A:353:ILE:HG13	1.57	0.45
1:A:415:GLY:C	1:A:416:HIS:CD2	2.94	0.45
1:A:500:HIS:CG	1:A:501:SER:N	2.84	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:GLN:HA	1:A:161:VAL:HB	1.97	0.45
1:A:287:GLN:HA	1:A:347:VAL:HG11	1.99	0.45
1:A:73:LEU:HD22	1:A:476:PRO:HD3	1.97	0.45
1:B:99:ALA:O	1:B:103:LYS:HG3	2.16	0.45
1:A:451:SER:O	1:A:485:ALA:HA	2.17	0.45
1:A:432:VAL:HG21	1:A:487:LEU:HD21	1.98	0.44
1:A:500:HIS:C	1:A:502:ASN:H	2.24	0.44
1:A:284:ASN:O	1:A:288:VAL:HG23	2.16	0.44
1:A:101:THR:O	1:A:105:GLU:HG2	2.18	0.44
1:A:384:HIS:CD2	1:A:384:HIS:H	2.34	0.44
1:A:421:THR:HG22	1:A:422:ALA:N	2.32	0.44
1:A:316:ILE:HD13	1:A:321:VAL:HA	2.00	0.44
1:B:86:PRO:O	1:B:133:ARG:NH1	2.40	0.44
1:A:349:GLU:C	1:A:351:VAL:N	2.76	0.43
1:B:106:LEU:HD22	1:B:127:PHE:CE1	2.53	0.43
1:A:204:LEU:HD11	1:A:329:VAL:HG21	1.99	0.43
1:B:504:ILE:HG23	1:B:506:SER:N	2.32	0.43
1:B:40:SER:HA	1:B:43:GLN:NE2	2.33	0.43
1:A:422:ALA:HB3	1:A:480:GLY:CA	2.48	0.43
1:B:141:ALA:O	1:B:144:SER:HB3	2.18	0.43
1:B:379:ALA:HA	1:B:453:ASN:ND2	2.33	0.43
1:A:2:ALA:HA	1:A:106:LEU:HD23	2.01	0.43
1:A:172:LYS:NZ	1:A:180:GLU:OE1	2.37	0.43
1:A:421:THR:HG23	1:A:484:HIS:ND1	2.33	0.43
1:B:274:ALA:HB3	1:B:277:ASN:CG	2.44	0.43
1:A:173:ARG:HH21	1:A:207:ASP:CB	2.32	0.43
1:B:290:ASP:OD1	1:B:293:THR:OG1	2.23	0.43
1:B:349:GLU:C	1:B:351:VAL:N	2.75	0.43
1:B:422:ALA:HB3	1:B:480:GLY:HA2	2.01	0.42
1:B:181:TYR:O	1:B:184:GLN:HB2	2.20	0.42
1:B:284:ASN:O	1:B:288:VAL:HG23	2.20	0.42
1:A:76:LYS:HE3	1:A:76:LYS:HB2	1.78	0.42
1:B:457:ILE:HD13	1:B:475:SER:HB2	2.02	0.42
1:A:24:LYS:HA	1:A:66:SER:O	2.19	0.42
1:B:79:GLY:HA2	1:B:167:PHE:CD2	2.55	0.42
1:B:210:ARG:HD3	1:B:362:GLU:OE2	2.19	0.42
1:A:23:THR:HG21	1:A:28:VAL:HA	2.01	0.42
1:B:271:PRO:C	1:B:273:PHE:N	2.77	0.42
1:B:315:GLY:HA3	1:B:323:HIS:CG	2.55	0.42
1:B:529:LEU:HD12	1:B:529:LEU:HA	1.90	0.42
1:A:350:LEU:O	1:A:350:LEU:HG	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:352:ASP:O	1:A:355:PHE:HB3	2.20	0.42
1:A:381:SER:HA	1:A:382:PRO:HD3	1.78	0.42
1:A:402:GLU:OE2	1:A:407:ARG:NH1	2.53	0.42
1:B:73:LEU:HD22	1:B:476:PRO:HD3	2.01	0.42
1:A:408:THR:CG2	1:A:409:GLY:H	2.32	0.41
1:A:421:THR:HG22	1:A:422:ALA:H	1.85	0.41
1:B:344:ILE:HB	1:B:345:PRO:HD3	2.01	0.41
1:B:400:THR:O	1:B:403:ASP:N	2.50	0.41
1:A:14:MET:HE3	1:A:14:MET:HB2	1.87	0.41
1:A:42:THR:O	1:A:43:GLN:HB2	2.19	0.41
1:B:352:ASP:CG	1:B:354:GLY:H	2.27	0.41
1:A:273:PHE:HE2	1:A:322:HIS:CE1	2.38	0.41
1:B:519:ASP:O	1:B:520:HIS:HB3	2.19	0.41
1:B:184:GLN:C	1:B:186:CYS:H	2.27	0.41
1:B:292:GLU:H	1:B:292:GLU:HG2	1.64	0.41
1:B:497:GLU:CG	1:B:498:LYS:H	2.31	0.41
1:A:529:LEU:HD12	1:A:529:LEU:HA	1.98	0.41
1:B:380:TYR:CE2	1:B:419:LYS:HE2	2.55	0.41
1:B:451:SER:HA	1:B:455:ARG:O	2.21	0.41
1:B:333:ILE:HG21	1:B:361:VAL:HG13	2.03	0.41
1:A:273:PHE:CE2	1:A:322:HIS:CE1	3.08	0.40
1:A:386:THR:HB	1:A:398:TRP:O	2.22	0.40
1:B:186:CYS:O	1:B:201:CYS:SG	2.79	0.40
1:B:407:ARG:HD3	1:B:534:LYS:HB2	2.03	0.40
1:B:445:LYS:HE3	1:B:445:LYS:HB3	1.24	0.40
1:B:166:ASN:HB3	1:B:169:THR:HB	2.02	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	471/535 (88%)	425 (90%)	39 (8%)	7 (2%)	8	28
1	B	482/535 (90%)	430 (89%)	47 (10%)	5 (1%)	12	38
All	All	953/1070 (89%)	855 (90%)	86 (9%)	12 (1%)	9	31

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	350	LEU
1	A	501	SER
1	A	519	ASP
1	B	350	LEU
1	A	467	ASP
1	B	78	GLY
1	B	261	SER
1	B	263	LEU
1	B	496	SER
1	A	78	GLY
1	A	132	SER
1	A	382	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	399/452 (88%)	385 (96%)	14 (4%)	32	67
1	B	407/452 (90%)	388 (95%)	19 (5%)	23	57
All	All	806/904 (89%)	773 (96%)	33 (4%)	27	62

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ILE
1	A	51	LYS
1	A	138	LEU
1	A	186	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	219	SER
1	A	289	ILE
1	A	312	SER
1	A	353	ILE
1	A	364	ILE
1	A	427	LEU
1	A	468	VAL
1	A	499	ILE
1	A	503	GLU
1	A	527	LEU
1	B	42	THR
1	B	56	THR
1	B	69	ASN
1	B	118	VAL
1	B	162	GLU
1	B	207	ASP
1	B	211	ASP
1	B	272	VAL
1	B	312	SER
1	B	353	ILE
1	B	396	VAL
1	B	408	THR
1	B	427	LEU
1	B	445	LYS
1	B	468	VAL
1	B	495	SER
1	B	500	HIS
1	B	504	ILE
1	B	520	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	71	ASN
1	A	117	GLN
1	A	324	ASN
1	A	484	HIS
1	B	151	ASN
1	B	175	GLN
1	B	366	ASN
1	B	372	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	500	HIS
1	B	520	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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	477/535 (89%)	0.59	42 (8%)	15 11	11, 32, 71, 98	0
1	B	488/535 (91%)	0.42	30 (6%)	27 20	13, 31, 68, 90	0
All	All	965/1070 (90%)	0.50	72 (7%)	20 15	11, 32, 70, 98	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	220	LEU	5.2
1	B	260	LEU	3.8
1	A	348	GLY	3.7
1	B	335	LEU	3.7
1	B	257	HIS	3.5
1	A	201	CYS	3.4
1	A	505	SER	3.4
1	A	274	ALA	3.4
1	B	272	VAL	3.4
1	A	409	GLY	3.3
1	A	350	LEU	3.2
1	A	275	GLY	3.2
1	A	534	LYS	3.1
1	A	267	THR	3.1
1	A	273	PHE	3.0
1	B	263	LEU	2.9
1	A	219	SER	2.9
1	B	218	GLU	2.9
1	A	294	ALA	2.9
1	A	424	ASN	2.8
1	B	274	ALA	2.8
1	A	200	SER	2.8
1	A	43	GLN	2.8
1	B	256	GLU	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	259	GLU	2.8
1	A	501	SER	2.8
1	A	342	GLN	2.8
1	B	277	ASN	2.8
1	B	342	GLN	2.7
1	A	291	SER	2.7
1	A	502	ASN	2.7
1	A	438	PRO	2.6
1	A	331	GLN	2.6
1	A	272	VAL	2.6
1	B	502	ASN	2.6
1	A	535	SER	2.6
1	B	220	LEU	2.6
1	A	531	PHE	2.6
1	A	499	ILE	2.5
1	B	495	SER	2.5
1	B	521	THR	2.5
1	B	504	ILE	2.5
1	A	39	LYS	2.5
1	A	500	HIS	2.4
1	B	520	HIS	2.4
1	B	271	PRO	2.4
1	A	44	GLY	2.4
1	B	522	LYS	2.3
1	A	202	ILE	2.3
1	B	186	CYS	2.3
1	B	339	MET	2.3
1	B	501	SER	2.3
1	A	352	ASP	2.3
1	B	500	HIS	2.3
1	B	187	ALA	2.2
1	A	408	THR	2.2
1	A	504	ILE	2.1
1	A	186	CYS	2.1
1	B	276	ALA	2.1
1	B	494	SER	2.1
1	A	355	PHE	2.1
1	B	523	VAL	2.1
1	A	410	PHE	2.1
1	A	341	ALA	2.1
1	A	349	GLU	2.1
1	A	278	TYR	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	278	TYR	2.1
1	A	322	HIS	2.0
1	B	350	LEU	2.0
1	B	258	PRO	2.0
1	A	344	ILE	2.0
1	A	347	VAL	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 oligosaccharides 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.