



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:39 AM EDT

PDB ID : 2PWD / pdb_00002pwd
Title : Crystal Structure of the Trehalulose Synthase MUTB from *Pseudomonas Mesoacidophila* MX-45 Complexed to the Inhibitor Deoxynojirmycin
Authors : Ravaud, S.; Robert, X.; Haser, R.; Aghajari, N.
Deposited on : 2007-05-11
Resolution : 1.80 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

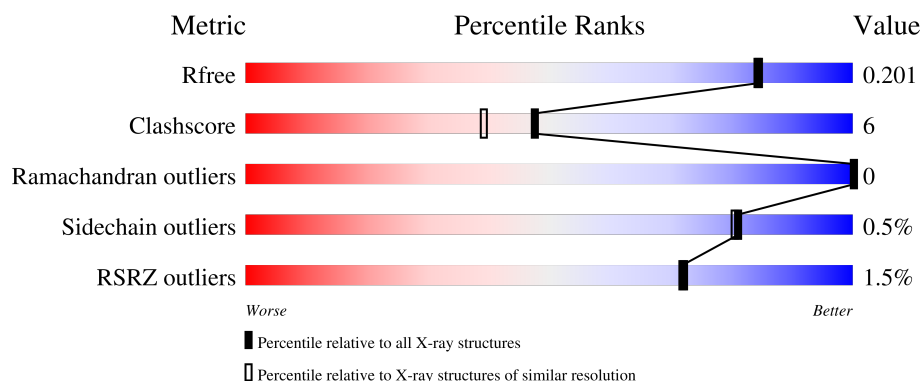
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	557	
1	B	557	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10591 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.

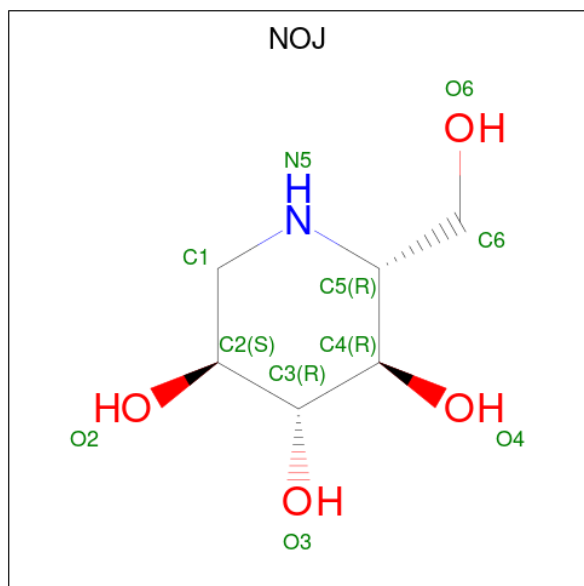
- Molecule 1 is a protein called Sucrose isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	557	Total	C	N	O	S	0	7	0
			4533	2894	774	850	15			
1	B	557	Total	C	N	O	S	0	7	0
			4519	2886	774	845	14			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

- Molecule 3 is 1-DEOXYNOJIRIMYCIN (CCD ID: NOJ) (formula: C₆H₁₃NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	6	1	4		
3	B	1	Total	C	N	O	0	0
			11	6	1	4		

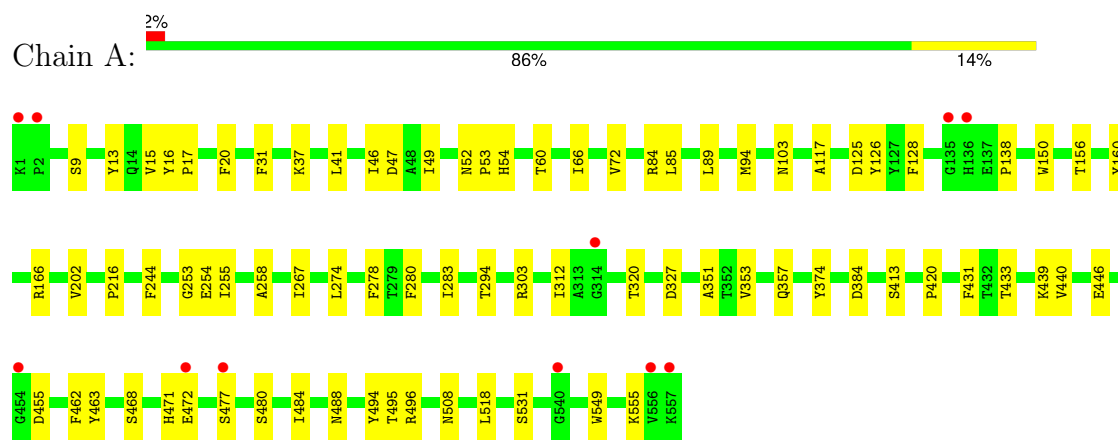
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	764	Total	O	0	0
			764	764		
4	B	751	Total	O	0	0
			751	751		

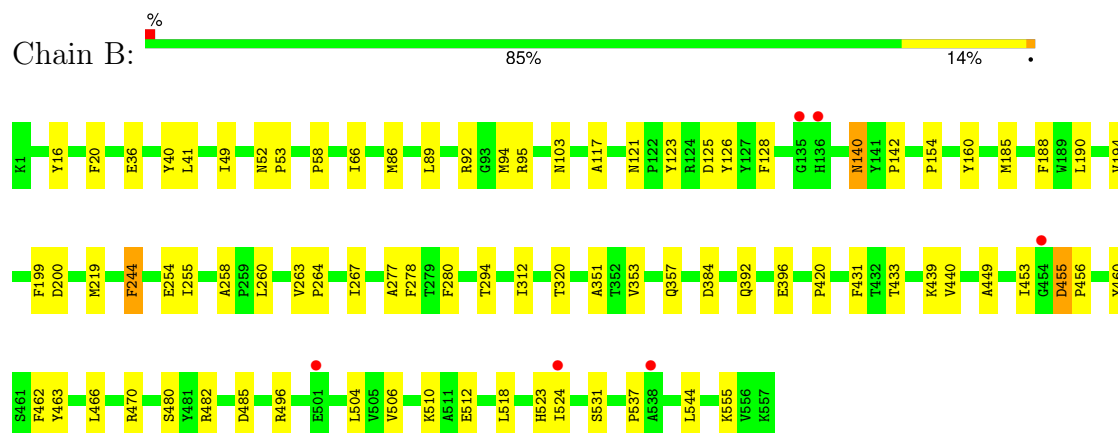
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Sucrose isomerase



• Molecule 1: Sucrose isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	63.40Å 72.00Å 82.00Å 67.20° 73.40° 70.90°	Depositor
Resolution (Å)	42.32 – 1.80 42.32 – 1.80	Depositor EDS
% Data completeness (in resolution range)	95.7 (42.32-1.80) 95.7 (42.32-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 1.60Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.169 , 0.205 0.166 , 0.201	Depositor DCC
R_{free} test set	5570 reflections (3.56%)	wwPDB-VP
Wilson B-factor (Å ²)	12.0	Xtriage
Anisotropy	0.383	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10591	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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

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

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	0.51	0/4670	0.94	16/6348 (0.3%)
1	B	0.51	0/4656	0.95	18/6333 (0.3%)
All	All	0.51	0/9326	0.95	34/12681 (0.3%)

There are no bond length outliers.

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	320	THR	N-CA-C	-8.03	97.97	110.42
1	B	320	THR	N-CA-C	-7.79	98.34	110.42
1	B	384	ASP	N-CA-C	7.24	121.16	110.30
1	B	244	PHE	N-CA-C	6.57	120.39	112.38
1	A	267	ILE	N-CA-C	6.54	120.56	113.43
1	A	384	ASP	N-CA-C	6.49	119.78	110.24
1	A	244	PHE	N-CA-C	6.46	120.26	112.38
1	B	126	TYR	N-CA-C	-6.23	105.64	113.18
1	A	433	THR	N-CA-C	-6.11	105.47	113.17
1	B	267	ILE	N-CA-C	6.00	119.97	113.43
1	A	103	ASN	N-CA-C	-5.95	104.74	112.23
1	B	433	THR	N-CA-C	-5.94	106.07	113.38
1	B	278	PHE	N-CA-C	-5.93	98.86	108.52
1	B	103	ASN	N-CA-C	-5.87	104.83	112.23
1	B	117	ALA	N-CA-C	5.83	118.41	111.71
1	B	485	ASP	CA-C-N	5.60	125.97	119.47
1	B	485	ASP	C-N-CA	5.60	125.97	119.47
1	A	126	TYR	N-CA-C	-5.41	106.64	113.18
1	A	455	ASP	CA-C-N	5.41	125.08	119.56
1	A	455	ASP	C-N-CA	5.41	125.08	119.56
1	B	16	TYR	N-CA-C	-5.38	97.93	109.81
1	A	60	THR	N-CA-C	-5.35	106.01	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	ILE	N-CA-C	5.29	116.20	108.58
1	A	555	LYS	N-CA-C	-5.28	100.69	109.46
1	B	66	ILE	N-CA-C	5.24	116.12	108.58
1	B	140	ASN	N-CA-C	5.22	118.77	112.93
1	A	413	SER	N-CA-C	5.21	117.78	110.23
1	A	278	PHE	N-CA-C	-5.20	100.25	108.73
1	A	16	TYR	N-CA-C	-5.18	98.35	109.81
1	B	58	PRO	N-CA-C	-5.16	107.68	114.03
1	B	455	ASP	CA-C-N	5.09	124.76	119.56
1	B	455	ASP	C-N-CA	5.09	124.76	119.56
1	B	555	LYS	N-CA-C	-5.08	101.02	109.46
1	A	117	ALA	N-CA-C	5.02	116.75	111.28

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	4533	0	4260	50	0
1	B	4519	0	4238	50	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	11	0	13	1	0
3	B	11	0	13	1	0
4	A	764	0	0	9	0
4	B	751	0	0	10	0
All	All	10591	0	8524	99	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 6.

All (99) 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:484:ILE:HD13	1:A:494:TYR:HA	1.59	0.82
1:B:89:LEU:HD23	1:B:94[B]:MET:HE3	1.66	0.77
1:B:439:LYS:HD3	4:B:9838:HOH:O	1.86	0.73
1:B:121:ASN:HD22	1:B:123:TYR:H	1.39	0.70
1:B:125:ASP:HB2	4:B:4824:HOH:O	1.93	0.69
1:A:31:PHE:HE2	1:A:72[A]:VAL:CG1	2.07	0.68
1:B:449:ALA:O	1:B:453:ILE:HG12	1.93	0.68
1:A:31:PHE:HE2	1:A:72[A]:VAL:HG11	1.59	0.67
1:A:89:LEU:HD23	1:A:94[B]:MET:HE3	1.78	0.66
1:B:92:ARG:HB2	1:B:94[B]:MET:HE2	1.79	0.64
1:A:294:THR:HG23	4:A:4619:HOH:O	1.99	0.62
1:A:468:SER:O	1:A:472:GLU:HG3	1.99	0.61
1:B:524:ILE:HD13	1:B:537:PRO:HG3	1.83	0.61
1:A:471:HIS:HD2	4:A:4720:HOH:O	1.85	0.59
1:B:260:LEU:HG	1:B:312:ILE:HG13	1.85	0.59
1:B:121:ASN:ND2	1:B:123:TYR:H	2.00	0.58
1:B:255:ILE:HG22	1:B:258:ALA:HB3	1.86	0.58
1:A:484:ILE:HD11	1:A:495:THR:HG23	1.84	0.58
1:A:255:ILE:HG22	1:A:258:ALA:HB3	1.87	0.56
1:B:142:PRO:HD3	1:B:219:MET:HE1	1.86	0.56
1:A:353:VAL:O	1:A:357:GLN:HG2	2.07	0.55
1:B:518:LEU:HD11	1:B:524:ILE:HG13	1.89	0.55
1:B:36:GLU:HG3	4:B:9853:HOH:O	2.08	0.54
1:A:31:PHE:HZ	1:A:54:HIS:HB2	1.74	0.53
1:A:9[A]:SER:HA	1:A:477:SER:OG	2.09	0.52
1:A:477:SER:HB2	4:A:4932:HOH:O	2.08	0.52
1:A:47:ASP:OD2	1:A:471:HIS:HE1	1.93	0.52
1:A:125:ASP:HB2	4:A:4617:HOH:O	2.11	0.51
1:A:13:TYR:HB3	1:A:49[A]:ILE:CD1	2.41	0.51
1:A:13:TYR:HB3	1:A:49[B]:ILE:CD1	2.41	0.51
1:A:84:ARG:HD3	4:A:5999:HOH:O	2.11	0.51
1:B:264:PRO:HG3	1:B:312:ILE:HG23	1.93	0.51
1:A:216:PRO:HD2	4:A:5611:HOH:O	2.11	0.49
1:B:420:PRO:HB2	1:B:440:VAL:HG22	1.94	0.49
1:A:13:TYR:HB3	1:A:49[B]:ILE:HD13	1.94	0.49
1:A:13:TYR:HB3	1:A:49[A]:ILE:HD13	1.94	0.49
1:B:95[B]:ARG:HD3	4:B:9841:HOH:O	2.13	0.49
1:B:353:VAL:O	1:B:357:GLN:HG2	2.13	0.48
1:B:420:PRO:HB3	1:B:431:PHE:CG	2.48	0.48
1:B:254:GLU:HG2	1:B:280:PHE:CE1	2.48	0.48
1:B:482:ARG:HD3	4:B:4920:HOH:O	2.12	0.47
1:B:537:PRO:HG3	1:B:544:LEU:HD21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:VAL:O	1:A:17:PRO:HD3	2.14	0.47
1:A:31:PHE:CZ	1:A:54:HIS:HB2	2.50	0.47
1:B:462:PHE:CZ	1:B:531:SER:HB3	2.50	0.47
1:B:462:PHE:CE2	1:B:466:LEU:HD11	2.51	0.46
1:A:20:PHE:HB3	4:A:4008:HOH:O	2.15	0.46
1:B:392:GLN:HA	1:B:396:GLU:OE1	2.16	0.46
1:A:9[B]:SER:HA	1:A:477:SER:OG	2.15	0.46
1:B:128:PHE:O	1:B:160:TYR:HA	2.15	0.46
1:A:202:VAL:CG1	1:A:255:ILE:HD13	2.46	0.46
1:B:40:TYR:HE1	1:B:453:ILE:HD11	1.81	0.46
1:A:128:PHE:O	1:A:160:TYR:HA	2.16	0.45
1:A:254:GLU:HG2	1:A:280:PHE:CE2	2.51	0.45
1:A:303:ARG:NH1	1:A:488:ASN:HB3	2.31	0.45
1:B:140:ASN:O	1:B:219:MET:HE1	2.17	0.45
1:A:420:PRO:HB3	1:A:431:PHE:CG	2.52	0.45
1:A:31:PHE:HE2	1:A:72[A]:VAL:HG13	1.81	0.45
1:A:508:ASN:O	1:A:549:TRP:HA	2.16	0.45
1:B:351:ALA:HB2	1:B:463:TYR:CE1	2.52	0.45
1:A:52:ASN:HB3	1:A:53:PRO:CD	2.46	0.45
1:B:294:THR:HG23	4:B:4879:HOH:O	2.15	0.45
1:B:523:HIS:HE1	4:B:6232:HOH:O	2.00	0.44
1:B:470[A]:ARG:NH2	4:B:4127:HOH:O	2.46	0.44
1:B:480:SER:O	1:B:496:ARG:HA	2.17	0.44
1:A:156:THR:HA	1:B:154:PRO:HB3	1.98	0.44
1:B:460:TYR:CD1	1:B:460:TYR:C	2.95	0.44
1:B:312:ILE:HD13	1:B:312:ILE:HA	1.86	0.43
1:A:46:ILE:HG21	1:A:49[A]:ILE:CD1	2.48	0.43
1:A:480:SER:O	1:A:496:ARG:HA	2.18	0.43
1:A:46:ILE:HG21	1:A:49[B]:ILE:CD1	2.48	0.43
1:A:41:LEU:HD13	1:A:49[A]:ILE:HD11	2.00	0.43
1:A:41:LEU:HD13	1:A:49[B]:ILE:HD11	2.00	0.43
1:B:86[B]:MET:HE3	4:B:4810:HOH:O	2.18	0.43
1:A:85:LEU:HD22	4:A:5981:HOH:O	2.18	0.43
1:A:253:GLY:HA3	1:A:274:LEU:HD13	2.01	0.43
1:A:420:PRO:HB2	1:A:440:VAL:HG22	2.01	0.43
1:B:263:VAL:N	1:B:264:PRO:CD	2.82	0.42
1:B:200:ASP:OD1	3:B:8001:NOJ:C1	2.67	0.42
1:B:255:ILE:HD12	1:B:277:ALA:HB1	2.00	0.42
1:A:462:PHE:CZ	1:A:531:SER:HB3	2.55	0.42
1:A:41:LEU:HD13	1:A:49[B]:ILE:CD1	2.49	0.42
1:A:351:ALA:HB2	1:A:463:TYR:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:PHE:HB3	4:B:4001:HOH:O	2.19	0.42
1:B:504:LEU:HG	1:B:506:VAL:HG23	2.01	0.42
1:A:41:LEU:HD13	1:A:49[A]:ILE:CD1	2.50	0.41
1:A:374:TYR:OH	1:A:439:LYS:HE2	2.20	0.41
1:A:37:LYS:HA	4:A:4244:HOH:O	2.20	0.41
1:B:455:ASP:HA	1:B:456:PRO:HD3	1.83	0.41
1:B:524:ILE:CD1	1:B:544:LEU:HD21	2.50	0.41
1:A:327:ASP:OD2	3:A:8000:NOJ:O2	2.29	0.41
1:B:190:LEU:HD23	1:B:194[A]:VAL:HG23	2.03	0.41
1:B:52:ASN:HB3	1:B:53:PRO:CD	2.51	0.41
1:B:185:MET:O	1:B:188:PHE:HB3	2.20	0.41
1:B:510:LYS:C	1:B:512:GLU:H	2.29	0.41
1:A:138:PRO:HD2	1:A:150:TRP:CG	2.56	0.40
1:B:199:PHE:HZ	1:B:244:PHE:CZ	2.39	0.40
1:B:41:LEU:HD13	1:B:49[A]:ILE:CD1	2.52	0.40
1:B:142:PRO:HD3	1:B:219:MET:CE	2.52	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	562/557 (101%)	545 (97%)	17 (3%)	0	100	100
1	B	562/557 (101%)	546 (97%)	16 (3%)	0	100	100
All	All	1124/1114 (101%)	1091 (97%)	33 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	469/475 (99%)	464 (99%)	5 (1%)	65	60
1	B	465/475 (98%)	465 (100%)	0	100	100
All	All	934/950 (98%)	929 (100%)	5 (0%)	81	80

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	ARG
1	A	283	ILE
1	A	312	ILE
1	A	446	GLU
1	A	518	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	221	ASN
1	A	228	GLN
1	A	262	GLN
1	A	471	HIS
1	A	498	GLN
1	B	62	ASN
1	B	121	ASN
1	B	136	HIS
1	B	221	ASN
1	B	228	GLN
1	B	262	GLN
1	B	498	GLN
1	B	523	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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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$
3	NOJ	A	8000	-	11,11,11	2.09	2 (18%)	13,15,15	1.23	1 (7%)
3	NOJ	B	8001	-	11,11,11	2.19	3 (27%)	13,15,15	1.29	2 (15%)

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
3	NOJ	A	8000	-	-	0/2/19/19	0/1/1/1
3	NOJ	B	8001	-	-	0/2/19/19	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	8000	NOJ	C1-C2	5.69	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	8001	NOJ	C1-C2	5.22	1.57	1.52
3	B	8001	NOJ	C5-N5	-2.74	1.43	1.47
3	B	8001	NOJ	C4-C5	2.31	1.57	1.52
3	A	8000	NOJ	C4-C5	2.23	1.57	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	8000	NOJ	O6-C6-C5	-2.73	104.48	111.10
3	B	8001	NOJ	O6-C6-C5	-2.55	104.92	111.10
3	B	8001	NOJ	C1-N5-C5	2.12	114.36	109.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	8000	NOJ	1	0
3	B	8001	NOJ	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 [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	557/557 (100%)	-0.28	11 (1%) 65 65	5, 13, 28, 50	7 (1%)
1	B	557/557 (100%)	-0.23	6 (1%) 78 78	6, 14, 28, 44	7 (1%)
All	All	1114/1114 (100%)	-0.26	17 (1%) 72 72	5, 14, 28, 50	14 (1%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	LYS	4.3
1	B	135	GLY	3.0
1	A	136	HIS	2.7
1	A	454	GLY	2.6
1	A	556	VAL	2.6
1	A	557	LYS	2.5
1	B	454	GLY	2.4
1	B	501	GLU	2.3
1	A	477	SER	2.2
1	A	314	GLY	2.2
1	A	2	PRO	2.2
1	B	538	ALA	2.2
1	B	136	HIS	2.1
1	A	472	GLU	2.1
1	A	540	GLY	2.1
1	B	524	ILE	2.0
1	A	135	GLY	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](#)

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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	NOJ	A	8000	11/11	0.96	0.06	8,9,10,11	0
3	NOJ	B	8001	11/11	0.96	0.06	9,10,11,12	0
2	CA	B	7000	1/1	0.97	0.05	15,15,15,15	0
2	CA	A	7001	1/1	0.99	0.05	11,11,11,11	0

6.5 Other polymers [i](#)

There are no such residues in this entry.