



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:00 PM GMT

PDB ID : 1MZO  
Title : Crystal structure of pyruvate formate-lyase with pyruvate  
Authors : Lehtio, L.; Leppanen, V.-M.; Kozarich, J.W.; Goldman, A.  
Deposited on : 2002-10-09  
Resolution : 2.70 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

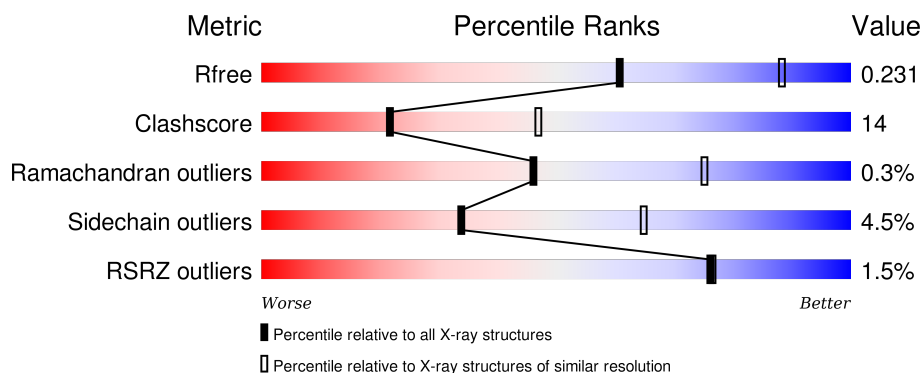
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	759	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 1%, orange 1%, yellow 26%, green 71%);"></div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 1%, orange 1%, yellow 26%, green 71%);"></div> </div> <div> <span style="position: absolute; top: -10px; left: 0; width: 100%;"></span> <span style="position: absolute; top: 10px; left: 0; width: 100%;"></span> <span style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 1%, orange 1%, yellow 26%, green 71%);"></span> <span style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 1%, orange 1%, yellow 26%, green 71%);"></span> </div> </div>
1	B	759	<div> <div style="width: 100%; height: 10px; position: relative;"> <div style="position: absolute; top: -10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 10px; left: 0; width: 100%;"></div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 2%, orange 2%, yellow 27%, green 71%);"></div> <div style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 2%, orange 2%, yellow 27%, green 71%);"></div> </div> <div> <span style="position: absolute; top: -10px; left: 0; width: 100%;"></span> <span style="position: absolute; top: 10px; left: 0; width: 100%;"></span> <span style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 2%, orange 2%, yellow 27%, green 71%);"></span> <span style="position: absolute; top: 0; left: 0; width: 100%; height: 100%; background: linear-gradient(to right, red 2%, orange 2%, yellow 27%, green 71%);"></span> </div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PGE	A	1001	-	-	-	X
3	PYR	B	2002	-	-	-	X

## 2 Entry composition [i](#)

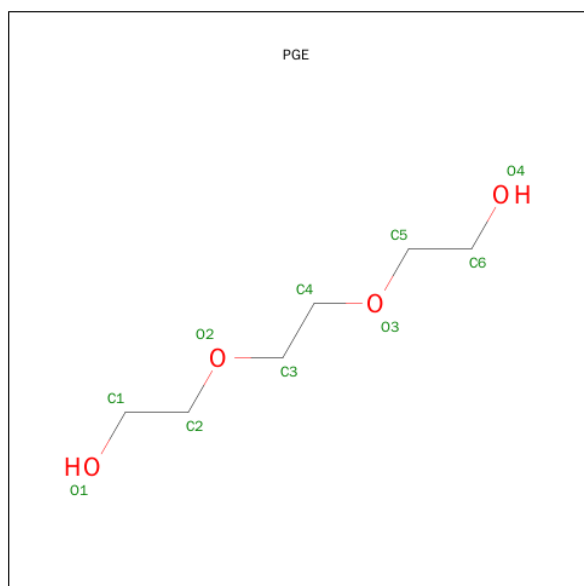
There are 4 unique types of molecules in this entry. The entry contains 12467 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Pyruvate formate-lyase.

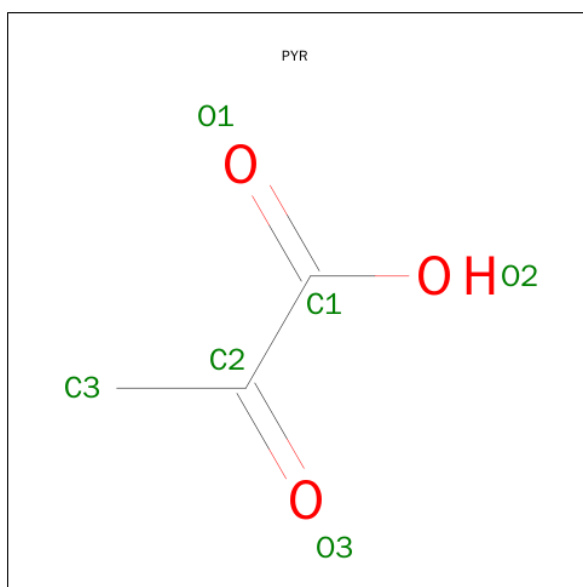
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	756	Total	C	N	O	S	0	0	0
			5965	3770	1020	1139	36			
1	B	756	Total	C	N	O	S	0	0	0
			5965	3770	1020	1139	36			

- Molecule 2 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula:  $C_6H_{14}O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 3 is PYRUVIC ACID (three-letter code: PYR) (formula:  $C_3H_4O_3$ ).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	276	Total	O	0	0
			276	276		
4	B	239	Total	O	0	0
			239	239		

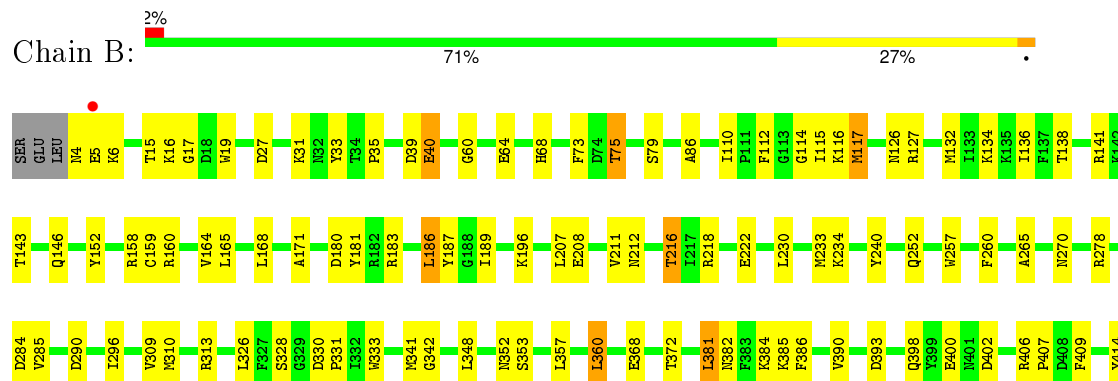
### 3 Residue-property plots

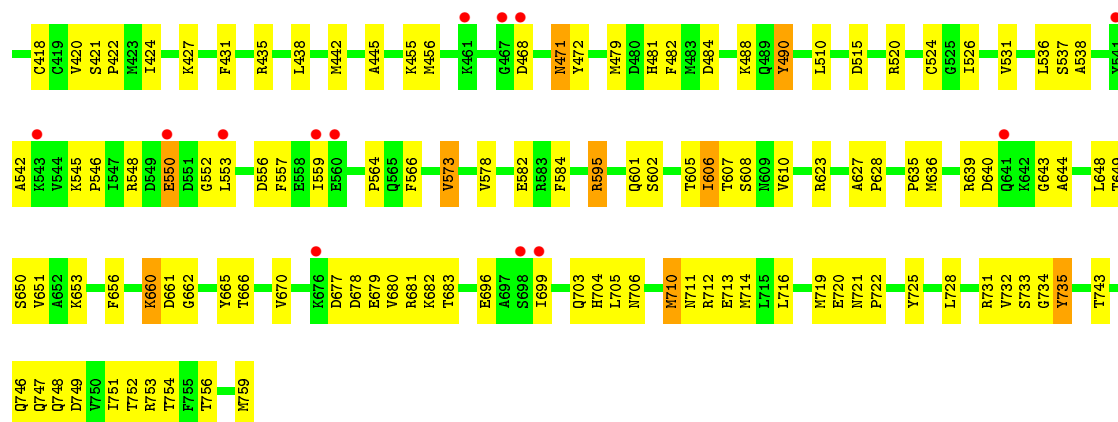
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

#### • Molecule 1: Pyruvate formate-lyase



#### • Molecule 1: Pyruvate formate-lyase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	158.35Å 158.35Å 159.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 19.79 – 2.68	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.70) 94.3 (19.79-2.68)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.32 (at 2.67Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.196 , 0.235 0.194 , 0.231	Depositor DCC
$R_{free}$ test set	2795 reflections (5.51%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.8	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 47.3	EDS
Estimated twinning fraction	0.019 for -h,l,k 0.004 for -l,-k,-h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 55885 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12467	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

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

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	0.37	0/6086	0.60	0/8222
1	B	0.38	0/6086	0.60	0/8222
All	All	0.37	0/12172	0.60	0/16444

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	181	TYR	Sidechain

### 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	5965	0	5889	169	0
1	B	5965	0	5889	165	0
2	A	10	0	14	1	1
3	A	6	0	3	1	0
3	B	6	0	3	0	0
4	A	276	0	0	12	0
4	B	239	0	0	7	0
All	All	12467	0	11798	332	1

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 14.

All (332) 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:602:SER:HB3	1:A:661:ASP:HB3	1.43	1.00
1:B:602:SER:HB3	1:B:661:ASP:HB3	1.44	0.97
1:B:606:ILE:HG22	1:B:607:THR:H	1.41	0.85
1:A:606:ILE:HG22	1:A:607:THR:H	1.43	0.83
1:A:115:ILE:HG22	4:A:2049:HOH:O	1.77	0.82
1:A:112:PHE:HD1	4:A:2137:HOH:O	1.63	0.80
1:A:341:MET:HB2	1:A:406:ARG:NH1	1.97	0.79
1:B:4:ASN:ND2	1:B:6:LYS:HB2	2.00	0.77
1:A:4:ASN:ND2	1:A:6:LYS:HB2	2.00	0.76
1:B:341:MET:HB2	1:B:406:ARG:NH1	2.00	0.76
1:B:4:ASN:HD21	1:B:6:LYS:HB2	1.50	0.75
1:A:4:ASN:HD21	1:A:6:LYS:HB2	1.51	0.75
1:A:420:VAL:HG23	1:A:662:GLY:HA3	1.68	0.74
1:A:40:GLU:HG2	1:A:386:PHE:CD1	2.23	0.74
1:B:40:GLU:HG2	1:B:386:PHE:CD1	2.22	0.73
1:A:333:TRP:HE1	1:A:735:TYR:HB3	1.53	0.73
1:B:420:VAL:HG23	1:B:662:GLY:HA3	1.70	0.73
1:A:564:PRO:HB2	1:A:573:VAL:HG22	1.71	0.73
1:A:39:ASP:HB3	1:A:382:ASN:ND2	2.04	0.71
1:B:666:THR:HA	1:B:706:ASN:HB2	1.72	0.71
1:B:564:PRO:HB2	1:B:573:VAL:HG22	1.72	0.71
1:B:39:ASP:HB3	1:B:382:ASN:ND2	2.04	0.71
1:A:328:SER:HB3	1:A:746:GLN:NE2	2.04	0.71
1:B:333:TRP:HE1	1:B:735:TYR:HB3	1.56	0.70
1:B:328:SER:HB3	1:B:746:GLN:NE2	2.06	0.70
1:A:666:THR:HA	1:A:706:ASN:HB2	1.73	0.70
1:B:115:ILE:HG21	1:B:138:THR:HG22	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:ARG:HD2	4:A:2200:HOH:O	1.92	0.68
1:B:720:GLU:C	1:B:722:PRO:HD3	2.13	0.68
1:A:720:GLU:C	1:A:722:PRO:HD3	2.14	0.68
1:A:115:ILE:HG21	1:A:138:THR:HG22	1.76	0.68
1:B:40:GLU:HG2	1:B:386:PHE:CG	2.28	0.67
1:B:212:ASN:O	1:B:216:THR:HG22	1.95	0.67
1:A:526:ILE:HD11	1:A:584:PHE:CD2	2.30	0.66
1:A:212:ASN:O	1:A:216:THR:HG22	1.95	0.66
1:A:40:GLU:HG2	1:A:386:PHE:CG	2.30	0.66
1:A:743:THR:OG1	1:A:746:GLN:HG3	1.96	0.66
1:B:526:ILE:HD11	1:B:584:PHE:CD2	2.31	0.65
1:B:696:GLU:HB2	1:B:699:ILE:CG2	2.26	0.65
1:A:696:GLU:HB2	1:A:699:ILE:CG2	2.27	0.65
1:B:743:THR:OG1	1:B:746:GLN:HG3	1.97	0.65
1:B:218:ARG:O	1:B:222:GLU:HG3	1.97	0.64
1:A:623:ARG:NH1	1:A:627:ALA:O	2.32	0.63
1:B:749:ASP:O	1:B:753:ARG:HG3	1.98	0.63
1:A:218:ARG:O	1:A:222:GLU:HG3	1.98	0.63
1:A:333:TRP:NE1	1:A:735:TYR:HB3	2.14	0.62
1:B:706:ASN:HD21	1:B:734:GLY:N	1.98	0.62
1:B:602:SER:HB3	1:B:661:ASP:CB	2.27	0.62
1:A:725:TYR:HB3	1:A:728:LEU:HB2	1.82	0.62
1:A:743:THR:O	1:A:747:GLN:HG3	1.99	0.62
1:B:623:ARG:NH1	1:B:627:ALA:O	2.33	0.61
1:A:605:THR:O	1:A:608:SER:HB2	2.00	0.61
1:B:725:TYR:HB3	1:B:728:LEU:HB2	1.82	0.61
1:B:696:GLU:HB2	1:B:699:ILE:HG23	1.82	0.61
1:A:696:GLU:HB2	1:A:699:ILE:HG23	1.82	0.61
1:A:656:PHE:O	1:A:660:LYS:HD2	2.00	0.61
1:B:333:TRP:NE1	1:B:735:TYR:HB3	2.16	0.61
1:A:706:ASN:HD21	1:A:734:GLY:N	1.99	0.61
1:A:749:ASP:O	1:A:753:ARG:HG3	2.01	0.61
1:A:420:VAL:CG2	1:A:662:GLY:HA3	2.31	0.60
1:B:743:THR:O	1:B:747:GLN:HG3	2.01	0.60
1:B:75:THR:HG21	4:B:2241:HOH:O	2.01	0.60
1:A:678:ASP:O	1:A:682:LYS:HG3	2.02	0.59
1:B:420:VAL:CG2	1:B:662:GLY:HA3	2.32	0.59
1:B:670:VAL:HG13	1:B:711:ASN:ND2	2.16	0.59
1:B:605:THR:O	1:B:608:SER:HB2	2.02	0.59
1:A:670:VAL:HG13	1:A:711:ASN:ND2	2.16	0.59
1:B:559:ILE:HD12	1:B:559:ILE:N	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:656:PHE:O	1:B:660:LYS:HD2	2.02	0.59
1:B:115:ILE:HG21	1:B:138:THR:CG2	2.33	0.59
1:B:644:ALA:HB2	1:B:756:THR:HG21	1.84	0.59
1:B:678:ASP:O	1:B:682:LYS:HG3	2.03	0.58
1:A:559:ILE:N	1:A:559:ILE:HD12	2.17	0.58
1:A:115:ILE:HG21	1:A:138:THR:CG2	2.34	0.58
1:B:39:ASP:HB3	1:B:382:ASN:HD22	1.68	0.58
1:B:606:ILE:HG22	1:B:607:THR:N	2.14	0.58
1:A:15:THR:HB	1:A:31:LYS:O	2.04	0.58
1:A:644:ALA:HB2	1:A:756:THR:HG21	1.85	0.58
1:A:39:ASP:HB3	1:A:382:ASN:HD22	1.68	0.58
1:B:548:ARG:HG3	1:B:548:ARG:HH11	1.69	0.58
1:B:566:PHE:O	1:B:635:PRO:HB3	2.04	0.58
1:B:15:THR:HB	1:B:31:LYS:O	2.04	0.58
1:B:278:ARG:HD2	4:B:2091:HOH:O	2.04	0.57
1:A:606:ILE:HG22	1:A:607:THR:N	2.16	0.56
1:A:110:ILE:HG13	1:A:270:ASN:HB3	1.87	0.56
1:B:402:ASP:OD2	1:B:406:ARG:NH1	2.38	0.56
1:A:431:PHE:CZ	1:A:520:ARG:HD3	2.40	0.56
1:A:341:MET:O	1:A:406:ARG:HD3	2.05	0.56
1:A:656:PHE:CD1	1:A:703:GLN:HG3	2.40	0.56
1:B:712:ARG:HH12	1:B:751:ILE:HB	1.70	0.56
1:B:431:PHE:CZ	1:B:520:ARG:HD3	2.41	0.56
1:B:110:ILE:HG13	1:B:270:ASN:HB3	1.87	0.56
1:A:548:ARG:HG3	1:A:548:ARG:HH11	1.71	0.56
1:A:402:ASP:OD2	1:A:406:ARG:NH1	2.40	0.55
1:B:341:MET:O	1:B:406:ARG:HD3	2.06	0.55
1:B:720:GLU:O	1:B:722:PRO:HD3	2.06	0.55
1:B:284:ASP:HB2	1:B:352:ASN:HB2	1.88	0.55
1:B:656:PHE:CD1	1:B:703:GLN:HG3	2.41	0.55
1:B:677:ASP:O	1:B:681:ARG:HG3	2.07	0.55
1:A:602:SER:HB3	1:A:661:ASP:CB	2.26	0.55
1:A:284:ASP:HB2	1:A:352:ASN:HB2	1.89	0.55
1:B:357:LEU:O	1:B:360:LEU:HB2	2.07	0.55
1:B:409:PHE:HE2	1:B:422:PRO:HB2	1.72	0.54
1:A:720:GLU:O	1:A:722:PRO:HD3	2.07	0.54
1:A:566:PHE:O	1:A:635:PRO:HB3	2.06	0.54
1:A:712:ARG:HH12	1:A:751:ILE:HB	1.72	0.54
1:A:677:ASP:O	1:A:681:ARG:HG3	2.07	0.54
1:B:595:ARG:HD3	4:B:2119:HOH:O	2.07	0.54
1:A:290:ASP:HB3	1:A:296:ILE:HG12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:ASP:HB3	1:B:296:ILE:HG12	1.89	0.53
1:A:33:TYR:CE1	1:A:35:PRO:HG3	2.43	0.53
1:A:357:LEU:O	1:A:360:LEU:HB2	2.08	0.53
1:B:712:ARG:NH1	1:B:751:ILE:HB	2.24	0.53
1:A:712:ARG:O	1:A:716:LEU:HD13	2.08	0.53
1:A:488:LYS:HD2	1:B:208:GLU:O	2.09	0.53
1:A:189:ILE:HG21	1:A:234:LYS:HG3	1.91	0.53
1:B:712:ARG:O	1:B:716:LEU:HD13	2.08	0.53
1:B:651:VAL:HG11	1:B:665:TYR:HB2	1.90	0.53
1:A:409:PHE:HE2	1:A:422:PRO:HB2	1.73	0.52
1:A:418:CYS:SG	3:A:2001:PYR:C2	2.97	0.52
1:A:372:THR:HG21	1:A:400:GLU:HG3	1.90	0.52
1:A:330:ASP:N	1:A:331:PRO:CD	2.73	0.52
1:B:372:THR:HG21	1:B:400:GLU:HG3	1.91	0.52
1:B:189:ILE:HG21	1:B:234:LYS:HG3	1.92	0.52
1:B:330:ASP:N	1:B:331:PRO:CD	2.73	0.52
1:B:132:MET:HE3	1:B:136:ILE:HG13	1.92	0.52
1:A:385:LYS:NZ	1:A:683:THR:HG22	2.25	0.52
1:A:651:VAL:HG11	1:A:665:TYR:HB2	1.91	0.51
1:A:165:LEU:HD11	1:A:490:TYR:HA	1.92	0.51
1:B:165:LEU:HD11	1:B:490:TYR:HA	1.92	0.51
1:A:180:ASP:HB3	1:A:183:ARG:HG3	1.91	0.51
1:A:677:ASP:OD2	1:A:679:GLU:HB2	2.11	0.51
1:A:208:GLU:O	1:B:488:LYS:HD2	2.10	0.51
1:A:550:GLU:HA	1:A:550:GLU:OE1	2.11	0.51
1:B:704:HIS:CG	1:B:705:LEU:N	2.79	0.51
1:B:385:LYS:NZ	1:B:683:THR:HG22	2.26	0.51
1:B:677:ASP:OD2	1:B:679:GLU:HB2	2.11	0.51
1:A:704:HIS:CG	1:A:705:LEU:N	2.79	0.51
1:B:643:GLY:HA3	1:B:759:MET:OXT	2.11	0.51
1:A:643:GLY:HA3	1:A:759:MET:OXT	2.12	0.50
1:A:146:GLN:HG2	4:A:2074:HOH:O	2.11	0.50
1:B:445:ALA:HA	1:B:482:PHE:CE2	2.46	0.50
1:B:186:LEU:HD13	1:B:187:TYR:CE1	2.47	0.50
1:A:116:LYS:HB2	1:A:117:MET:HE1	1.93	0.50
1:B:420:VAL:O	1:B:422:PRO:HD3	2.11	0.50
1:A:222:GLU:CD	1:A:595:ARG:HH22	2.15	0.50
1:A:712:ARG:NH1	1:A:751:ILE:HB	2.26	0.50
1:B:648:LEU:HD23	1:B:665:TYR:HE2	1.77	0.50
1:A:328:SER:CB	1:A:746:GLN:NE2	2.73	0.50
1:A:649:THR:O	1:A:653:LYS:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:ASP:HA	4:A:2108:HOH:O	2.12	0.49
1:A:66:ARG:HD2	4:A:2207:HOH:O	2.12	0.49
1:B:649:THR:O	1:B:653:LYS:HG3	2.12	0.49
1:A:445:ALA:HA	1:A:482:PHE:CE2	2.48	0.49
1:A:112:PHE:HE1	4:A:2141:HOH:O	1.95	0.49
1:A:420:VAL:O	1:A:422:PRO:HD3	2.12	0.49
1:B:158:ARG:HG2	1:B:456:MET:CE	2.42	0.49
1:B:132:MET:O	1:B:132:MET:HE3	2.11	0.49
1:A:471:ASN:HD22	1:A:472:TYR:N	2.11	0.49
1:B:132:MET:CE	1:B:136:ILE:HG13	2.43	0.49
1:A:222:GLU:OE2	1:A:595:ARG:NH2	2.46	0.49
1:B:116:LYS:HB2	1:B:117:MET:HE1	1.94	0.49
1:A:696:GLU:HB2	1:A:699:ILE:HG22	1.95	0.49
1:A:19:TRP:HD1	1:A:27:ASP:OD1	1.95	0.49
1:B:696:GLU:HB2	1:B:699:ILE:HG22	1.94	0.48
1:A:648:LEU:HD23	1:A:665:TYR:HE2	1.78	0.48
1:B:490:TYR:CE2	1:B:524:CYS:HB3	2.47	0.48
1:B:60:GLY:O	1:B:64:GLU:HG3	2.12	0.48
1:A:132:MET:CE	1:A:136:ILE:HG13	2.44	0.48
1:B:471:ASN:HD22	1:B:472:TYR:N	2.10	0.48
1:B:186:LEU:HD13	1:B:187:TYR:CZ	2.48	0.48
1:B:550:GLU:OE1	1:B:550:GLU:HA	2.12	0.48
1:A:186:LEU:HD13	1:A:187:TYR:CE1	2.48	0.48
1:B:222:GLU:CD	1:B:595:ARG:HH22	2.16	0.48
1:A:165:LEU:HD22	1:A:168:LEU:HD11	1.95	0.48
1:B:33:TYR:CE1	1:B:35:PRO:HG3	2.48	0.48
1:B:381:LEU:HD22	1:B:384:LYS:HD2	1.95	0.48
1:B:180:ASP:HB3	1:B:183:ARG:HG3	1.95	0.48
1:B:748:GLN:O	1:B:752:THR:HG23	2.13	0.48
1:B:33:TYR:HA	1:B:285:VAL:HG22	1.96	0.48
1:B:468:ASP:O	1:B:545:LYS:HG3	2.14	0.48
1:A:158:ARG:HG2	1:A:456:MET:CE	2.44	0.48
1:A:372:THR:CG2	1:A:400:GLU:HG3	2.44	0.48
1:A:400:GLU:OE2	1:A:704:HIS:HD2	1.97	0.48
1:A:719:MET:SD	1:A:751:ILE:HD13	2.54	0.47
1:A:132:MET:HE3	1:A:132:MET:O	2.13	0.47
1:A:381:LEU:HD22	1:A:384:LYS:HD2	1.96	0.47
1:A:548:ARG:HG3	1:A:548:ARG:NH1	2.29	0.47
1:B:445:ALA:HA	1:B:482:PHE:CD2	2.50	0.47
1:A:526:ILE:CG1	1:A:601:GLN:HE21	2.28	0.47
1:B:406:ARG:N	1:B:407:PRO:HD2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:526:ILE:HG13	1:A:601:GLN:NE2	2.29	0.47
1:B:158:ARG:HG2	1:B:456:MET:HE2	1.96	0.47
1:B:19:TRP:HD1	1:B:27:ASP:OD1	1.96	0.47
1:B:313:ARG:HG2	1:B:368:GLU:O	2.14	0.47
1:A:112:PHE:HD2	1:A:141:ARG:CZ	2.26	0.47
1:A:748:GLN:O	1:A:752:THR:HG23	2.15	0.47
1:A:468:ASP:O	1:A:545:LYS:HG3	2.15	0.47
1:B:526:ILE:HG13	1:B:601:GLN:NE2	2.30	0.47
1:B:636:MET:HB2	1:B:639:ARG:HD2	1.97	0.47
1:A:33:TYR:HA	1:A:285:VAL:HG22	1.97	0.47
1:B:468:ASP:O	1:B:546:PRO:HD2	2.15	0.47
1:A:60:GLY:O	1:A:64:GLU:HG3	2.15	0.47
1:B:16:LYS:O	1:B:31:LYS:HD3	2.15	0.46
1:B:372:THR:CG2	1:B:400:GLU:HG3	2.45	0.46
1:A:186:LEU:HD13	1:A:187:TYR:CZ	2.50	0.46
1:B:719:MET:SD	1:B:751:ILE:HD13	2.55	0.46
1:A:490:TYR:CE2	1:A:524:CYS:HB3	2.50	0.46
1:B:386:PHE:O	1:B:390:VAL:HG23	2.16	0.46
1:B:328:SER:CB	1:B:746:GLN:NE2	2.76	0.46
1:A:636:MET:HB2	1:A:639:ARG:HD2	1.96	0.46
1:A:406:ARG:N	1:A:407:PRO:HD2	2.31	0.46
1:B:409:PHE:CE2	1:B:422:PRO:HB2	2.49	0.46
1:B:537:SER:OG	1:B:564:PRO:HG2	2.16	0.46
1:A:17:GLY:HA3	1:A:31:LYS:HD2	1.98	0.46
1:B:360:LEU:HD23	1:B:390:VAL:CG1	2.46	0.46
1:A:159:CYS:HB3	1:A:165:LEU:HB2	1.98	0.46
1:B:159:CYS:HB3	1:B:165:LEU:HB2	1.97	0.46
1:B:134:LYS:O	1:B:138:THR:HG23	2.16	0.46
1:B:455:LYS:HG2	1:B:553:LEU:CD2	2.46	0.46
1:B:414:TYR:HA	1:B:424:ILE:HA	1.98	0.46
1:B:548:ARG:HG3	1:B:548:ARG:NH1	2.27	0.45
1:B:278:ARG:HG3	4:B:2208:HOH:O	2.15	0.45
1:A:158:ARG:HG2	1:A:456:MET:HE1	1.99	0.45
1:B:159:CYS:HB3	1:B:164:VAL:HG13	1.99	0.45
1:A:313:ARG:HG2	1:A:368:GLU:O	2.15	0.45
1:A:601:GLN:HG2	1:A:602:SER:N	2.32	0.45
1:A:386:PHE:O	1:A:390:VAL:HG23	2.16	0.45
1:B:112:PHE:HD2	1:B:141:ARG:CZ	2.28	0.45
1:B:442:MET:HE1	1:B:536:LEU:HG	1.98	0.45
1:A:537:SER:OG	1:A:564:PRO:HG2	2.16	0.45
1:B:222:GLU:OE2	1:B:595:ARG:NH2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:400:GLU:OE2	1:B:704:HIS:HD2	2.00	0.45
1:A:445:ALA:HA	1:A:482:PHE:CD2	2.52	0.45
1:B:526:ILE:CG1	1:B:601:GLN:HE21	2.29	0.45
1:A:159:CYS:HB3	1:A:164:VAL:HG13	1.97	0.45
1:B:160:ARG:HA	1:B:165:LEU:O	2.17	0.45
1:A:230:LEU:O	1:A:233:MET:HB2	2.16	0.45
1:B:265:ALA:HB1	1:B:510:LEU:HD11	1.99	0.45
1:A:538:ALA:O	1:A:542:ALA:HB3	2.17	0.45
1:B:17:GLY:HA3	1:B:31:LYS:HD2	1.99	0.45
1:A:414:TYR:HA	1:A:424:ILE:HA	1.98	0.45
1:B:165:LEU:HD22	1:B:168:LEU:HD11	1.98	0.45
1:A:409:PHE:CE2	1:A:422:PRO:HB2	2.50	0.44
1:A:353:SER:O	1:A:357:LEU:HD13	2.17	0.44
1:B:79:SER:HB3	1:B:110:ILE:HD13	2.00	0.44
1:B:601:GLN:HG2	1:B:602:SER:N	2.32	0.44
1:A:112:PHE:CD1	4:A:2137:HOH:O	2.49	0.44
1:A:16:LYS:O	1:A:31:LYS:HD3	2.17	0.44
1:A:309:VAL:O	1:A:313:ARG:HG3	2.18	0.44
1:B:538:ALA:O	1:B:542:ALA:HB3	2.17	0.44
1:A:360:LEU:HD23	1:A:390:VAL:CG1	2.48	0.44
1:B:73:PHE:CZ	1:B:127:ARG:HG3	2.52	0.44
1:B:353:SER:O	1:B:357:LEU:HD13	2.17	0.44
1:A:160:ARG:HA	1:A:165:LEU:O	2.18	0.44
1:A:73:PHE:CZ	1:A:127:ARG:HG3	2.51	0.44
1:A:713:GLU:OE1	1:A:713:GLU:N	2.50	0.44
1:B:481:HIS:O	1:B:484:ASP:HB2	2.17	0.44
1:B:114:GLY:HA2	1:B:143:THR:CB	2.48	0.44
1:B:677:ASP:OD1	1:B:680:VAL:HG23	2.18	0.44
1:B:610:VAL:HA	1:B:628:PRO:HB3	1.99	0.44
1:B:526:ILE:HD11	1:B:584:PHE:CE2	2.52	0.44
1:A:468:ASP:O	1:A:546:PRO:HD2	2.17	0.44
1:A:241:GLY:HA3	2:A:1001:PGE:H4	1.99	0.44
1:B:578:VAL:O	1:B:582:GLU:HG3	2.18	0.44
1:A:526:ILE:HD11	1:A:584:PHE:CE2	2.53	0.44
1:A:712:ARG:HH11	1:A:712:ARG:HG3	1.83	0.44
1:B:310:MET:O	1:B:313:ARG:HB2	2.18	0.44
1:A:677:ASP:OD1	1:A:680:VAL:HG23	2.18	0.43
1:B:556:ASP:OD1	1:B:557:PHE:N	2.51	0.43
1:A:427:LYS:HG2	1:A:515:ASP:OD1	2.18	0.43
1:B:710:MET:HB2	1:B:714:MET:CE	2.49	0.43
1:A:265:ALA:HB1	1:A:510:LEU:HD11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:578:VAL:O	1:A:582:GLU:HG3	2.18	0.43
1:B:713:GLU:OE1	1:B:713:GLU:N	2.51	0.43
1:B:559:ILE:HD12	1:B:559:ILE:H	1.84	0.43
1:A:114:GLY:HA2	1:A:143:THR:CB	2.48	0.43
1:A:54:TRP:HE1	1:A:727:GLN:HE22	1.67	0.43
1:A:640:ASP:OD1	1:A:754:THR:HG21	2.19	0.43
1:A:455:LYS:HG2	1:A:553:LEU:CD2	2.49	0.43
1:A:710:MET:HB2	1:A:714:MET:CE	2.49	0.43
1:A:733:SER:HB2	4:A:2076:HOH:O	2.18	0.43
1:A:610:VAL:HA	1:A:628:PRO:HB3	2.00	0.43
1:A:132:MET:HE3	1:A:136:ILE:HG13	2.00	0.43
1:A:481:HIS:O	1:A:484:ASP:HB2	2.18	0.43
1:B:230:LEU:O	1:B:233:MET:HB2	2.19	0.43
1:A:134:LYS:O	1:A:138:THR:HG23	2.18	0.43
1:A:650:SER:O	1:A:653:LYS:HB2	2.19	0.43
1:A:732:VAL:HG23	1:A:735:TYR:CE2	2.54	0.42
1:A:559:ILE:HD12	1:A:559:ILE:H	1.83	0.42
1:B:309:VAL:O	1:B:313:ARG:HG3	2.18	0.42
1:A:526:ILE:CG1	1:A:601:GLN:NE2	2.82	0.42
1:B:360:LEU:HD12	1:B:360:LEU:HA	1.90	0.42
1:B:146:GLN:HG2	4:B:2158:HOH:O	2.19	0.42
1:B:158:ARG:NH1	4:B:2179:HOH:O	2.51	0.42
1:B:86:ALA:HA	1:B:240:TYR:CZ	2.55	0.42
1:B:64:GLU:O	1:B:68:HIS:N	2.53	0.42
1:B:531:VAL:HG12	1:B:636:MET:CG	2.50	0.42
1:B:640:ASP:OD1	1:B:754:THR:HG21	2.19	0.42
1:B:333:TRP:HB3	1:B:418:CYS:HA	2.00	0.42
1:A:110:ILE:C	4:A:2137:HOH:O	2.58	0.42
1:A:385:LYS:HE3	1:A:683:THR:HG23	2.02	0.42
1:A:333:TRP:HB3	1:A:418:CYS:HA	2.01	0.42
1:B:712:ARG:HH11	1:B:712:ARG:HG3	1.85	0.42
1:B:650:SER:O	1:B:653:LYS:HB2	2.19	0.42
1:B:732:VAL:HG23	1:B:735:TYR:CE2	2.55	0.42
1:A:748:GLN:NE2	1:A:751:ILE:HD11	2.34	0.42
1:B:421:SER:HA	1:B:422:PRO:HD2	1.93	0.41
1:B:720:GLU:C	1:B:721:ASN:HD22	2.24	0.41
1:B:342:GLY:HA3	4:B:2172:HOH:O	2.19	0.41
1:A:79:SER:HB3	1:A:110:ILE:HD13	2.02	0.41
1:A:720:GLU:C	1:A:721:ASN:HD22	2.23	0.41
1:B:748:GLN:NE2	1:B:751:ILE:HD11	2.35	0.41
1:A:435:ARG:HB3	1:A:435:ARG:HE	1.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:MET:HG2	1:B:171:ALA:O	2.21	0.41
1:B:548:ARG:HD3	1:B:552:GLY:O	2.21	0.41
1:A:86:ALA:HA	1:A:240:TYR:CZ	2.55	0.41
1:A:548:ARG:HD3	1:A:552:GLY:O	2.20	0.41
1:B:165:LEU:HA	1:B:165:LEU:HD23	1.79	0.41
1:A:281:THR:HB	4:A:2005:HOH:O	2.20	0.41
1:A:442:MET:HE1	1:A:536:LEU:HG	2.03	0.41
1:A:38:GLY:C	1:A:382:ASN:HD22	2.24	0.41
1:B:196:LYS:HA	1:B:196:LYS:HD3	1.88	0.41
1:A:211:VAL:O	1:A:216:THR:HG21	2.20	0.41
1:B:427:LYS:HG2	1:B:515:ASP:OD1	2.21	0.41
1:A:556:ASP:OD1	1:A:557:PHE:N	2.50	0.40
1:B:526:ILE:CG1	1:B:601:GLN:NE2	2.84	0.40
1:A:47:THR:HG23	4:A:2054:HOH:O	2.21	0.40
1:B:211:VAL:O	1:B:216:THR:HG21	2.20	0.40
1:A:531:VAL:HG12	1:A:636:MET:CG	2.51	0.40
1:B:398:GLN:HB3	1:B:731:ARG:NH2	2.37	0.40
1:A:388:ALA:O	1:A:392:ILE:HG13	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1001:PGE:C1	2:A:1001:PGE:O1[8_776]	1.46	0.74

## 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	754/759 (99%)	708 (94%)	44 (6%)	2 (0%)	46 75
1	B	754/759 (99%)	706 (94%)	46 (6%)	2 (0%)	46 75

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1508/1518 (99%)	1414 (94%)	90 (6%)	4 (0%)	46 75

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	606	ILE
1	A	733	SER
1	B	606	ILE
1	B	733	SER

### 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	635/638 (100%)	606 (95%)	29 (5%)	33 64
1	B	635/638 (100%)	607 (96%)	28 (4%)	35 65
All	All	1270/1276 (100%)	1213 (96%)	57 (4%)	34 65

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLU
1	A	40	GLU
1	A	75	THR
1	A	117	MET
1	A	126	ASN
1	A	152	TYR
1	A	165	LEU
1	A	186	LEU
1	A	207	LEU
1	A	216	THR
1	A	252	GLN
1	A	257	TRP
1	A	260	PHE
1	A	326	LEU

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Mol	Chain	Res	Type
1	A	348	LEU
1	A	360	LEU
1	A	381	LEU
1	A	393	ASP
1	A	435	ARG
1	A	438	LEU
1	A	471	ASN
1	A	479	MET
1	A	490	TYR
1	A	550	GLU
1	A	573	VAL
1	A	595	ARG
1	A	660	LYS
1	A	710	MET
1	A	735	TYR
1	B	5	GLU
1	B	40	GLU
1	B	75	THR
1	B	117	MET
1	B	126	ASN
1	B	152	TYR
1	B	186	LEU
1	B	207	LEU
1	B	216	THR
1	B	252	GLN
1	B	257	TRP
1	B	260	PHE
1	B	326	LEU
1	B	348	LEU
1	B	360	LEU
1	B	381	LEU
1	B	393	ASP
1	B	435	ARG
1	B	438	LEU
1	B	471	ASN
1	B	479	MET
1	B	490	TYR
1	B	550	GLU
1	B	573	VAL
1	B	595	ARG
1	B	660	LYS
1	B	710	MET

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Mol	Chain	Res	Type
1	B	735	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	ASN
1	A	126	ASN
1	A	358	ASN
1	A	382	ASN
1	A	410	ASN
1	A	430	GLN
1	A	471	ASN
1	A	489	GLN
1	A	589	GLN
1	A	601	GLN
1	A	684	ASN
1	A	711	ASN
1	A	721	ASN
1	A	727	GLN
1	A	748	GLN
1	B	4	ASN
1	B	126	ASN
1	B	358	ASN
1	B	382	ASN
1	B	410	ASN
1	B	430	GLN
1	B	471	ASN
1	B	589	GLN
1	B	601	GLN
1	B	684	ASN
1	B	711	ASN
1	B	721	ASN
1	B	727	GLN
1	B	748	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	PGE	A	1001	-	9,9,9	0.83	0	8,8,8	0.74	0
3	PYR	A	2001	-	2,5,5	1.08	0	2,6,6	0.53	0
3	PYR	B	2002	-	2,5,5	1.08	0	2,6,6	0.61	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PGE	A	1001	-	-	0/7/7/7	0/0/0/0
3	PYR	A	2001	-	-	0/0/4/4	0/0/0/0
3	PYR	B	2002	-	-	0/0/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	PGE	1	1
3	A	2001	PYR	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	756/759 (99%)	-0.33	9 (1%) 81 81	25, 43, 74, 96	0
1	B	756/759 (99%)	-0.29	14 (1%) 70 70	25, 45, 74, 95	0
All	All	1512/1518 (99%)	-0.31	23 (1%) 76 76	25, 44, 74, 96	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	468	ASP	4.2
1	B	550	GLU	3.6
1	B	699	ILE	3.4
1	A	550	GLU	3.2
1	B	641	GLN	3.1
1	A	6	LYS	3.0
1	A	721	ASN	2.8
1	B	5	GLU	2.7
1	B	553	LEU	2.7
1	A	4	ASN	2.7
1	B	676	LYS	2.6
1	A	699	ILE	2.6
1	A	720	GLU	2.5
1	B	560	GLU	2.5
1	B	698	SER	2.5
1	B	467	GLY	2.3
1	B	461	LYS	2.2
1	A	696	GLU	2.2
1	A	698	SER	2.2
1	A	744	LYS	2.2
1	B	541	TYR	2.1
1	B	543	LYS	2.1
1	B	559	ILE	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](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	PYR	B	2002	6/6	0.94	0.17	2.91	46,47,50,50	0
2	PGE	A	1001	10/10	0.90	0.22	2.56	46,55,61,63	1
3	PYR	A	2001	6/6	0.97	0.11	-0.86	32,33,33,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.