Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 05:50 pm BST

PDB ID	:	3CS0
Title	:	Crystal structure of DegP24
Authors	:	Krojer, T.; Sawa, J.; Schaefer, E.; Saibil, H.R.; Ehrmann, M.; Clausen, T.
Deposited on	:	2008-04-08
Resolution	:	3.00 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 following versions of software and data (see references ⓘ) were used in the production of this report:

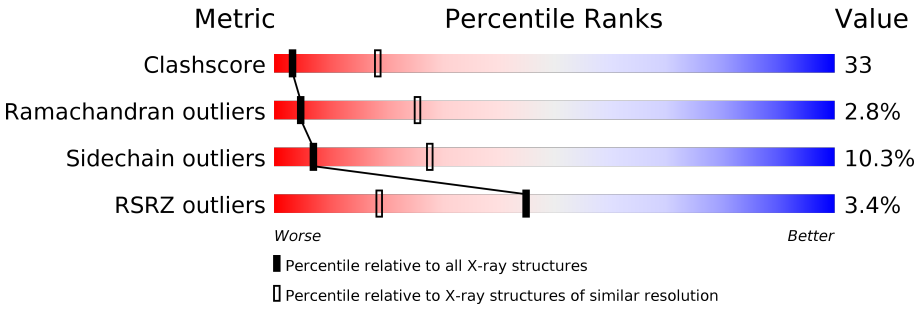
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 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 <=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	448	3%, 45%, 36%, 5%, 13%
2	B	5	100%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2893 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 Periplasmic serine endoprotease DegP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	Se	0	0	0
			2867	1783	506	565	13			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	210	ALA	SER	engineered mutation	UNP P0C0V0

- Molecule 2 is a protein called pentapeptide.

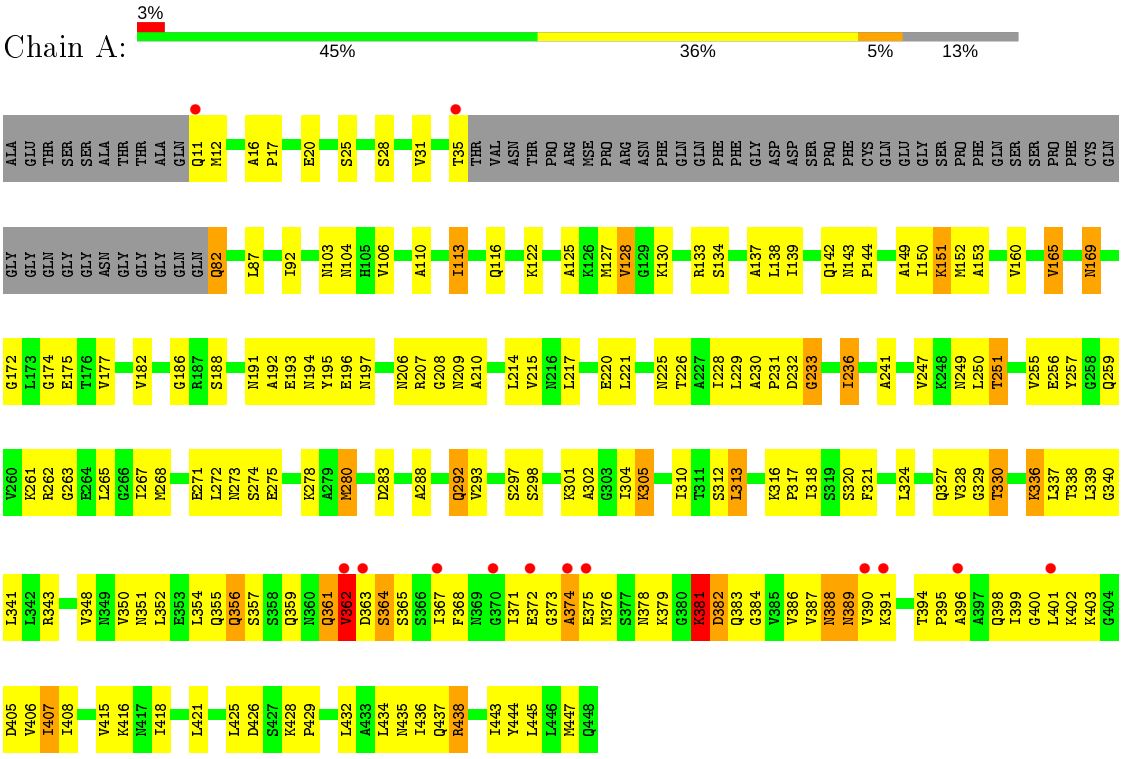
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	5	Total	C	N	O	0	0	0
			26	15	5	6			

3 Residue-property plots (i)

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.

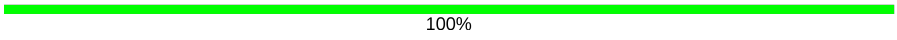
- Molecule 1: Periplasmic serine endoprotease DegP

Chain A:



- Molecule 2: pentapeptide

Chain B:



There are no outlier residues recorded for this chain.

4 Data and refinement statistics (i)

Property	Value	Source
Space group	F 4 3 2	Depositor
Cell constants a, b, c, α, β, γ	253.93Å 253.93Å 253.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 3.00 48.87 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (15.00-3.00) 98.9 (48.87-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.37 (at 3.01Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.212 , 0.274 0.208 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	67.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 70.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	2893	wwPDB-VP
Average B, all atoms (Å^2)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.46	0/2879	0.72	0/3865

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	2867	0	2957	193	0
2	B	26	0	7	0	0
All	All	2893	0	2964	193	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 33.

All (193) 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:364:SER:HA	1:A:376:MSE:HE2	1.39	1.05
1:A:382:ASP:HB3	1:A:416:LYS:HB3	1.38	1.02
1:A:206:ASN:H	1:A:209:ASN:HD22	1.06	1.02
1:A:372:GLU:HB2	1:A:395:PRO:HD2	1.39	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:ASN:HB3	1:A:194:ASN:HD22	1.27	0.96
1:A:191:ASN:HB3	1:A:194:ASN:ND2	1.85	0.91
1:A:313:LEU:HB2	1:A:318:ILE:HD11	1.50	0.91
1:A:341:LEU:HB2	1:A:348:VAL:HB	1.55	0.88
1:A:374:ALA:HB2	1:A:390:VAL:HG12	1.55	0.86
1:A:247:VAL:O	1:A:251:THR:HB	1.77	0.85
1:A:259:GLN:NE2	1:A:378:ASN:H	1.79	0.81
1:A:373:GLY:HA3	1:A:396:ALA:HB3	1.62	0.80
1:A:259:GLN:HE21	1:A:378:ASN:ND2	1.80	0.80
1:A:367:ILE:HD12	1:A:376:MSE:HE3	1.64	0.77
1:A:368:PHE:HB3	1:A:371:ILE:HD13	1.67	0.76
1:A:405:ASP:OD1	1:A:438:ARG:HD3	1.86	0.76
1:A:280:MSE:HA	1:A:280:MSE:HE3	1.67	0.76
1:A:432:LEU:HD23	1:A:447:MSE:SE	2.35	0.76
1:A:367:ILE:HG21	1:A:421:LEU:HD12	1.67	0.75
1:A:206:ASN:H	1:A:209:ASN:ND2	1.85	0.75
1:A:405:ASP:HB3	1:A:436:ILE:HD12	1.67	0.75
1:A:379:LYS:HB2	1:A:386:VAL:HG23	1.70	0.74
1:A:272:LEU:HD13	1:A:272:LEU:O	1.88	0.73
1:A:103:ASN:HD22	1:A:210:ALA:HB1	1.54	0.72
1:A:362:VAL:HG11	1:A:418:ILE:HD13	1.70	0.72
1:A:374:ALA:HB2	1:A:390:VAL:HA	1.72	0.72
1:A:150:ILE:HD13	1:A:221:LEU:HB2	1.71	0.72
1:A:374:ALA:HB2	1:A:390:VAL:CG1	2.21	0.71
1:A:16:ALA:HB3	1:A:17:PRO:HD3	1.73	0.71
1:A:133:ARG:O	1:A:194:ASN:HB3	1.91	0.71
1:A:374:ALA:HA	1:A:389:ASN:O	1.91	0.70
1:A:249:ASN:HD22	1:A:330:THR:CG2	2.03	0.69
1:A:153:ALA:HB2	1:A:220:GLU:HB3	1.74	0.69
1:A:390:VAL:HG22	1:A:403:LYS:HG2	1.75	0.69
1:A:228:ILE:O	1:A:228:ILE:HG13	1.92	0.68
1:A:169:ASN:HD22	1:A:169:ASN:C	1.97	0.67
1:A:188:SER:HB2	1:A:196:GLU:HG3	1.76	0.67
1:A:271:GLU:OE1	1:A:320:SER:HB2	1.94	0.67
1:A:262:ARG:H	1:A:359:GLN:NE2	1.90	0.67
1:A:259:GLN:HE22	1:A:378:ASN:H	1.41	0.66
1:A:142:GLN:O	1:A:143:ASN:HB2	1.96	0.66
1:A:273:ASN:HD21	1:A:275:GLU:HB2	1.60	0.66
1:A:304:ILE:HG12	1:A:341:LEU:HD11	1.80	0.64
1:A:337:LEU:HD11	1:A:352:LEU:HB2	1.80	0.64
1:A:11:GLN:NE2	1:A:12:MSE:HG3	2.13	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:VAL:HG22	1:A:215:VAL:HG22	1.80	0.63
1:A:231:PRO:HD2	1:A:236:ILE:HD12	1.79	0.63
1:A:104:ASN:HD22	1:A:130:LYS:HB2	1.64	0.63
1:A:288:ALA:HB1	1:A:321:PHE:HD1	1.64	0.62
1:A:338:THR:HG22	1:A:351:ASN:OD1	1.99	0.62
1:A:151:LYS:HD3	1:A:152:MSE:N	2.15	0.62
1:A:374:ALA:HB2	1:A:390:VAL:CA	2.31	0.61
1:A:11:GLN:HE22	1:A:12:MSE:HG3	1.65	0.60
1:A:436:ILE:HD11	1:A:438:ARG:NH1	2.17	0.60
1:A:396:ALA:O	1:A:401:LEU:HB2	2.02	0.60
1:A:337:LEU:C	1:A:337:LEU:HD12	2.22	0.59
1:A:206:ASN:N	1:A:209:ASN:HD22	1.90	0.59
1:A:432:LEU:HG	1:A:434:LEU:CD2	2.33	0.59
1:A:396:ALA:O	1:A:399:ILE:HG22	2.03	0.58
1:A:128:VAL:CG2	1:A:138:LEU:HD12	2.34	0.58
1:A:374:ALA:CB	1:A:390:VAL:HG12	2.29	0.58
1:A:305:LYS:HD3	1:A:343:ARG:NH2	2.19	0.58
1:A:35:THR:H	1:A:82:GLN:NE2	2.01	0.58
1:A:262:ARG:H	1:A:359:GLN:HE22	1.49	0.57
1:A:249:ASN:HD22	1:A:330:THR:HG22	1.68	0.57
1:A:359:GLN:OE1	1:A:361:GLN:HG2	2.04	0.57
1:A:103:ASN:ND2	1:A:210:ALA:HB1	2.20	0.56
1:A:265:LEU:CD2	1:A:339:LEU:HD11	2.36	0.56
1:A:263:GLY:C	1:A:354:LEU:HD22	2.26	0.56
1:A:379:LYS:HB2	1:A:386:VAL:CG2	2.34	0.56
1:A:381:LYS:O	1:A:383:GLN:N	2.38	0.56
1:A:191:ASN:CB	1:A:194:ASN:ND2	2.65	0.56
1:A:35:THR:H	1:A:82:GLN:HE21	1.54	0.56
1:A:405:ASP:CB	1:A:436:ILE:HD12	2.34	0.56
1:A:259:GLN:HG2	1:A:378:ASN:HD21	1.69	0.56
1:A:249:ASN:HB2	1:A:330:THR:HG23	1.88	0.56
1:A:113:ILE:HD11	1:A:139:ILE:HD12	1.89	0.55
1:A:229:LEU:O	1:A:230:ALA:HB2	2.07	0.55
1:A:432:LEU:HB3	1:A:447:MSE:HB2	1.87	0.55
1:A:259:GLN:HG2	1:A:378:ASN:ND2	2.22	0.55
1:A:297:SER:O	1:A:301:LYS:HG3	2.06	0.54
1:A:336:LYS:HD2	1:A:336:LYS:C	2.28	0.54
1:A:371:ILE:HG22	1:A:396:ALA:HB2	1.90	0.54
1:A:169:ASN:HD21	1:A:172:GLY:C	2.12	0.53
1:A:432:LEU:HG	1:A:434:LEU:HD22	1.90	0.53
1:A:337:LEU:CD1	1:A:352:LEU:HB2	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:THR:N	1:A:82:GLN:NE2	2.56	0.53
1:A:82:GLN:O	1:A:82:GLN:HG3	2.10	0.52
1:A:371:ILE:HG22	1:A:371:ILE:O	2.08	0.52
1:A:133:ARG:HB3	1:A:195:TYR:CD1	2.45	0.52
1:A:373:GLY:HA2	1:A:394:THR:HB	1.91	0.52
1:A:256:GLU:O	1:A:257:TYR:CG	2.64	0.51
1:A:343:ARG:HG2	1:A:348:VAL:HG21	1.93	0.51
1:A:128:VAL:HG22	1:A:138:LEU:HD12	1.92	0.51
1:A:92:ILE:HG22	1:A:149:ALA:HA	1.93	0.50
1:A:265:LEU:HD13	1:A:328:VAL:HG21	1.94	0.50
1:A:104:ASN:HA	1:A:137:ALA:HB2	1.93	0.50
1:A:268:MSE:CG	1:A:292:GLN:HG3	2.42	0.50
1:A:364:SER:HB3	1:A:374:ALA:O	2.12	0.50
1:A:265:LEU:HD21	1:A:339:LEU:HD11	1.94	0.49
1:A:195:TYR:CE2	1:A:329:GLY:HA3	2.47	0.49
1:A:288:ALA:HB3	1:A:310:ILE:HB	1.93	0.49
1:A:261:LYS:HA	1:A:359:GLN:HE22	1.77	0.49
1:A:363:ASP:C	1:A:365:SER:H	2.15	0.49
1:A:151:LYS:HD3	1:A:152:MSE:H	1.77	0.49
1:A:153:ALA:HB2	1:A:220:GLU:CB	2.43	0.48
1:A:207:ARG:HH11	1:A:207:ARG:HG3	1.77	0.48
1:A:356:GLN:O	1:A:357:SER:HB2	2.13	0.48
1:A:169:ASN:HD21	1:A:172:GLY:CA	2.26	0.48
1:A:251:THR:O	1:A:255:VAL:HG23	2.14	0.48
1:A:400:GLY:O	1:A:445:LEU:HD21	2.13	0.48
1:A:373:GLY:HA3	1:A:396:ALA:CB	2.39	0.48
1:A:133:ARG:HB3	1:A:195:TYR:HD1	1.77	0.48
1:A:363:ASP:OD1	1:A:375:GLU:HG2	2.14	0.48
1:A:396:ALA:HB1	1:A:401:LEU:HD12	1.95	0.48
1:A:361:GLN:O	1:A:362:VAL:C	2.52	0.47
1:A:142:GLN:O	1:A:143:ASN:CB	2.61	0.47
1:A:371:ILE:N	1:A:371:ILE:HD12	2.28	0.47
1:A:35:THR:N	1:A:82:GLN:HE21	2.12	0.47
1:A:103:ASN:HB2	1:A:106:VAL:HG23	1.95	0.47
1:A:355:GLN:O	1:A:356:GLN:O	2.33	0.47
1:A:387:VAL:O	1:A:387:VAL:HG13	2.15	0.47
1:A:374:ALA:CB	1:A:390:VAL:HA	2.43	0.47
1:A:160:VAL:HA	1:A:182:VAL:CG1	2.45	0.47
1:A:274:SER:O	1:A:278:LYS:HG3	2.14	0.46
1:A:301:LYS:HE3	1:A:355:GLN:HE22	1.79	0.46
1:A:381:LYS:HB2	1:A:381:LYS:NZ	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:GLN:HG3	1:A:361:GLN:NE2	2.30	0.46
1:A:387:VAL:HG13	1:A:403:LYS:HA	1.98	0.46
1:A:341:LEU:CB	1:A:348:VAL:HB	2.37	0.46
1:A:336:LYS:HD2	1:A:337:LEU:N	2.31	0.46
1:A:363:ASP:O	1:A:365:SER:N	2.49	0.46
1:A:381:LYS:HG3	1:A:382:ASP:N	2.31	0.46
1:A:407:ILE:HG23	1:A:434:LEU:HD12	1.98	0.46
1:A:160:VAL:HA	1:A:182:VAL:HG12	1.98	0.45
1:A:302:ALA:HB1	1:A:350:VAL:CG2	2.47	0.45
1:A:435:ASN:HB2	1:A:444:TYR:CE1	2.51	0.45
1:A:305:LYS:HB2	1:A:343:ARG:HH21	1.82	0.45
1:A:363:ASP:C	1:A:365:SER:N	2.70	0.45
1:A:373:GLY:HA2	1:A:394:THR:CB	2.45	0.45
1:A:134:SER:OG	1:A:250:LEU:HD13	2.17	0.45
1:A:116:GLN:NE2	1:A:122:LYS:HE3	2.32	0.45
1:A:160:VAL:O	1:A:182:VAL:O	2.35	0.45
1:A:169:ASN:ND2	1:A:169:ASN:C	2.68	0.45
1:A:259:GLN:HE21	1:A:378:ASN:CG	2.21	0.44
1:A:375:GLU:HB2	1:A:388:ASN:HB2	1.98	0.44
1:A:236:ILE:O	1:A:236:ILE:HG23	2.18	0.44
1:A:395:PRO:O	1:A:398:GLN:HB2	2.18	0.44
1:A:293:VAL:HG11	1:A:304:ILE:O	2.18	0.44
1:A:381:LYS:HG2	1:A:383:GLN:HG2	2.00	0.44
1:A:405:ASP:CG	1:A:436:ILE:HD12	2.37	0.44
1:A:231:PRO:O	1:A:232:ASP:HB3	2.18	0.44
1:A:401:LEU:HA	1:A:401:LEU:HD23	1.84	0.43
1:A:359:GLN:O	1:A:359:GLN:HG3	2.18	0.43
1:A:367:ILE:HD12	1:A:376:MSE:CE	2.42	0.43
1:A:407:ILE:HG12	1:A:436:ILE:HG22	1.99	0.43
1:A:438:ARG:HG3	1:A:443:ILE:HD13	2.00	0.43
1:A:152:MSE:HE1	1:A:247:VAL:HG12	2.00	0.43
1:A:425:LEU:HD21	1:A:432:LEU:HD22	1.99	0.43
1:A:103:ASN:HD21	1:A:226:THR:HA	1.83	0.43
1:A:138:LEU:HD13	1:A:138:LEU:C	2.38	0.43
1:A:262:ARG:N	1:A:359:GLN:HE22	2.14	0.43
1:A:436:ILE:HD11	1:A:438:ARG:HH11	1.82	0.43
1:A:169:ASN:O	1:A:208:GLY:HA3	2.19	0.43
1:A:128:VAL:HG21	1:A:138:LEU:HD12	2.01	0.43
1:A:406:VAL:HB	1:A:437:GLN:HG3	2.00	0.43
1:A:408:ILE:HG22	1:A:435:ASN:O	2.19	0.43
1:A:191:ASN:OD1	1:A:193:GLU:HG2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:LEU:CD1	1:A:328:VAL:HG21	2.49	0.42
1:A:390:VAL:HG22	1:A:403:LYS:CG	2.46	0.42
1:A:390:VAL:HG11	1:A:402:LYS:HA	2.02	0.42
1:A:375:GLU:O	1:A:388:ASN:N	2.50	0.42
1:A:113:ILE:HG12	1:A:125:ALA:O	2.19	0.42
1:A:35:THR:O	1:A:35:THR:HG22	2.19	0.42
1:A:165:VAL:HG22	1:A:215:VAL:CG2	2.48	0.42
1:A:169:ASN:ND2	1:A:172:GLY:CA	2.82	0.42
1:A:169:ASN:ND2	1:A:174:GLY:H	2.17	0.42
1:A:186:GLY:HA2	1:A:197:ASN:OD1	2.19	0.42
1:A:267:ILE:HD11	1:A:321:PHE:HE1	1.84	0.42
1:A:31:VAL:HG13	1:A:110:ALA:HB1	2.02	0.41
1:A:127:MSE:HG3	1:A:128:VAL:N	2.35	0.41
1:A:232:ASP:O	1:A:233:GLY:C	2.58	0.41
1:A:292:GLN:HB2	1:A:292:GLN:HE21	1.70	0.41
1:A:316:LYS:HA	1:A:317:PRO:HD3	1.97	0.41
1:A:384:GLY:HA2	1:A:415:VAL:O	2.20	0.41
1:A:312:SER:OG	1:A:340:GLY:HA3	2.21	0.41
1:A:373:GLY:CA	1:A:394:THR:HB	2.49	0.41
1:A:225:ASN:HD22	1:A:241:ALA:HB2	1.85	0.41
1:A:379:LYS:O	1:A:381:LYS:O	2.38	0.41
1:A:428:LYS:N	1:A:429:PRO:HD3	2.36	0.41
1:A:143:ASN:N	1:A:144:PRO:CD	2.83	0.41
1:A:206:ASN:O	1:A:209:ASN:HB2	2.21	0.41
1:A:383:GLN:OE1	1:A:383:GLN:HA	2.21	0.41

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	388/448 (87%)	348 (90%)	29 (8%)	11 (3%)	5 25

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	356	GLN
1	A	362	VAL
1	A	374	ALA
1	A	192	ALA
1	A	233	GLY
1	A	391	LYS
1	A	364	SER
1	A	382	ASP
1	A	388	ASN
1	A	407	ILE
1	A	381	LYS

5.3.2 Protein sidechains (i)

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	312/342 (91%)	280 (90%)	32 (10%)	7 28

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	GLU
1	A	25	SER
1	A	28	SER
1	A	82	GLN
1	A	87	LEU
1	A	113	ILE
1	A	128	VAL
1	A	151	LYS
1	A	165	VAL
1	A	169	ASN
1	A	175	GLU
1	A	177	VAL
1	A	214	LEU
1	A	217	LEU

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Mol	Chain	Res	Type
1	A	236	ILE
1	A	251	THR
1	A	280	MSE
1	A	283	ASP
1	A	292	GLN
1	A	298	SER
1	A	305	LYS
1	A	313	LEU
1	A	324	LEU
1	A	327	GLN
1	A	330	THR
1	A	336	LYS
1	A	361	GLN
1	A	362	VAL
1	A	381	LYS
1	A	389	ASN
1	A	426	ASP
1	A	438	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	82	GLN
1	A	103	ASN
1	A	104	ASN
1	A	116	GLN
1	A	169	ASN
1	A	194	ASN
1	A	209	ASN
1	A	225	ASN
1	A	245	ASN
1	A	249	ASN
1	A	259	GLN
1	A	273	ASN
1	A	292	GLN
1	A	355	GLN
1	A	359	GLN
1	A	378	ASN

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, 95^{th} 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	379/448 (84%)	-0.09	13 (3%) 45 19	26, 65, 130, 156	0
2	B	0/5	-	-	-	-
All	All	379/453 (83%)	-0.09	13 (3%) 45 19	26, 65, 130, 156	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	390	VAL	3.4
1	A	396	ALA	3.0
1	A	391	LYS	3.0
1	A	362	VAL	2.7
1	A	11	GLN	2.4
1	A	35	THR	2.4
1	A	375	GLU	2.4
1	A	372	GLU	2.3
1	A	370	GLY	2.2
1	A	367	ILE	2.2
1	A	401	LEU	2.1
1	A	374	ALA	2.1
1	A	363	ASP	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

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.