



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:17 AM GMT

PDB ID : 2WKJ
Title : CRYSTAL STRUCTURE OF THE E192N MUTANT OF E.COLI N-ACETYLNEURAMINIC ACID LYASE IN COMPLEX WITH PYRUVATE AT 1.45Å RESOLUTION IN SPACE GROUP P212121
Authors : Campeotto, I.; Carr, S.B.; Trinh, C.H.; Nelson, A.S.; Berry, A.; Phillips, S.E.V.; Pearson, A.R.
Deposited on : 2009-06-11
Resolution : 1.45 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
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

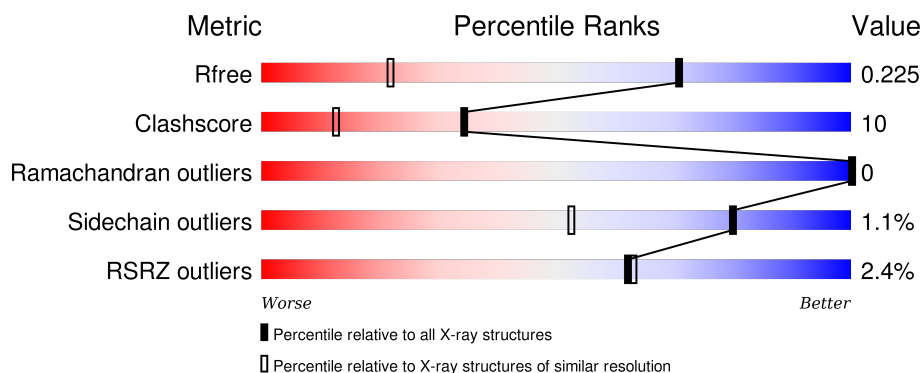
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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	1278 (1.48-1.44)
Clashscore	102246	1336 (1.48-1.44)
Ramachandran outliers	100387	1320 (1.48-1.44)
Sidechain outliers	100360	1320 (1.48-1.44)
RSRZ outliers	91569	1279 (1.48-1.44)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	303	<div> <div>3%</div> <div>88%</div> <div>9%</div> <div>..</div> </div>
1	B	303	<div> <div>%</div> <div>86%</div> <div>12%</div> <div>..</div> </div>
1	C	303	<div> <div>%</div> <div>85%</div> <div>13%</div> <div>.</div> </div>
1	D	303	<div> <div>4%</div> <div>85%</div> <div>13%</div> <div>..</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	1PE	A	1297	-	-	X	X
2	1PE	C	1297	-	-	-	X
3	PYR	C	1298[A]	-	-	-	X
3	PYR	C	1298[B]	-	-	-	X
3	PYR	D	1297	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10677 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.

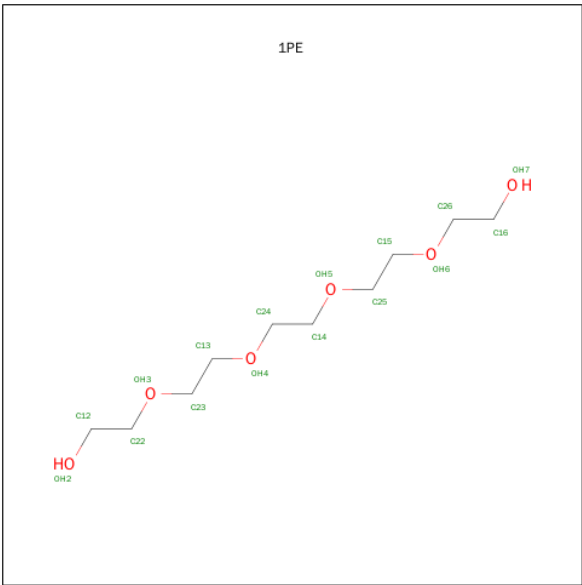
- Molecule 1 is a protein called N-ACETYLNEURAMINATE LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	8	0
			2342	1497	394	440	11			
1	B	298	Total	C	N	O	S	0	7	0
			2341	1492	398	440	11			
1	C	298	Total	C	N	O	S	0	5	0
			2329	1485	396	436	12			
1	D	298	Total	C	N	O	S	0	4	0
			2324	1482	394	437	11			

There are 4 discrepancies between the modelled and reference sequences:

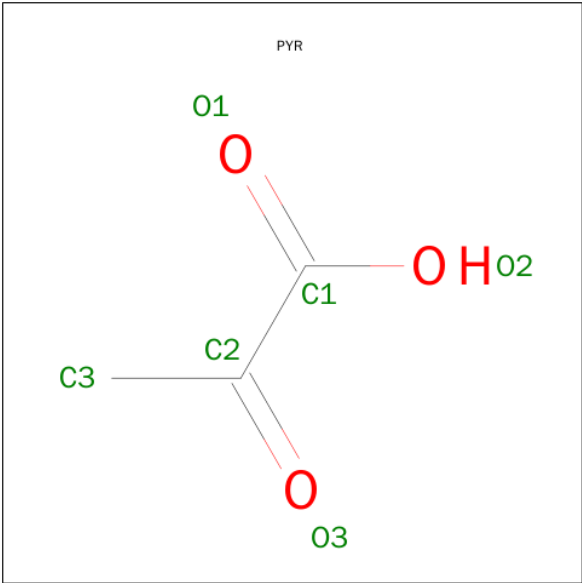
Chain	Residue	Modelled	Actual	Comment	Reference
A	192	ASN	GLU	ENGINEERED MUTATION	UNP P0A6L4
B	192	ASN	GLU	ENGINEERED MUTATION	UNP P0A6L4
C	192	ASN	GLU	ENGINEERED MUTATION	UNP P0A6L4
D	192	ASN	GLU	ENGINEERED MUTATION	UNP P0A6L4

- Molecule 2 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: C₁₀H₂₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	5	3		
2	C	1	Total	C	O	0	0
			8	5	3		

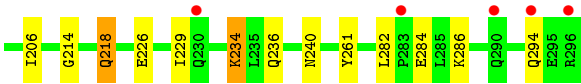
- Molecule 3 is PYRUVIC ACID (three-letter code: PYR) (formula: C₃H₄O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	1
			12	6	6		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	345	Total 345	O 345	0	0
4	B	347	Total 347	O 347	0	0
4	C	340	Total 340	O 340	0	0
4	D	275	Total 275	O 275	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.33Å 108.05Å 148.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	87.33 – 1.45 61.14 – 1.45	Depositor EDS
% Data completeness (in resolution range)	95.9 (87.33-1.45) 95.9 (61.14-1.45)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.42 (at 1.45Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.167 , 0.189 0.210 , 0.225	Depositor DCC
R_{free} test set	11158 reflections (5.51%)	DCC
Wilson B-factor (Å ²)	13.4	Xtriage
Anisotropy	0.503	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 40.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Outliers	2 of 213077 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10677	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 76.71 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 9.8480e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: KPI, PYR, 1PE

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	0.56	0/2392	0.70	2/3236 (0.1%)
1	B	0.50	0/2388	0.65	3/3231 (0.1%)
1	C	0.54	0/2370	0.70	2/3206 (0.1%)
1	D	0.52	0/2359	0.67	0/3193
All	All	0.53	0/9509	0.68	7/12866 (0.1%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	244	ASP	CB-CG-OD1	6.98	124.58	118.30
1	B	244	ASP	CB-CG-OD1	6.26	123.94	118.30
1	C	244	ASP	CB-CG-OD2	-6.14	112.77	118.30
1	B	244	ASP	CB-CG-OD2	-5.91	112.98	118.30
1	A	210	TYR	CB-CG-CD1	5.58	124.35	121.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2342	0	2376	60	0
1	B	2341	0	2365	34	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2329	0	2354	44	0
1	D	2324	0	2342	56	1
2	A	8	0	9	9	0
2	C	8	0	9	0	0
3	C	12	0	6	0	0
3	D	6	0	3	0	0
4	A	345	0	0	15	0
4	B	347	0	0	8	0
4	C	340	0	0	10	0
4	D	275	0	0	17	0
All	All	10677	0	9464	189	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 10.

The worst 5 of 189 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:C:9[B]:MET:CE	1:C:77:ILE:HD12	1.44	1.46
1:C:9[B]:MET:CE	1:C:77:ILE:CD1	1.95	1.43
1:C:9[B]:MET:HE1	1:C:77:ILE:CD1	1.44	1.43
1:D:9[B]:MET:CE	1:D:77:ILE:HD12	1.63	1.28
1:D:9[B]:MET:HE1	1:D:77:ILE:CD1	1.69	1.22

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)
1:B:123:ARG:NH2	1:D:226:GLU:OE2[4_555]	2.06	0.14

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	303/303 (100%)	298 (98%)	5 (2%)	0	100	100
1	B	302/303 (100%)	296 (98%)	6 (2%)	0	100	100
1	C	300/303 (99%)	294 (98%)	6 (2%)	0	100	100
1	D	299/303 (99%)	293 (98%)	6 (2%)	0	100	100
All	All	1204/1212 (99%)	1181 (98%)	23 (2%)	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	250/250 (100%)	246 (98%)	4 (2%)	70	35
1	B	249/250 (100%)	246 (99%)	3 (1%)	78	48
1	C	247/250 (99%)	245 (99%)	2 (1%)	86	66
1	D	246/250 (98%)	242 (98%)	4 (2%)	70	35
All	All	992/1000 (99%)	979 (99%)	13 (1%)	80	45

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	218	GLN
1	B	263	ASP
1	D	218[A]	GLN
1	B	166	GLN
1	D	166	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	240	ASN
1	C	118	HIS
1	D	181	HIS

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Mol	Chain	Res	Type
1	B	260	HIS
1	C	79	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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
1	KPI	A	165	1	10,13,14	1.00	0	9,15,17	0.77	0
1	KPI	B	165	1	10,13,14	1.14	1 (10%)	9,15,17	0.96	0
1	KPI	C	165	1	10,13,14	1.04	0	9,15,17	0.83	0
1	KPI	D	165	1	10,13,14	1.08	1 (10%)	9,15,17	0.80	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
1	KPI	A	165	1	-	0/8/14/16	0/0/0/0
1	KPI	B	165	1	-	0/8/14/16	0/0/0/0
1	KPI	C	165	1	-	0/8/14/16	0/0/0/0
1	KPI	D	165	1	-	0/8/14/16	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	165	KPI	CX1-NZ	2.16	1.32	1.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	165	KPI	CX1-NZ	2.81	1.33	1.29

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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	1PE	A	1297	2	7,7,15	0.43	0	6,6,14	1.16	1 (16%)
2	1PE	C	1297	2	7,7,15	0.72	0	6,6,14	0.40	0
3	PYR	C	1298[A]	-	2,5,5	1.09	0	2,6,6	0.37	0
3	PYR	C	1298[B]	-	2,5,5	0.78	0	2,6,6	0.43	0
3	PYR	D	1297	-	2,5,5	0.81	0	2,6,6	0.65	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	1PE	A	1297	2	-	0/5/5/13	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	1PE	C	1297	2	-	0/5/5/13	0/0/0/0
3	PYR	C	1298[A]	-	-	0/0/4/4	0/0/0/0
3	PYR	C	1298[B]	-	-	0/0/4/4	0/0/0/0
3	PYR	D	1297	-	-	0/0/4/4	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1297	1PE	C23-OH3-C22	-2.23	103.71	113.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1297	1PE	9	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	297/303 (98%)	0.11	8 (2%) 58 58	8, 12, 29, 71	0
1	B	297/303 (98%)	0.05	3 (1%) 84 85	9, 14, 26, 42	0
1	C	297/303 (98%)	-0.09	4 (1%) 79 80	8, 12, 23, 41	0
1	D	297/303 (98%)	0.24	13 (4%) 38 38	9, 14, 32, 75	0
All	All	1188/1212 (98%)	0.08	28 (2%) 62 63	8, 13, 29, 75	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	THR	6.1
1	D	1	HIS	6.0
1	A	5	LEU	5.8
1	D	3	THR	5.2
1	D	5	LEU	4.2

6.2 Non-standard residues in protein, DNA, RNA chains [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, 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	LLDF	B-factors(Å ²)	Q<0.9
1	KPI	C	165	14/15	0.97	0.07	-	8,9,12,13	0
1	KPI	D	165	14/15	0.96	0.09	-	8,10,13,16	0
1	KPI	A	165	14/15	0.97	0.08	-	8,8,11,11	0
1	KPI	B	165	14/15	0.97	0.07	-	11,12,14,14	0

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, 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	LLDF	B-factors(Å ²)	Q<0.9
3	PYR	C	1298[A]	6/6	0.80	0.27	45.29	12,14,15,15	6
3	PYR	C	1298[B]	6/6	0.80	0.27	17.89	36,37,37,38	6
3	PYR	D	1297	6/6	0.84	0.20	13.19	23,28,28,31	0
2	1PE	C	1297	8/16	0.85	0.23	3.59	91,92,92,92	8
2	1PE	A	1297	8/16	0.84	0.19	2.37	18,20,22,22	8

6.5 Other polymers [i](#)

There are no such residues in this entry.